

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2005, 11:47:33 ; Search time 89 Seconds  
(without alignments)  
2216.267 Million cell updates/sec

Title: US-09-807-660C-2

Perfect score: 2698

Sequence: 1 MEDTKESNVKTFCSKNILAI.....VAIIGLLIIFHKPSYFWKDMV 510

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A\_Geneseq\_16Dec04:\*
- 1: Geneseqp1980s:\*
  - 2: Geneseqp1990s:\*
  - 3: Geneseqp2000s:\*
  - 4: Geneseqp2001s:\*
  - 5: Geneseqp2002s:\*
  - 6: Geneseqp2003s:\*
  - 7: Geneseqp2003bs:\*
  - 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2698	100.0	510	2	AAW04334 Human lym
2	2698	100.0	510	2	AAW04264 Human CD3
3	2698	100.0	510	3	AAV70910 Human sol
4	2698	100.0	510	3	AAV70887 Human sol
5	2698	100.0	510	4	AAV71917 Human CD3
6	2698	100.0	510	7	ADJ57262 Human CD3
7	2698	100.0	510	8	ADL24295 Human CD3
8	2698	100.0	510	8	ADQ9453 Human CD3
9	2698	100.0	510	8	ADR69210 Human CD3
10	2698	100.0	510	8	ADR69042 Human CD3
11	2698	100.0	510	8	ADU17924 Human CD3
12	2698	100.0	510	8	ADU84674 Human can
13	2698	100.0	510	8	ADR87821 Human CD3
14	2698	100.0	511	8	ADK60421 Angiogene
15	2698	100.0	511	8	ADK60722 Angiogene
16	2698	100.0	511	8	ADP73345 CD39 lymph
17	2677	99.2	517	7	ADN95839 Human BEC
18	2677	99.2	517	8	ADK60221 Angiogene
19	2677	99.2	517	8	ADK60522 Angiogene
20	2677	99.2	517	8	ADP73145 Angiogene
21	2673	99.1	522	8	ABO84672 Human can
22	2469	91.5	529	8	ABM83376 Human dia
23	2358	87.4	464	3	AAV70922 Human sol
24	2358	87.4	464	3	AAV70899 Protein e
25	2348	87.0	439	4	AAV71918 Soluble h

26	2348	87.0	454	3	AAV70913 Human sol
27	2348	87.0	454	3	AAV70890 Protein e
28	2348	87.0	463	3	AAV70925 Human sol
29	2348	87.0	463	3	AAV70902 Protein e
30	2348	87.0	473	3	AAV70924 Human sol
31	2348	87.0	473	3	AAV70901 Protein e
32	2348	87.0	474	3	AAV70923 Human sol
33	2348	87.0	474	3	AAV70900 Protein e
34	2348	87.0	476	3	AAV70911 Human CD3
35	2348	87.0	476	3	AAV70888 Protein e
36	2348	87.0	478	3	AAV70914 Human sol
37	2348	87.0	478	3	AAV70891 Protein e
38	2348	87.0	487	3	AAV70921 Human sol
39	2348	87.0	487	3	AAV70898 Protein e
40	2311	85.7	503	8	ABM83377 Human dia
41	2297	85.1	476	3	AAV70912 Human CD3
42	2297	85.1	476	3	AAV70889 Protein e
43	2144	79.5	402	8	ABO84671 Human can
44	2016	74.7	377	7	ADI62735 Human apo
45	1293	47.9	311	8	ABO84673 Human can

ALIGNMENTS

RESULT 1  
AAW04334  
ID AAW04334 standard; protein; 510 AA.  
AC AAW04334;  
XX  
DT 29-DEC-1996 (first entry)  
XX  
DE Human lymphoid cell activation antigen CD39.  
XX  
KW ATP diphosphohydrolase; ATPDase; bovine aorta; pig pancreas; apyrase;  
KW CD39; lymphoid cell activation antigen; enzyme; platelet aggregation;  
KW thrombogenicity; anti-haemostatic.  
XX  
OS Homo sapiens.  
XX  
FN WO9632471-A2.  
XX  
PD 17-OCT-1996.  
XX  
PF 10-APR-1996; 96WO-CA000223.  
XX  
PR 10-APR-1995; 95US-00419204.  
XX  
FA (UYSH ) UNIV SHERBROOKE.  
XX  
PI Beaudoin AR, Sevigny J;  
XX  
DR WPI, 1996-477122/47.  
XX  
DR N-PSDB; AAT38516.  
XX  
PT Isolated ATP di-phospho-hydrolase enzymes - have anti-haemostatic  
XX activity, useful for reducing platelet aggregation and thrombogenicity.  
XX  
PS Claim 17; Page 42-44; 60pp; English.  
XX  
XX  
CC The bovine aorta (AAW04335 and AAW04338 and AAW04340) and porcine  
CC pancreatic (AAW04339) ATPDases have been partially sequenced. The  
CC sequences have been found to be highly homologous to a human lymphoid  
CC cell activation antigen designated CD39 (Maliszewski et al. (1994). J.  
CC Immunol.: 3574-3583). The complete sequences of the ATPDases types I and  
CC II have not been obtained yet. Assuming that the CD39 gene product is an  
CC ATPDase type II, the use of CD39 in the reduction of platelet aggregation  
CC and of thrombogenicity may be contemplated, as well as a process of  
CC making ATPDases using the CD39 sequence (AAT38516)  
XX  
SQ Sequence 510 AA;

DR	N-PSDB; AAT33966.				
XX	Gene therapy of inflammatory or immunological stimulation of platelet				
PT	aggregation - using CD39 protein with ATP di:phospho:hydrolase activity,				
PT	useful for preventing or alleviating thrombotic condition in mammalian				
PT	subject.				
XX					
PS	Claim 3; Page 39; 65pp; English.				
XX					
CC	Non-human transgenic or somatic recombinant mammals, whose cells contain				
CC	a heterologous DNA encoding a polypeptide (especially human CD39 protein)				
CC	having ATP-diphosphohydrolase activity under cellular activating				
CC	conditions is claimed. In particular the animal is a pig and its cells				
CC	(or tissues or organs) can be used for transplantation. DNA coding for				
CC	human CD39 is also useful for genetically modifying a mammalian cell to				
CC	render it less susceptible to an inflammatory or immunological stimulus				
CC	and platelet aggregation. The modified cells can be used to prevent or				
CC	alleviate a thrombotic condition. The present sequence is that of the				
CC	human CD39 protein and was disclosed in J.Immunol. 153 (8) (1994) 3574-				
CC	3584				
XX					
SQ	Sequence 510 AA;				
	Query Match	100.0%;	Score 2698;	DB 2;	Length 510;
	Best Local Similarity	100.0%;	Pred. No. 5.2e-262;		
	Matches 510;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGVILDAGSSHT	60		
Db	1	MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGVILDAGSSHT	60		
QY	61	SLYIYKWPAAEKENDTGTVHQQVEECRVKPGISKVFQVNEIGIYLTDCMERAREVIPRSQ	120		
Db	61	SLYIYKWPAAEKENDTGTVHQQVEECRVKPGISKVFQVNEIGIYLTDCMERAREVIPRSQ	120		
QY	121	HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDQGARIITGOEGAYGWI	180		
Db	121	HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDQGARIITGOEGAYGWI	180		
QY	181	TINYLKGFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFR	240		
Db	181	TINYLKGFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFR	240		
QY	241	LYGKDVNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDPCHPHGYKKVNVNVDLYKTP	300		
Db	241	LYGKDVNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDPCHPHGYKKVNVNVDLYKTP	300		
QY	301	CTKRFEMTLPFQOFEIQGIGNYQOCHQSILELFNTSYCPYSQCAFNGIFLPLQGDGFAP	360		
Db	301	CTKRFEMTLPFQOFEIQGIGNYQOCHQSILELFNTSYCPYSQCAFNGIFLPLQGDGFAP	360		
QY	361	SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQWPBEIKTSYAGVKEKYLSEYCFSGTYIL	420		
Db	361	SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQWPBEIKTSYAGVKEKYLSEYCFSGTYIL	420		
QY	421	SLLLQGYHFTADSWEHIFHGKIQTGSDAGWTGLGYMLNLTNMI PAEQPLSTPLSHSTYVFL	480		
Db	421	SLLLQGYHFTADSWEHIFHGKIQTGSDAGWTGLGYMLNLTNMI PAEQPLSTPLSHSTYVFL	480		
QY	481	MVLFSLVLFTVAIIIGLLIFHKPSYFWKDMV	510		
Db	481	MVLFSLVLFTVAIIIGLLIFHKPSYFWKDMV	510		
RESULT 2					
AAW04264					
ID	AAW04264 standard; protein; 510 AA.				
AC	AAW04264;				
XX					
DT	29-MAY-1997 (first entry)				
XX					
DE	Human CD39 protein.				
XX					
KW	Human; lymphocyte activation marker; gene therapy;				
KW	ATP diphosphohydrolase; transgenic animal; pig; porcine; graft; donor;				
KW	transplantation; endothelial cell; prosthetic device;				
KW	platelet aggregation; inhibition; intravascular.				
XX					
OS	Homo sapiens.				
XX					
PN	WO9630532-A1.				
XX					
PD	03-OCT-1996.				
XX					
PF	22-MAR-1996; 96WO-EP001270.				
XX					
PR	24-MAR-1995; 95US-00410371.				
PR	12-FEB-1996; 96US-00600383.				
XX					
PA	(SANO ) SANDOZ LTD.				
PA	(NEWB-) NEW ENGLAND DEACONESS HOSPITAL.				
XX					
PI	Bach FH, Robson S;				
XX					
XX	WPI; 1996-455377/45.				
DR					
DR N-PSDB; AAT33966.					
Gene therapy of inflammatory or immunological stimulation of platelet					
aggregation - using CD39 protein with ATP di:phospho:hydrolase activity,					
useful for preventing or alleviating thrombotic condition in mammalian					
subject.					
Claim 3; Page 39; 65pp; English.					
Non-human transgenic or somatic recombinant mammals, whose cells contain					
a heterologous DNA encoding a polypeptide (especially human CD39 protein)					
having ATP-diphosphohydrolase activity under cellular activating					
conditions is claimed. In particular the animal is a pig and its cells					
(or tissues or organs) can be used for transplantation. DNA coding for					
human CD39 is also useful for genetically modifying a mammalian cell to					
render it less susceptible to an inflammatory or immunological stimulus					
and platelet aggregation. The modified cells can be used to prevent or					
alleviate a thrombotic condition. The present sequence is that of the					
human CD39 protein and was disclosed in J.Immunol. 153 (8) (1994) 3574-					
3584					
Sequence 510 AA;					
Query Match					
Best Local Similarity					
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGVILDAGSSHT	60		
Db	1	MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGVILDAGSSHT	60		
QY	61	SLYIYKWPAAEKENDTGTVHQQVEECRVKPGISKVFQVNEIGIYLTDCMERAREVIPRSQ	120		
Db	61	SLYIYKWPAAEKENDTGTVHQQVEECRVKPGISKVFQVNEIGIYLTDCMERAREVIPRSQ	120		
QY	121	HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDQGARIITGOEGAYGWI	180		
Db	121	HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDQGARIITGOEGAYGWI	180		
QY	181	TINYLKGFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFR	240		
Db	181	TINYLKGFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFR	240		
QY	241	LYGKDVNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDPCHPHGYKKVNVNVDLYKTP	300		
Db	241	LYGKDVNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDPCHPHGYKKVNVNVDLYKTP	300		
QY	301	CTKRFEMTLPFQOFEIQGIGNYQOCHQSILELFNTSYCPYSQCAFNGIFLPLQGDGFAP	360		
Db	301	CTKRFEMTLPFQOFEIQGIGNYQOCHQSILELFNTSYCPYSQCAFNGIFLPLQGDGFAP	360		
QY	361	SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQWPBEIKTSYAGVKEKYLSEYCFSGTYIL	420		
Db	361	SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQWPBEIKTSYAGVKEKYLSEYCFSGTYIL	420		
QY	421	SLLLQGYHFTADSWEHIFHGKIQTGSDAGWTGLGYMLNLTNMI PAEQPLSTPLSHSTYVFL	480		
Db	421	SLLLQGYHFTADSWEHIFHGKIQTGSDAGWTGLGYMLNLTNMI PAEQPLSTPLSHSTYVFL	480		
QY	481	MVLFSLVLFTVAIIIGLLIFHKPSYFWKDMV	510		
Db	481	MVLFSLVLFTVAIIIGLLIFHKPSYFWKDMV	510		
RESULT 3					
AAAY70910					
ID	AAAY70910 standard; protein; 510 AA.				
XX					
AC	AAAY70910;				
XX					
DT	17-AUG-2000 (first entry)				
XX					
DE	Human soluble CD39 protein.				

XX Soluble CD39; human; apyrase activity; platelet activation; inhibitor;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;  
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;  
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;  
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;  
KW antilanginal; cerebroprotective; antiarteriosclerotic; anticoagulant;  
KW cardiatic; vasotropic; thrombolytic.

OS Homo sapiens.

XX Key Location/Qualifiers  
FH Domain 17..37  
FT /label= Transmembrane domain  
FT /note= "N-terminal end"

FT Modified-site 73..75  
FT /note= "Asn is N-glycosylated"

FT Modified-site 227..229  
FT /note= "Asn is N-glycosylated"

FT Modified-site 292..294  
FT /note= "Asn is N-glycosylated"

FT Modified-site 334..336  
FT /note= "Asn is N-glycosylated"

FT Modified-site 371..373  
FT /note= "Asn is N-glycosylated"

FT Modified-site 457..459  
FT /note= "Asn is N-glycosylated"

FT Modified-site 477..499  
FT /label= Transmembrane domain  
FT /note= "C-terminal end"

XX WO200023459-A1.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US022955.

XX 16-OCT-1998; 98US-0104585P.

XX 06-NOV-1998; 98US-0107466P.

XX 13-AUG-1999; 99US-0149010P.

XX (IMMV ) IMMUNEX CORP.

XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;

XX WPI; 2000-339644/29.

XX N-FSDB; AAD00205.

XX New soluble CD39 polypeptides having apyrase activity, useful for  
PT inhibiting angiogenesis and treating unstable angina, myocardial  
PT infarction, stroke, coronary artery disease or injury.

XX Claim 1a; Fig 1; 122pp; English.

XX The present sequence is the human soluble CD39 protein, a cell surface  
XX molecule, having apyrase activity. It is derived from a human B cell line  
XX cDNA library, referred to as MP-1. Soluble CD39 is constructed by  
XX removing the N- and C-terminal transmembrane domains. It retains the  
XX capacity to metabolise ATP and ADP at relevant concentrations and the  
XX ability to block and reverse ADP-induced platelet activation and  
XX recruitment, including platelet aggregation. Soluble CD39 polypeptides  
XX are useful for inhibiting angiogenesis. It is useful for the treatment of  
XX unstable angina, myocardial infarction, stroke, coronary artery disease  
XX or injury, atherosclerosis, peripheral vascular occlusion, preclampsia,  
XX embolism, platelet-associated ischaemic disorders including lung,  
XX coronary and cerebral ischaemia, thrombotic disorders including coronary,  
XX peripheral and cerebral artery thrombosis, intracardiac and venous  
XX thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary  
XX embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful  
XX for preventing thrombus formation or reformation, occlusion, reocclusion,  
XX stenosis or restenosis of blood vessels or stroke

SQ Sequence 510 AA;  
Query Match 100.0%; Score 2698; DB 3; Length 510;  
Best Local Similarity 100.0%; Pred. No. 5.2e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEDTKESNVKTFCSKNILAILGFSIIAIVALLAVGLTQNKALPENVKYIGIVLDAGSSHT 60  
DB 1 MEDTKESNVKTFCSKNILAILGFSIIAIVALLAVGLTQNKALPENVKYIGIVLDAGSSHT 60  
QY 61 SLIYIKWPAEKENDTGVVHVEECRVKPGGSKVQKNEIGIYLTDCMERAREVIPSQ 120  
DB 61 SLIYIKWPAEKENDTGVVHVEECRVKPGGSKVQKNEIGIYLTDCMERAREVIPSQ 120  
QY 121 HQETPVYLGATAGMRLLRMESEELADRLVDVVERSLSNYPDFQGARITITGOEEGAYGI 180  
DB 121 HQETPVYLGATAGMRLLRMESEELADRLVDVVERSLSNYPDFQGARITITGOEEGAYGI 180  
QY 181 TINVLLGKFSQKTRWFSIVPYETNNQETFFGALDILGGASTQTVTFPQNTIESPDNALQPR 240  
DB 181 TINVLLGKFSQKTRWFSIVPYETNNQETFFGALDILGGASTQTVTFPQNTIESPDNALQPR 240  
QY 241 LYGKDYNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDCFHPGYKKVNVSDLYKTP 300  
DB 241 LYGKDYNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDCFHPGYKKVNVSDLYKTP 300  
QY 301 CTKEFEMTLPPQOFEIOGIGNYQCHOSILELFTNSYCPYSQCAFNGIFLPPLOQDFGAF 360  
DB 301 CTKEFEMTLPPQOFEIOGIGNYQCHOSILELFTNSYCPYSQCAFNGIFLPPLOQDFGAF 360  
QY 361 SAFYFVMKFLNLTSEKVSQEKVTEMKKFCQAPWEEIKTSYAGVKYKLSYCFSGTVIL 420  
DB 361 SAFYFVMKFLNLTSEKVSQEKVTEMKKFCQAPWEEIKTSYAGVKYKLSYCFSGTVIL 420  
QY 421 SLLLOQYHFTADSWEHIFHFKIQQSDAGWTGLYMLNTNMIPAEQRLSTPLSHSTYVFL 480  
DB 421 SLLLOQYHFTADSWEHIFHFKIQQSDAGWTGLYMLNTNMIPAEQRLSTPLSHSTYVFL 480  
QY 481 MVFLSLVLTVAIIGLLIFHFKPSYFWKDMV 510  
DB 481 MVFLSLVLTVAIIGLLIFHFKPSYFWKDMV 510  
RESULT 4  
AA70887  
ID AA70887 standard; protein; 510 AA.  
AC AA70887;  
XX  
DT 17-AUG-2000 (first entry)  
XX  
DE Human soluble CD39 protein.  
XX  
KW Soluble CD39; ADP-induced platelet activation; stroke; platelet aggregation;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;  
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;  
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;  
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;  
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;  
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;  
KW occlusion; reocclusion; stenosis; restenosis; antilanginal; cardiatic;  
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;  
KW coronary ischaemia; vascular occlusion.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 17..37  
FT /label= Transmembrane domain  
FT Modified-site 73..75  
FT /note= "Asn is N-glycosylated"

FT	Modified-site	/note= "Aen is N-glycosylated"	Db	181	TINYLKGFQKTRWFSIVPYETNNQETFGALDGGASTQVTFVQNQTIESPDNALQFR	240
FT	292..294					
FT	Modified-site	/note= "Aen is N-glycosylated"	Qy	241	LYGKDYNYTHSFLCYGKDQALWQKLAKDIOVASNEILRDCPHGPGYKVVNVSDLYKTP	300
FT	334..336					
FT	Modified-site	/note= "Aen is N-glycosylated"	Db	241	LYGKDYNYTHSFLCYGKDQALWQKLAKDIOVASNEILRDCPHGPGYKVVNVSDLYKTP	300
FT	371..373					
FT	Modified-site	/note= "Aen is N-glycosylated"	Qy	301	CTKRFEMLTFFQOFIEIGIGNYQQCHQSILELNFNTSYCPYSQCAFNGIFLPLPLQGDGFAG	360
FT	371..373					
FT	Modified-site	/note= "Aen is N-glycosylated"	Db	301	CTKRFEMLTFFQOFIEIGIGNYQQCHQSILELNFNTSYCPYSQCAFNGIFLPLPLQGDGFAG	360
FT	457..459					
FT	Modified-site	/note= "Aen is N-glycosylated"	Qy	361	SAFYFVMKFLNLTSEKVSQEKVTENMKKPCAPQBEIKTSYAGVKEKYLSEYCFSGSTYIL	420
FT	477..499					
FT	Domain	/label= Transmembrane_domain	Db	361	SAFYFVMKFLNLTSEKVSQEKVTENMKKPCAPQBEIKTSYAGVKEKYLSEYCFSGSTYIL	420
FT	477..499					
XX	W0200023094-A2.					
XX	27-APR-2000.					
XX	13-OCT-1999;	99WO-US023641.				
XX	16-OCT-1998;	98US-0104585P.				
PR	06-NOV-1998;	98US-0107466P.				
PR	13-AUG-1999;	99US-0149010P.				
XX	(IMMV ) IMMUNEX CORP.					
PA	(CORR ) CORNELL RES FOUND INC.					
XX	Maliszewski CR, Gayle RB, Marcus AJ;					
XX	WPI; 2000-339518/29.					
DR	N-PSDB; AAD00200.					
XX	Inhibiting platelet activation and recruitment, useful for treating a					
PT	mammal suffering from unstable angina, myocardial infarction, stroke					
PT	coronary artery disease or injury, comprises administering soluble CD39					
PT	polypeptides.					
XX	Claim 2; Fig 1; 118pp; English.					
PS	The present sequence is soluble CD39 having apyrase activity. Soluble					
CC	CD39 retains the capacity of wildtype CD39 to metabolise ATP and ADP at					
CC	physiologically relevant concentrations as well as the ability to block					
CC	and reverse ADP-induced platelet activation and recruitment including					
CC	platelet aggregation. This is used in the treatment of unstable angina,					
CC	myocardial infarction, stroke, coronary artery disease or injury.					
CC	atherosclerosis, peripheral vascular occlusion, preclampsia, embolism,					
CC	platelet-associated ischaemic disorder including lung ischaemia, coronary					
CC	ischaemia and cerebral ischaemia, thrombotic disorder including coronary					
CC	artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis,					
CC	peripheral artery thrombosis, venous thrombosis, thrombosis,					
CC	coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),					
CC	transient ischaemic attack. Soluble CD39 is also useful for preventing					
CC	thrombus formation or reformation, occlusion, reocclusion, stenosis or					
CC	restenosis of blood vessels or stroke					
XX	Sequence 510 AA;					
Qy	Query Match	100.0%; Score 2698; DB 3; Length 510;				
Best	Local Similarity	100.0%; Pred. No. 5.2e-262;				
Matches	510; Conservative	0; Mismatches	0; Indels	0; Gaps	0;	
Qy	1	MEDTKESNVTFCNKILAILGFSSIIAVIALLAGLTQNKALPENVKYGVILVDASSHT	60			
Db	1	MEDTKESNVTFCNKILAILGFSSIIAVIALLAGLTQNKALPENVKYGVILVDASSHT	60			
Qy	61	SLYIKWPAEKENDTGVMHQBECRVKPGISKFQKWEIGIYLTDCMERAREVTPRSQ	120			
Db	61	SLYIKWPAEKENDTGVMHQBECRVKPGISKFQKWEIGIYLTDCMERAREVTPRSQ	120			
Qy	121	HQSTPYVLGATAGMRLRMESELAQRLDVLVRSLSNYPDFQGARITTGQEGAYGWI	180			
Db	121	HQSTPYVLGATAGMRLRMESELAQRLDVLVRSLSNYPDFQGARITTGQEGAYGWI	180			
Qy	181	TINYLKGFQKTRWFSIVPYETNNQETFGALDGGASTQVTFVQNQTIESPDNALQFR	240			



Query Match 100.0%; Score 2698; DB 4; Length 510;  
Best Local Similarity 100.0%; Pred. No. 5.2e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60  
DB 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60

QY 61 SLIYIKWPAEKENDTGTVHVEECRVKPGISKFGKQVNEIGIYITDCMERAREVIPSQ 120  
DB 61 SLIYIKWPAEKENDTGTVHVEECRVKPGISKFGKQVNEIGIYITDCMERAREVIPSQ 120

QY 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARITGOEGAYGWI 180  
DB 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARITGOEGAYGWI 180

QY 181 TINYLLGKFSQKTRWFSIVPVTNNQETFGALDLGGASTQVTFVPOQTIESPDNALQFR 240  
DB 181 TINYLLGKFSQKTRWFSIVPVTNNQETFGALDLGGASTQVTFVPOQTIESPDNALQFR 240

QY 241 LYGDYNNVYTHSFLCYGKDQALWQKLAKDIQVANSNEILRDPCHFPGYKVVNSDLYKTP 300  
DB 241 LYGDYNNVYTHSFLCYGKDQALWQKLAKDIQVANSNEILRDPCHFPGYKVVNSDLYKTP 300

QY 301 CTKRFEMTLPPQOPEIQTIGNYQOCHQSILELFTNYSYCPYSQCAFNGIFLPPLOQDFGAF 360  
DB 301 CTKRFEMTLPPQOPEIQTIGNYQOCHQSILELFTNYSYCPYSQCAFNGIFLPPLOQDFGAF 360

QY 361 SAFYFVMKFLNLTSEKVSQEKTEMMKFCAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420  
DB 361 SAFYFVMKFLNLTSEKVSQEKTEMMKFCAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420

QY 421 SLLLOGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMPASOPLSTPLSHSTYVFL 480  
DB 421 SLLLOGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMPASOPLSTPLSHSTYVFL 480

QY 481 MVFLSLVLTVAIIGLLIFHKPSPYFWMKDV 510  
DB 481 MVFLSLVLTVAIIGLLIFHKPSPYFWMKDV 510

RESULT 6

ADJ57262

ID ADJ57262 standard; protein; 510 AA.

XX AC ADJ57262;

XX DE

DT 06-MAY-2004 (first entry)

XX DE Human CD39 polypeptide.

XX DE

KW CD39; nucleoside diphosphate; thrombolytic; anticoagulant;  
KW cardiovascular; cytostatic; antibacterial; immunosuppressive; vasotropic;  
KW cardiant; antianginal; antiarteriosclerotic; gynaecological;  
KW cerebroprotective; cancer; human; apyrase; enzyme.

XX OS Homo sapiens.

XX FH Key

FT Domain Location/Qualifiers

FT 55..61 /note = ACR1

FT 125..135 /note = ACR2

FT 171..183 /note = ACR3

FT 213..220 /note = ACR4

FT 447..454 /note = ACR5

FT 447..454 /note = ACR5

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

PD 28-AUG-2003.

XX PF 19-FEB-2003; 2003WO-US004845.

XX PR 20-FEB-2002; 2002US-0358303P.

XX PA (GEHO ) GEN HOSPITAL CORP.

XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX PI Elmaleh DR, Robson SC, Papisov MI;

XX DR MPI, 2003-778966/73.

XX DR N-FSDB; ADJ57261.

New enzyme polymer conjugate used for treating abnormal levels of extracellular nucleotides or platelet aggregation, graft transplant, cardiovascular disease, cancer and sepsis.

XX Claim 20; SEQ ID NO 2; 82pp; English.

The invention relates to a conjugate (I) comprising an enzyme and a biodegradable polymer, where (i) enzymatic activity of the enzyme is higher relative to that of the enzyme in the absence of the biodegradable polymer, or (ii) the half life of the enzyme is longer than that of the polymer in the absence of the polymer. The enzymatic activity (i) is at least 10 (preferably at least 100) times higher in the presence of the polymer. The enzyme is a multimeric, soluble and/or extracellular enzyme, preferably an apyrase, especially a soluble form of CD39 and catalyzes hydrolysis of nucleoside diphosphate. The conjugate can be used to treat diseases relating to abnormal levels of extracellular nucleotides or abnormal aggregation of platelets, particularly cardiovascular disease, cancer, sepsis or a disease related to graft transplant. (I) is also used for treating coronary artery disease or injury following myocardial infarction, unstable angina, atherosclerosis, pre-eclampsia, embolism, platelet associated ischaemic disorders including lung, coronary and cerebral ischaemia, reocclusion following thrombosis, thrombotic disorders, and thrombosis and coagulopathies associated with exposure to a foreign or injured tissue surface, in combination with angioplasty, carotid endarterectomy, anastomosis of vascular grafts and chronic cardiovascular devices. The present sequence represents a human CD39 polypeptide.

XX SQ Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 7; Length 510;  
Best Local Similarity 100.0%; Pred. No. 5.2e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60

DB 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60

QY 61 SLIYIKWPAEKENDTGTVHVEECRVKPGISKFGKQVNEIGIYITDCMERAREVIPSQ 120

DB 61 SLIYIKWPAEKENDTGTVHVEECRVKPGISKFGKQVNEIGIYITDCMERAREVIPSQ 120

QY 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARITGOEGAYGWI 180

DB 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARITGOEGAYGWI 180

QY 181 TINYLLGKFSQKTRWFSIVPVTNNQETFGALDLGGASTQVTFVPOQTIESPDNALQFR 240

DB 181 TINYLLGKFSQKTRWFSIVPVTNNQETFGALDLGGASTQVTFVPOQTIESPDNALQFR 240

QY 241 LYGDYNNVYTHSFLCYGKDQALWQKLAKDIQVANSNEILRDPCHFPGYKVVNSDLYKTP 300

DB 241 LYGDYNNVYTHSFLCYGKDQALWQKLAKDIQVANSNEILRDPCHFPGYKVVNSDLYKTP 300

QY 301 CTKRFEMTLPPQOPEIQTIGNYQOCHQSILELFTNYSYCPYSQCAFNGIFLPPLOQDFGAF 360

DB 301 CTKRFEMTLPPQOPEIQTIGNYQOCHQSILELFTNYSYCPYSQCAFNGIFLPPLOQDFGAF 360

QY 361 SAFYFVMKFLNLTSEKVSQEKTEMMKFCAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420

XX SQ

```

Db      361  SAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPMEEIKTSYAGVKEKYLSEYCFSGTYIL 420
      421  SLLQGYHFTADSWEHIFGKIQGS DAGWTGLGYMLNLTNMIIPAEQPLSTPLSHSTYVFL 480
      421  SLLQGYHFTADSWEHIFGKIQGS DAGWTGLGYMLNLTNMIIPAEQPLSTPLSHSTYVFL 480
Qy      481  MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510
      481  MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510
Db      481  MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510
      481  MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510

RESULT 7
ADL24295
ID   ADL24295 standard; protein; 510 AA.
XX
AC   ADL24295;
DT   03-JUN-2004 (first entry)
XX
DE   Human CD39.
XX
KW   cardiovascular disease; IL-17; interleukin; IL-18; 4-1BB; CD30; OX40;
KW   antagonist.
XX
OS   Homo sapiens.
XX
PN   WO2004019866-A2.
XX
PD   11-MAR-2004.
XX
PF   21-AUG-2003; 2003WO-US026354.
XX
PR   28-AUG-2002; 2002US-0406418P.
PR   12-AUG-2003; 2003US-0494457P.
XX
PA   (IMMUNEX ) IMMUNEX CORP.
XX
PI   Burton PB, Deisher TA;
XX
DR   WPI; 2004-239107/22.
DR   N-PSDB; ADL24294.
XX
PT   Use of IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists, for treating a
PT   cardiovascular disease, e.g. chronic immune myocarditis, congestive heart
PT   failure, aneurysm, angina, embolism, restenosis, ischemia or
PT   thrombocytopenic purpura.
XX
PS   Disclosure; Page 133-134; 135pp; English.
XX
CC   The present invention relates to a method of treating cardiovascular
CC   disease in a subject, comprising administering an IL-17, IL-18, 4-1BB,
CC   CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40
CC   antagonists are useful for treating cardiovascular disorders, e.g.
CC   (chronic immune) myocarditis, congestive heart failure, aneurysms,
CC   angina, embolism, restenosis, ischemia or thrombocytopenic purpura. The
CC   present sequence is a polypeptide used in the exemplification of the
CC   invention.
XX
SQ   Sequence 510 AA;

```

```

Query Match      100.0%; Score 2698; DB 8; Length 510;
Best Local Similarity 100.0%; Pred. No. 5.2e-262;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1  MEDTKSNVKTFCCKNLAIFGSSIIAVALLAVGLTONKALPENVKYGIVLDAAGSSHT 60
      1  MEDTKSNVKTFCCKNLAIFGSSIIAVALLAVGLTONKALPENVKYGIVLDAAGSSHT 60
Db      61  SLIYIKWPAEKENDTGVVHQVEECRVKPGISKVFQKVNIEIGIYLTDCMERAREVIPSQ 120
      61  SLIYIKWPAEKENDTGVVHQVEECRVKPGISKVFQKVNIEIGIYLTDCMERAREVIPSQ 120

```

```

Qy      121  HOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLSNYPDFQGARIIITGOEEGAYGWI 180
      121  HOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLSNYPDFQGARIIITGOEEGAYGWI 180
Qy      181  TTYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVFNQNTIESPDNALQPR 240
      181  TTYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVFNQNTIESPDNALQPR 240
Qy      241  LYKDYNNVYTHSFLCYGKQDALWQKLAKDIQVASNEILLRDCPFHFGYKKVNVSDLYKTP 300
      241  LYKDYNNVYTHSFLCYGKQDALWQKLAKDIQVASNEILLRDCPFHFGYKKVNVSDLYKTP 300
Qy      301  CTKRFEMTLPFOQFEIQIGNYQQCHOSILELFTNTSYCPYSCAFNGIFLPLQGDGAF 360
      301  CTKRFEMTLPFOQFEIQIGNYQQCHOSILELFTNTSYCPYSCAFNGIFLPLQGDGAF 360
Qy      361  SAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPMEEIKTSYAGVKEKYLSEYCFSGTYIL 420
      361  SAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPMEEIKTSYAGVKEKYLSEYCFSGTYIL 420
Qy      421  SLLQGYHFTADSWEHIFGKIQGS DAGWTGLGYMLNLTNMIIPAEQPLSTPLSHSTYVFL 480
      421  SLLQGYHFTADSWEHIFGKIQGS DAGWTGLGYMLNLTNMIIPAEQPLSTPLSHSTYVFL 480
Qy      481  MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510
      481  MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510
Db      481  MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510
      481  MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510

RESULT 8
ADQ99453
ID   ADQ99453 standard; protein; 510 AA.
XX
AC   ADQ99453;
DT   23-SEP-2004 (first entry)
XX
DE   Human CD39 protein.
XX
KW   CD39-like protein; gene mapping; molecular weight marker;
KW   food supplement; anti-thrombotic; anti-tissue graft rejection agent;
KW   ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase;
KW   NTPase; human; enzyme.
XX
OS   Homo sapiens.
XX
FH   Key Location/Qualifiers
FT   Region 47..68
FT   Region /note= "Apyrase region (ACR) I"
FT   Region 124..142
FT   Region /note= "Apyrase region (ACR) II"
FT   Region 169..191
FT   Region /note= "Apyrase region (ACR) III"
FT   Region 207..228
FT   Region /note= "Apyrase region (ACR) IV"
XX
PN   US6759214-B1.
XX
PD   06-JUL-2004.
XX
PF   13-JUL-2001; 2001US-00908510.
XX
PR   29-JAN-1999; 99US-00240639.
XX
PA   (NUVE-) NUVELO INC.
XX
PI   Chadwick BP, Friesch A;
XX
DR   WPI; 2004-515395/49.
XX
PT   New CD-39-like polypeptides and polynucleotides, useful in chromosome and
PT   gene mapping, as molecular weight markers, as food supplements, or as
PT   anti-thrombotic or anti-tissue graft rejection agents.

```

XX Example; Fig 8; 104pp; English.

XX The invention relates to novel CD39-like polypeptides (CD39-like nucleotide triphosphatase; NTPase) and nucleic acid molecules encoding such polypeptides. CD39-like polynucleotides may be used as hybridisation probes, PCR primers and in chromosome and gene mapping. Polypeptides of the invention may be used as molecular weight markers, as food supplements, as anti-thrombotic or anti-tissue graft rejection agents, or for regulating ATP neurotransmission in smooth muscle, peripheral ganglia or brain. Sequences of the invention are useful in modulating ecto-ATPase activity and for identifying compounds that modulate ecto-ATPase activity. The present sequence is human CD39 protein, a member of the CD39-like protein family. Note: This sequence is stated to be the same as that shown as SEQ ID NO:13 in the sequence listing of the specification. However this sequence has additional residues at its ends.

XX Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 8; Length 510; Best Local Similarity 100.0%; Pred. No. 5.2e-262; Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKSNVKTFCSKNIIAILGFSIIIVALLAVGLTQNKALPENVKYGVLDAGSSHT 60

Db 1 MEDTKSNVKTFCSKNIIAILGFSIIIVALLAVGLTQNKALPENVKYGVLDAGSSHT 60

Qy 61 SLIYIKVPAEKENDGVHVQVECKVKGPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120

Db 61 SLIYIKVPAEKENDGVHVQVECKVKGPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120

Qy 121 HQETPVYLGATAGMRLRMESEELADRLVDVVERSLSNYPDFQGARITGOEGAYGWI 180

Db 121 HQETPVYLGATAGMRLRMESEELADRLVDVVERSLSNYPDFQGARITGOEGAYGWI 180

Qy 181 TINYLKGFQSKTRWFSIVPVTNNQETFGALDLGGASTQVTFVPPQNTIESPDNALQFR 240

Db 181 TINYLKGFQSKTRWFSIVPVTNNQETFGALDLGGASTQVTFVPPQNTIESPDNALQFR 240

Qy 241 LYGDYNYVTHSFLCYGKDQALWOKLAKDIOVASNEILRDPCEHPGKVVNVSDLYKTP 300

Db 241 LYGDYNYVTHSFLCYGKDQALWOKLAKDIOVASNEILRDPCEHPGKVVNVSDLYKTP 300

Qy 301 CTKRFEMLTPQPEIQIGNYQOCHQSIELFNSTSYCPYSQCAFNGIFLPPLOQDFGAF 360

Db 301 CTKRFEMLTPQPEIQIGNYQOCHQSIELFNSTSYCPYSQCAFNGIFLPPLOQDFGAF 360

Qy 361 SAFYVVKFLNLTSEKVSQEKVTENMKKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTVIL 420

Db 361 SAFYVVKFLNLTSEKVSQEKVTENMKKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTVIL 420

Qy 421 SLLQGVHFTADSWEHIFIGKIOGSDAGWTLYGMLNLTNNIPAEQPLSTPLSHSTYVFL 480

Db 421 SLLQGVHFTADSWEHIFIGKIOGSDAGWTLYGMLNLTNNIPAEQPLSTPLSHSTYVFL 480

Qy 481 MVFLSLVFTVAIIGLLIFHKPSPFWKDMV 510

Db 481 MVFLSLVFTVAIIGLLIFHKPSPFWKDMV 510

RESULT 9

ADR69210

ID ADR69210 standard; protein; 510 AA.

XX

AC ADR69210;

XX

XX 04-NOV-2004 (first entry)

XX

XX Human CD39 protein #3.

XX

XX CD39-like protein; autoimmune deficiency disorder;

KW connective tissue disease; multiple sclerosis;

KW systemic lupus erythematosus; rheumatoid arthritis;

KW autoimmune pulmonary inflammation; Guillain-Barre syndrome;

KW autoimmune thyroiditis; insulin dependent diabetes mellitus;

KW myasthenia gravis; graft-versus-host disease;

KW autoimmune inflammatory eye disease; allergic disorder; asthma;

KW respiratory disorder; myeloid or lymphoid cell deficiency;

KW periodontal disease; tooth repair process; inflammatory bowel disease;

KW Crohn's disease; leukaemia; nervous system disorder; anticoagulant;

KW food supplement; anti-tissue graft rejection; ATP neurotransmission;

XX gene therapy; human.

XX Homo sapiens.

XX

Key Location/Qualifiers

Region 47..68

FT /note= "Apyrase region (ACR) I "

FT 124..142

FT /note= "Apyrase region (ACR)II"

FT 169..191

FT /note= "Apyrase region (ACR) III "

FT 207..228

FT /note= "Apyrase region (ACR) IV"

XX

US6780410-B1.

XX

24-AUG-2004.

XX

13-JUL-2001; 2001US-00905744.

XX

29-JAN-1999; 99US-00240639.

XX

(NUVE-) NUVELO INC.

XX

Chadwick BP, Frischauf A;

PI

XX

WPI; 2004-613270/59.

DR

XX

New isolated CD39LA polypeptide and polynucleotide, useful for preventing, treating, or ameliorating multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or graft-versus-host disease.

XX

Example; Fig 8; 103pp; English.

XX

The present invention relates to CD39-like polypeptide and its encoding polynucleotide. The invention is useful for preventing, treating or ameliorating autoimmune deficiency disorders including connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease or autoimmune inflammatory eye disease, allergic disorders including asthma and other respiratory problems, myeloid or lymphoid cell deficiencies, periodontal diseases and other tooth repair processes, inflammatory conditions including inflammatory bowel disease and Crohn's disease, leukaemia and nervous system disorders. The invention is also useful as an anticoagulant for inhibiting platelet aggregation, food supplement, anti-tissue graft rejection agents, for regulating neurotransmission by ATP in smooth muscle, peripheral ganglia or brain and in gene therapy. The present sequence is a human CD39 protein. Note: This sequence is stated to be the same as that shown as SEQ ID 13 in sequence listing, however these sequences differ.

XX

SQ Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 8; Length 510; Best Local Similarity 100.0%; Pred. No. 5.2e-262; Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKSNVKTFCSKNIIAILGFSIIIVALLAVGLTQNKALPENVKYGVLDAGSSHT 60

Db 1 MEDTKSNVKTFCSKNIIAILGFSIIIVALLAVGLTQNKALPENVKYGVLDAGSSHT 60

QY 61 SLVIYKPAEKENDTGVVHQVEECRVKPGISKFVQVNEIGIYLTDCCMERAREVIPSQ 120  
Db 61 SLVIYKPAEKENDTGVVHQVEECRVKPGISKFVQVNEIGIYLTDCCMERAREVIPSQ 120  
QY 121 HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPFDQFQARIITGOEAGYWI 180  
Db 121 HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPFDQFQARIITGOEAGYWI 180  
QY 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPOQNTIESPDNALQPR 240  
Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPOQNTIESPDNALQPR 240  
QY 241 LYGKDVNVYTHSLFCYQKQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSDLYKTP 300  
Db 241 LYGKDVNVYTHSLFCYQKQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSDLYKTP 300  
QY 301 CTKRFEWTLPPFOQFEIQQIGNYQQCHQSILELFTNTSCYPSQCAFNGIFLPLQGDGAF 360  
Db 301 CTKRFEWTLPPFOQFEIQQIGNYQQCHQSILELFTNTSCYPSQCAFNGIFLPLQGDGAF 360  
QY 361 SAFYFVWKFLNLTSEKVSQEKVTEMKFKCAQPBWEIKTSYAGVKBYKYLSEYCFSGTYIL 420  
Db 361 SAFYFVWKFLNLTSEKVSQEKVTEMKFKCAQPBWEIKTSYAGVKBYKYLSEYCFSGTYIL 420  
QY 421 SLLSQYHFTADSWEHIFIGIKIQGSDAGWTLGYMLNLNMIAPAEOLSTPLSHSTYVFL 480  
Db 421 SLLSQYHFTADSWEHIFIGIKIQGSDAGWTLGYMLNLNMIAPAEOLSTPLSHSTYVFL 480  
QY 481 MVLFSVLVFTVAIIGLLIFHKPSYFWKDMV 510  
Db 481 MVLFSVLVFTVAIIGLLIFHKPSYFWKDMV 510

RESULT 10  
ADRE69042  
ID ADRE69042 standard; protein; 510 AA.  
AC ADRE69042;  
XX  
XX  
XX 04-NOV-2004 (first entry)  
XX Human CD39 protein #3.  
XX CD39-like protein; CD39-like nucleotide triphosphatase; NTPase; cancer;  
KW leukaemia; acute lymphocytic leukaemia; acute myelocytic leukaemia;  
KW chronic leukaemia; autoimmune disorder; multiple sclerosis;  
KW rheumatoid arthritis; Guillain-Barre syndrome;  
KW insulin dependent diabetes mellitus; myasthenia gravis;  
KW graft-versus-host disease; GVHD; allergic disorder; asthma;  
KW respiratory disorder; inflammatory disorder; septic shock;  
KW systemic inflammatory response syndrome; SIRS; Crohn's disease;  
KW central nervous system disorder; peripheral nervous system disorder;  
KW ischaemia; Parkinson's disease; Alzheimer's disease; Huntington's chorea;  
KW systemic lupus erythematosus;  
KW human immunodeficiency virus-associated myelopathy;  
KW transverse myelopathy; nutritional disorder; vitamin B12 deficiency;  
KW folic acid deficiency; Wernicke disease; tobacco-alcohol amblyopia;  
KW Marchiafava-Bignami disease; haemostatic activity; thrombolytic activity;  
KW nutritional supplement; ecto-ATPase activity; cytosolic; immunotherapy;  
human; enzyme.  
XX  
XX Homo sapiens.

XX Key Location/Qualifiers  
FH Region 47..68 /note="Apyrase (ACR) I"  
FT Region 124..142 /note="Apyrase (ACR) II"  
FT Region 169..191 /note="Apyrase (ACR) III"  
FT Region 202..228 /note="Apyrase (ACR) IV"  
XX

PN US6780977-B1.  
XX  
PD 24-AUG-2004.  
XX  
PF 27-MAR-2002; 2002US-00107660.  
XX  
PR 29-JAN-1999; 99US-00240639.  
PR 13-JUL-2001; 2001US-00905589.  
XX (NUVE-) NUVELO INC.  
PA  
PI Chadwick BP, Frieschauf A;  
XX  
XX WPI: 2004-613273/59.  
DR GENBANK: S73813.  
XX  
PT New antibody or its fragment that specifically binds to CD39L3  
PT polypeptide, useful for detecting and purifying CD39L3 polypeptide, for  
PT treating leukemia, and for detecting and preventing metastatic spread of  
PT cancerous cells.  
XX  
PS Example; Fig 8; 102pp; English.  
XX  
CC The present invention provides novel CD39-like polypeptides (CD39-like  
CC nucleotide triphosphatase; NTPase) and their encoding polynucleotides.  
CC The invention is useful in treating cancer, leukaemia and related  
CC disorders such as acute lymphocytic leukaemia, acute myelocytic leukaemia  
CC and chronic leukaemia, autoimmune disorders such as multiple sclerosis,  
CC rheumatoid arthritis, Guillain-Barre syndrome, insulin dependent diabetes  
CC mellitus, myasthenia gravis and graft-versus-host disease, allergic  
CC disorders such as asthma, respiratory disorders, inflammatory disorders  
CC such as septic shock, systemic inflammatory response syndrome (SIRS) and  
CC Crohn's disease, central and peripheral nervous system disorders such as  
CC ischaemia, Parkinson's disease, Alzheimer's disease, Huntington's chorea,  
CC systemic lupus erythematosus, human immunodeficiency virus-associated  
CC myelopathy and transverse myelopathy and nutritional disorders such as  
CC vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-  
CC alcohol amblyopia and Marchiafava-Bignami disease. The invention also has  
CC haemostatic and thrombolytic activity. The invention acts as a cytosolic  
CC and modulates ecto-ATPase activity. The invention serves as nutritional supplements  
CC agent and is useful in immunotherapy. The present sequence is human CD39  
CC protein. Note: This sequence is described in the specification as being  
CC the same as the human CD39 protein represented in SEQ ID NO: 13 of the  
CC sequence listing, however the two sequences are different.  
XX  
SQ Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 8; Length 510;  
Best Local Similarity 100.0%; Pred. No. 5.2e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEDTKESNVKTPCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGVILDAGSSHT 60  
Db 1 MEDTKESNVKTPCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYGVILDAGSSHT 60  
QY 61 SLVIYKPAEKENDTGVVHQVEECRVKPGISKFVQVNEIGIYLTDCCMERAREVIPSQ 120  
Db 61 SLVIYKPAEKENDTGVVHQVEECRVKPGISKFVQVNEIGIYLTDCCMERAREVIPSQ 120  
QY 121 HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPFDQFQARIITGOEAGYWI 180  
Db 121 HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPFDQFQARIITGOEAGYWI 180  
QY 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPOQNTIESPDNALQPR 240  
Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPOQNTIESPDNALQPR 240  
QY 241 LYGKDVNVYTHSLFCYQKQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSDLYKTP 300  
Db 241 LYGKDVNVYTHSLFCYQKQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSDLYKTP 300  
QY 301 CTKRFEWTLPPFOQFEIQQIGNYQQCHQSILELFTNTSCYPSQCAFNGIFLPLQGDGAF 360  
XX

Db 301 CTKEFMTLPFOQFEIQQIGNVQQCHQSILELNTSYCPYSQCAFNGIFLPLQDGFAP 360  
QY 361 SAFYFVKFLNLTSEKVSQEKVTEMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420  
Db 361 SAFYFVKFLNLTSEKVSQEKVTEMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420  
QY 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480  
Db 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480  
QY 481 MVLFSLVLTVAIIIGLLIFHKPSYFWKDMV 510  
Db 481 MVLFSLVLTVAIIIGLLIFHKPSYFWKDMV 510

RESULT 11  
ID ADS17924  
XX ADS17924 standard; protein; 510 AA.

AC ADS17924;

DT 18-NOV-2004 (first entry)

DE Human CD39 protein #3.

XX CD39-like protein; gene mapping; food supplement; ecto-ATPase activity;  
KW gene therapy; multiple sclerosis; rheumatoid arthritis;  
KW autoimmune thyroiditis; diabetes mellitus; myasthenia gravis;  
KW autoimmune inflammatory eye disease; osteoporosis; osteoarthritis;  
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
KW leukaemia; nervous system disorder; neuroprotective; antidiabetic;  
KW antirheumatic; antithyroid; immunosuppressive; antidiabetic;  
KW muscular-gen; ophthalmological; osteopathic; nootropic; antiparkinsonian;  
KW cytostatic; human; CD39 protein.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 47..68  
FT /note= "Apyrase region (ACR) I"  
FT Region 124..142  
FT /note= "Apyrase region (ACR) II"  
FT Region 169..191  
FT /note= "Apyrase region (ACR) III"  
FT Region 207..228  
FT /note= "Apyrase region (ACR) IV"

XX US6787328-B1.

XX 07-SEP-2004.

XX 13-JUL-2001; 2001US-00905732.

XX 29-JAN-1999; 99US-00240639.

XX (NUVE-) NUVELO INC.

XX Chadwick BP, Frieschauf A;

XX WPI; 2004-632929/61.

XX New isolated CD39L4 polynucleotide, useful for preventing, treating, or  
PT ameliorating multiple sclerosis, rheumatoid arthritis, diabetes,  
PT osteoporosis, Alzheimer's disease, amyotrophic lateral sclerosis, or  
PT leukemia.

XX Example; Fig 8; 103pp; English.

XX The present invention relates to a CD39-like polypeptides and the  
CC encoding polynucleotides. The CD39L4 polynucleotide is useful as  
CC hybridisation probes, as primers for PCR, for chromosome or gene mapping,  
CC in the recombinant production of protein, and in generation of antisense  
CC DNA or RNA. The protein of the invention is used as molecular weight

CC markers, and as food supplements and for modulating ecto-ATPase activity  
CC and for identifying compounds that can be utilised for modulating ecto-  
CC ATPase activity. The invention is useful for preventing, treating or  
CC ameliorating a medical condition, e.g. multiple sclerosis, rheumatoid  
CC arthritis, autoimmune thyroiditis, diabetes mellitus, myasthenia gravis,  
CC autoimmune inflammatory eye disease, osteoporosis, osteoarthritis,  
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
CC leukaemia or nervous system disorders and in gene therapy. The present  
CC sequence is the human CD39 protein. Note: This sequence is stated to be  
CC the same as that shown as SEQ ID 13 in sequence listing, however these  
CC sequences differ.  
XX  
SQ Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 8; Length 510;  
Best Local Similarity 100.0%; Pred. No. 5.2e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDTKESNVKTFCSKNILAILGFFSIIIAVALLAVGLTQNKALPENVKYGI VLDAGSSHT 60  
Db 1 MEDTKESNVKTFCSKNILAILGFFSIIIAVALLAVGLTQNKALPENVKYGI VLDAGSSHT 60  
QY 61 SLIYIKWPAEKENDTGVVHVQVEECRVKGGISKFQKVEIGIYLTDCMERAREVIPSQ 120  
Db 61 SLIYIKWPAEKENDTGVVHVQVEECRVKGGISKFQKVEIGIYLTDCMERAREVIPSQ 120  
QY 121 HQETPVYLGATAGWRLRLMESEELADRVLDVVERSLSNYPDFQGARITTGEEGAYGI 180  
Db 121 HQETPVYLGATAGWRLRLMESEELADRVLDVVERSLSNYPDFQGARITTGEEGAYGI 180  
QY 181 TINYLLGKFSQKTRWFSIVPVTNNQETFGALDLGGASTQVTFVQNTIESPDNALQPR 240  
Db 181 TINYLLGKFSQKTRWFSIVPVTNNQETFGALDLGGASTQVTFVQNTIESPDNALQPR 240  
QY 241 LYGKDYNVYTHSFLCYGKDQALWQKLAQDIQVANSNEILRDCPFHGYKKVNVSDLYKTP 300  
Db 241 LYGKDYNVYTHSFLCYGKDQALWQKLAQDIQVANSNEILRDCPFHGYKKVNVSDLYKTP 300  
QY 301 CTKEFMTLPFOQFEIQQIGNVQQCHQSILELNTSYCPYSQCAFNGIFLPLQDGFAP 360  
Db 301 CTKEFMTLPFOQFEIQQIGNVQQCHQSILELNTSYCPYSQCAFNGIFLPLQDGFAP 360  
QY 361 SAFYFVKFLNLTSEKVSQEKVTEMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420  
Db 361 SAFYFVKFLNLTSEKVSQEKVTEMMKFCQAPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420  
QY 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480  
Db 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480  
QY 481 MVLFSLVLTVAIIIGLLIFHKPSYFWKDMV 510  
Db 481 MVLFSLVLTVAIIIGLLIFHKPSYFWKDMV 510

RESULT 12

ABO84674

ID ABO84674 standard; protein; 510 AA.

XX ABO84674;

DT 18-NOV-2004 (first entry)

DE Human cancer-associated protein HP20-011.5.

XX Human; cancer-associated protein; cytostatic; cancer; leukaemia;  
KW lymphoma; CAP.

XX Homo sapiens.

XX WO2004074320-A2.

XX 02-SEP-2004.



XX Example; Fig 8; 102pp; English.  
XX The invention relates to CD39-like polypeptides (CD39-like nucleotide-  
triphosphatase; NTPase) and their corresponding polynucleotides. The  
invention also relates to a method for making CD39L proteins. The methods  
and compositions of the invention are useful for the diagnosis,  
prevention and/or treatment of diseases or conditions associated with  
aberrant expression or activity of the CD39-like polypeptide, such as HIV  
infection, hepatitis, multiple sclerosis, systemic lupus erythematosus,  
rheumatoid arthritis, Guillain-Barre syndrome, thyroiditis, diabetes,  
myasthenia gravis, graft-versus-host disease (GVHD) and asthma. The  
present sequence is the human CD39 protein. Note: This sequence is  
described in the specification as being the same as the human CD39  
protein represented in SEQ ID NO: 13 of the sequence listing, however the  
two sequences are different.

XX Sequence 510 AA;

Query Match 100.0%; Score 2698; DB 8; Length 510;  
Best Local Similarity 100.0%; Pred. No. 5.2e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEDTKSNVTKFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGVLDAGSSHT 60  
Db 1 MEDTKSNVTKFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGVLDAGSSHT 60  
QY 61 SLVIYKWPABKENDTGVVHVQVEECRVKPGISKVQKNEIGIYLTDCMERAREVIPSQ 120  
Db 61 SLVIYKWPABKENDTGVVHVQVEECRVKPGISKVQKNEIGIYLTDCMERAREVIPSQ 120  
QY 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARITQEEGAYCWI 180  
Db 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARITQEEGAYCWI 180  
QY 181 TINYLLGKFSQKTRWFSIVPVETNNQETFGALDGGASTQVTFVQNOTTIESPNALQFR 240  
Db 181 TINYLLGKFSQKTRWFSIVPVETNNQETFGALDGGASTQVTFVQNOTTIESPNALQFR 240  
QY 241 LYGKDNVYVTHSFLCYGKDQALWQKLADIOVASNEILRDCPFHGYKKVNVSDLYKTP 300  
Db 241 LYGKDNVYVTHSFLCYGKDQALWQKLADIOVASNEILRDCPFHGYKKVNVSDLYKTP 300  
QY 301 CTKRFEMTLPFQOPEIQIGNYQQCHQSIQELFNISYCPYSCAFNGIFLPLQDGFAG 360  
Db 301 CTKRFEMTLPFQOPEIQIGNYQQCHQSIQELFNISYCPYSCAFNGIFLPLQDGFAG 360  
QY 361 SAFYVWKFNLMTSEKVSQEKVTEMKFKCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420  
Db 361 SAFYVWKFNLMTSEKVSQEKVTEMKFKCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420  
QY 421 SLLLGQYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMPAEQPLSTPLSHSTYVFL 480  
Db 421 SLLLGQYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMPAEQPLSTPLSHSTYVFL 480  
QY 481 MVLFSLVLTVAIIIGLLIFHRPSYFWKDMV 510  
Db 481 MVLFSLVLTVAIIIGLLIFHRPSYFWKDMV 510

RESULT 14

ADK60421  
ID ADK60421 standard; protein; 511 AA.  
XX AC ADK60421;  
XX AC ADK60421;  
XX DT 06-MAY-2004 (first entry)  
XX DE Angiogenesis differentially expressed protein #61.  
KW vasotrophic; antirheumatic; antiarthritic; hypotensive; antianginal;  
KW antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy;  
KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;

KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;  
KW ovary hyperstimulation; psoriasis; endometriosis; restenosis;  
KW angioplasty; cicatrization; peripheral vascular disease; hypertension;  
KW vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis;  
KW ischemia; angina; myocardial infarction; chronic heart disease;  
KW cardiac congestion; macular degeneration; osteoporosis.  
OS Homo sapiens.  
XX FR2836687-A1.  
XX 05-SEP-2003.  
XX 11-APR-2002; 2002FR-00004546.  
XX 04-MAR-2002; 2002FR-00002717.  
XX (GENE-) GENE SIGNAL.  
XX (ALMA/) AL MAHMOOD S.  
XX Colin S, Schneider C, Al Mahmood S;  
XX MPI: 2004-013912/02.  
XX N-FSDB; ADK60414.  
XX Compositions for diagnosing, prognosing and treating angiogenic disorders  
XX including tumor vascularization and heart disease, comprise nucleic acid  
XX or polypeptide differentially expressed in angiogenesis.  
XX Claim 7; SEQ ID NO 297; 424pp; French.

The invention relates to a novel pharmaceutical composition active on  
angiogenesis comprising an endothelial cell nucleic acid whose expression  
is induced by an angiogenic factor and inhibited by an angiostatic agent  
or its complement or fragment, a polypeptide sequence encoded by the  
nucleic acid or its fragment, a molecule capable of inhibiting expression  
of the nucleic acid or a molecule which binds to the polypeptide  
sequence. The invention is used to diagnose, prognose or treat an  
angiogenic disorder in a mammal, particularly a human. The disorder is  
particularly tumor vascularization, a retinopathy, rheumatoid arthritis,  
Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,  
endometriosis associated with neovascularization, restenosis due to  
angioplasty, overproduction of tissue due to cicatrization, a peripheral  
vascular disease, hypertension, vascular inflammation, Raynaud disease,  
aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,  
myocardial infarction, chronic heart disease, cardiac congestion or  
macular degeneration due to age or osteoporosis. This sequence  
corresponds to a protein encoded by a differentially expressed DNA used  
in the composition of the invention.

XX Sequence 511 AA;

Query Match 100.0%; Score 2698; DB 8; Length 511;  
Best Local Similarity 100.0%; Pred. No. 5.3e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEDTKSNVTKFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGVLDAGSSHT 60  
Db 2 MEDTKSNVTKFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGVLDAGSSHT 61  
QY 61 SLVIYKWPABKENDTGVVHVQVEECRVKPGISKVQKNEIGIYLTDCMERAREVIPSQ 120  
Db 62 SLVIYKWPABKENDTGVVHVQVEECRVKPGISKVQKNEIGIYLTDCMERAREVIPSQ 121  
QY 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARITQEEGAYCWI 180  
Db 122 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARITQEEGAYCWI 181  
QY 181 TINYLLGKFSQKTRWFSIVPVETNNQETFGALDGGASTQVTFVQNOTTIESPNALQFR 240  
Db 182 TINYLLGKFSQKTRWFSIVPVETNNQETFGALDGGASTQVTFVQNOTTIESPNALQFR 241  
QY 241 LYGKDNVYVTHSFLCYGKDQALWQKLADIOVASNEILRDCPFHGYKKVNVSDLYKTP 300

Db 242 LYCKDYNVYTHSLFCYKQALAKQAKDIQVANSNEILRDPCHFGYKVVNVSDLYKTP 301  
Qy 301 CTRKRFEMTLFPQOFETQIGNYQQCHQSILELNTSYCPYSQCAFNGIFLPPQLQDGFAG 360  
Db 302 CTRKRFEMTLFPQOFETQIGNYQQCHQSILELNTSYCPYSQCAFNGIFLPPQLQDGFAG 361  
Qy 361 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKESYLSEYCFSGTYIL 420  
Db 362 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKESYLSEYCFSGTYIL 421  
Qy 421 SLLQGYHFTADSWEHIFGKIQGSAGWTLGYMLNLTNMIPEOPLSTPLSHSYVFL 480  
Db 422 SLLQGYHFTADSWEHIFGKIQGSAGWTLGYMLNLTNMIPEOPLSTPLSHSYVFL 481  
Qy 481 MVLFSVLVFTVAIIGLLIFHKPSYFWKDMV 510  
Db 482 MVLFSVLVFTVAIIGLLIFHKPSYFWKDMV 511

RESULT 15

ADK60722  
ID ADK60722 standard; protein; 511 AA.  
AC ADK60722;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
XX Angiogenesis differentially expressed protein #61.  
XX vasotropic; antiarheumatic; antiarthritic; hypotensive; antianginal;  
KW antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy;  
KW angiogenesis; endothelial cell; diagnosis; tumor vascularization;  
KW retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;  
KW ovary hyperstimulation; psoriasis; endometriosis; restenosis;  
KW angioplasty; cicatrization; peripheral vascular disease; hypertension;  
KW vascular inflammation; Raynaud's disease; aneurism; thrombophlebitis;  
KW ischemia; angina; myocardial infarction; chronic heart disease;  
KW cardiac congestion; macular degeneration; osteoporosis.  
XX  
OS Homo sapiens.  
XX  
XX FR2836686-A1.  
XX  
XX  
PD 05-SEP-2003.  
XX  
XX 04-MAR-2002; 2002FR-00002717.  
XX  
XX 04-MAR-2002; 2002FR-00002717.  
XX  
XX (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
XX  
XX Colin S, Schneider C, Al Mahmood S;  
XX  
XX WPI; 2004-013911/02.  
DR N-PSDB; ADK60715.  
XX  
XX  
XX Compositions containing nucleic acid or polypeptide differentially  
PT expressed in angiogenesis are useful to diagnose, prognose and treat  
PT angiogenic disorders including tumor vascularization and heart disease.  
XX  
XX  
PS Claim 7; SEQ ID NO 297; 405pp; French.  
XX

The invention relates to a novel pharmaceutical composition active on  
CC angiogenesis comprising an endothelial cell nucleic acid whose expression  
CC is induced by an angiogenic factor and inhibited by an angiostatic agent  
CC or its complement or fragment, a polypeptide sequence encoded by the  
CC nucleic acid or its fragment, a molecule capable of inhibiting expression  
CC of the nucleic acid or a molecule which binds to the polypeptide  
CC sequence. The invention is used to diagnose, prognose or treat an  
CC angiogenic disorder in a mammal, particularly a human. The disorder is  
CC particularly tumor vascularization, a retinopathy, rheumatoid arthritis,

CC Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis,  
CC endometriosis associated with neovascularization, restenosis due to  
CC angioplasty, overproduction of tissue due to cicatrization, a peripheral  
CC vascular disease, hypertension, vascular inflammation, Raynaud disease,  
CC aneurism, arterial restenosis, thrombophlebitis, ischemia, angina,  
CC myocardial infarction, chronic heart disease, cardiac congestion or  
CC macular degeneration due to age or osteoporosis. This sequence  
CC corresponds to a protein encoded by a differentially expressed DNA used  
CC in the composition of the invention.

XX Sequence 511 AA;

Qy SQ Query Match 100.0%; Score 2698; DB 8; Length 511;  
Best Local Similarity 100.0%; Pred. No. 5.3e-262;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEDTKESNVKTFCSKNILAILGFSIIAVIALVGLTONKALPENVKYGIIVLDAGSSHT 60  
Db 2 MEDTKESNVKTFCSKNILAILGFSIIAVIALVGLTONKALPENVKYGIIVLDAGSSHT 61  
Qy 61 SLIYIKWPAEKENDTGVVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120  
Db 62 SLIYIKWPAEKENDTGVVHQVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 121  
Qy 121 HQETPVYLGATAGMRLLRMESEELADRVLDVVVERSLSNYPDFQGARIIITGOEEGAYGWI 180  
Db 122 HQETPVYLGATAGMRLLRMESEELADRVLDVVVERSLSNYPDFQGARIIITGOEEGAYGWI 181  
Qy 181 TINYLLGKPSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPONQTIESP DNALQFR 240  
Db 182 TINYLLGKPSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPONQTIESP DNALQFR 241  
Qy 241 LYGKDYNVVYTHSFLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSDLYKTP 300  
Db 242 LYGKDYNVVYTHSFLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSDLYKTP 301  
Qy 301 CTKRFEWTLFPQOFETQIGNYQQCHQSILELNTSYCPYSQCAFNGIFLPPQLQDGFAG 360  
Db 302 CTKRFEWTLFPQOFETQIGNYQQCHQSILELNTSYCPYSQCAFNGIFLPPQLQDGFAG 361  
Qy 361 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKESYLSEYCFSGTYIL 420  
Db 362 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKESYLSEYCFSGTYIL 421  
Qy 421 SLLQGYHFTADSWEHIFGKIQGSAGWTLGYMLNLTNMIPEOPLSTPLSHSYVFL 480  
Db 422 SLLQGYHFTADSWEHIFGKIQGSAGWTLGYMLNLTNMIPEOPLSTPLSHSYVFL 481  
Qy 481 MVLFSVLVFTVAIIGLLIFHKPSYFWKDMV 510  
Db 482 MVLFSVLVFTVAIIGLLIFHKPSYFWKDMV 511

Search completed: September 21, 2005, 16:19:46  
Job time : 92 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2005, 15:52:40 ; Search time 25 Seconds  
(without alignments)  
1962.822 Million cell updates/sec

Title: US-09-807-660C-2  
Perfect score: 2698  
Sequence: 1 MEDTKESNVKTFCSKNILAI.....VAIIIGLIIFHKPSYFWKDMV 510

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: Piri: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length DB ID	Description	
1	2698	100.0	510 2 I56242	lymphoid cell acti	
2	511.5	19.0	483 2 D86276	hypothetical prote	
3	469.5	17.4	405 2 E86276	hypothetical prote	
4	455.5	16.9	630 2 S50463	hypothetical prote	
5	435.5	16.1	572 2 T40856	probable nucleotid	
6	421	15.6	516 2 G84442	probable nucleosid	
7	413.5	15.3	485 2 T34147	hypothetical prote	
8	402.5	14.9	508 2 C86276	7A19.33 protein -	
9	397	14.7	557 2 T16696	hypothetical prote	
10	381.5	14.1	556 2 T39109	probable guanosine	
11	374.5	13.9	455 2 S48859	nucleoside triphos	
12	352	13.0	1052 2 T04439	hypothetical prote	
13	341.5	12.7	454 2 J04616	apyrase (EC 3.6.1.	
14	332	12.3	479 2 T23508	hypothetical prote	
15	322.5	12.0	518 2 A40732	guanosine-diphosph	
16	171	6.3	628 2 A55421	nucleoside-triphos	
17	145.5	5.4	369 2 S77299	C4-dicarboxylase-b	
18	122.5	4.5	727 2 T47541	beta-galactosidase	
19	113	4.2	665 2 T18979	hypothetical prote	
20	107.5	4.0	307 2 T27332	hypothetical prote	
21	101.5	3.8	417 2 S53410	Mg2+ transporter h	
22	101.5	3.8	451 2 G59859	hypothetical prote	
23	101.5	3.8	716 2 T21516	hypothetical prote	
24	101	3.7	1415 2 A72369	(R)-2-hydroxygluta	
25	100	3.7	3848 2 T17414	TipC protein - sli	
26	99	3.7	473 2 T15986	hypothetical prote	
27	99	3.7	1951 2 B43963	RNA viral polymera	
28	98.5	3.7	536 2 B90195	hypothetical prote	
29	98.5	3.7	590 2 AB1411	autolysin, N-acety	

30	98.5	3.7	764	2	AB1695	p60-related protei
31	98.5	3.7	797	2	D86247	hypothetical prote
32	98.5	3.7	989	2	B84532	hypothetical prote
33	98.5	3.7	1509	2	B89985	hypothetical prote
34	98	3.6	371	2	T05213	hypothetical prote
35	97.5	3.6	392	2	A96738	hypothetical prote
36	97.5	3.6	402	2	A97743	penicillin-binding
37	97	3.6	494	2	T03774	probable histidine
38	97	3.6	4436	2	E71086	hypothetical prote
39	96.5	3.6	1013	2	JC2314	chitin synthase (E
40	96	3.6	883	2	B85725	probable fibrial
41	96	3.6	1028	2	I51173	myosin I beta - bu
42	96	3.6	1658	2	D86890	DNA-directed DNA p
43	95.5	3.5	461	2	G91228	probable permease
44	95.5	3.5	461	2	F86075	probable permease
45	95.5	3.5	591	2	F89770	hypothetical prote

ALIGNMENTS

RESULT 1

I56242

lymphoid cell activation antigen - human

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C:Accession: I56242

R:Maliszewski, C.R.; Delespesse, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.; J. Immunol. 153, 3574-3583, 1994

A>Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural ch

A:Reference number: I56242; MUID:95015846; PMID:7930580

A:Accession: I56242

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-510 <RES>

A:Cross-references: UNIPROT:P49961; GB:S73813; NID:G765255; PIDN:AAB32152.1; PID:G765255

C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 100.0%; Score 2698; DB 2; Length 510;

Best Local Similarity 100.0%; Pred. No. 4.1e-206;

Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYIGIVLDAGSSHT	60
Db	1	MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVGLTQNKALPENVKYIGIVLDAGSSHT	60
Qy	61	SLYIYKWPAAEKENDTGVVHVQVECRVKGPGISKVKQKNEIGIYLTDCMERAREVIPRSQ	120
Db	61	SLYIYKWPAAEKENDTGVVHVQVECRVKGPGISKVKQKNEIGIYLTDCMERAREVIPRSQ	120
Qy	121	HQETPVYLGATAGMRLRMSEELADRLVDVVERSLSNYPDFQGARIITGOEAGYGI	180
Db	121	HQETPVYLGATAGMRLRMSEELADRLVDVVERSLSNYPDFQGARIITGOEAGYGI	180
Qy	181	TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPQNQTIESPDNALQFR	240
Db	181	TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPQNQTIESPDNALQFR	240
Qy	241	LYGKDYNYVTHSFICYGKDQALWQKLADIQVASNEILRDCPFHGYKKVNVVSDLYKTP	300
Db	241	LYGKDYNYVTHSFICYGKDQALWQKLADIQVASNEILRDCPFHGYKKVNVVSDLYKTP	300
Qy	301	CTKRFEMTLPPQOEIIOGIGNYQOCHOSIIELEFNSTYCPYSQCAFNGIFLPLQDGFAG	360
Db	301	CTKRFEMTLPPQOEIIOGIGNYQOCHOSIIELEFNSTYCPYSQCAFNGIFLPLQDGFAG	360
Qy	361	SAFYFVMKFLNLTSEKVSQEKVTMMKFKCAQPWEEIKNTSYAGVKEKYLSEYCSGTIYL	420
Db	361	SAFYFVMKFLNLTSEKVSQEKVTMMKFKCAQPWEEIKNTSYAGVKEKYLSEYCSGTIYL	420
Qy	421	SLLLQGHFTADSWEHIFHGKIQSDAGWTGLGMLNLTNNIPAEQPLSTPLSHSTYVFL	480
Db	421	SLLLQGHFTADSWEHIFHGKIQSDAGWTGLGMLNLTNNIPAEQPLSTPLSHSTYVFL	480

p60-related protei  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
penicillin-binding  
probable histidine  
hypothetical prote  
chitin synthase (E  
probable fibrin  
myosin I beta - bu  
DNA-directed DNA p  
probable permealase  
probable permealase  
hypothetical prote



Query Match 16.9%; Score 455.5; DB 2; Length 630;  
Best Local Similarity 25.0%; Pred. No. 5.4e-28;  
Matches 139; Conservative 103; Mismatches 170; Indels 145; Gaps 25;

QY 46 NVKGVILDGAGSHSTSIYIKWP-----AEKENDTGV-----VHOVEECRVK-GPGI 91  
DB 7 NDRFGVIDAGSGSRHIVFKWQTESLLHATWQDSQSIQSQVPHIHQEKDWTFLKPL 66

QY 92 SKFVQKNE-IGIYLTDCMERAREVPRSQHQTTPVYLGATAGMRLLRMESEBELADRVLD 150  
DB 67 SFEKKPQDAYKSHIRPLDFAKNILPESHWSCPVFIQATAGMRL--PQDIQSSILD 123

QY 151 VVERSLNYPDP-----QGARIITGOBEGAYGWTITVYLLGKFSQKTRWFSIVPYETN 204  
DB 124 GLCQGL-KHPAEFLVEDCSAQIQVIDGETELGYGLGLNLYLGHFNYP-----EVS 175

QY 205 NQETFGALDGGASTQVTFVPQNO-----TIESPDNALQFRLYGKDYNYTH 251  
DB 176 DHTFGMDGGASTQIAFAPHDSGEIARHDDIATIFLRSVNGDLQ-----KWDVFS 229

QY 252 SFLCYGKQALMOKLARDIQVA-----SNEILRDPCHFPGYKVVNVSDLYKT 299  
DB 230 TWLFGCANQARRYLALINTLPENTNDYENDDFSTRNLNDPCMPRG-----SSTDF--- 281

QY 300 PCKTRFEMILPFOQFRIQIGIGNYQOCHOSILE-LFNYSYCPYSQCAFNGIFLPPLOGDF- 357  
DB 282 ----EPKDTI----FHAGSGNYEQCTKSIYPLLLKNMPCDDPCFLFNGVHAPRI--DFA 331

QY 358 ----CAFSAFYVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEI-----KTSYAGVKEK 407  
DB 332 NDKFICTSEYWTANDVFKLGG-YNFDKPSKLRFCNSNMTQILANSKDGYSNIPEN 390

QY 408 YLSEYCFSGTYILSLLOQY----HFTADSGWEIHH-----FTGKIQSGDAGTGLGYML-- 456  
DB 391 FLKDACFKGNVNLILHEGDFMPRIDVA-ENVNDRPLFQSVKEKVEERELSWTLGRILLY 449

QY 457 -----NLTNMPAE-----QPLSTPLSHSTYVFLMWLF 484  
DB 450 ASGSILAGNDRFMVGIAPSERRTKTKGKFIPOKLESDQLRKQSSLSNKGFLMWFAII 509

QY 485 SLVFLPTVAIGLLIFHK 501  
DB 510 CCIFY-----LIFHR 519

RESULT 5  
T40856  
probable nucleoside triphosphatase - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T40856  
R:Ramppeiger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1999  
A:Reference number: Z21952  
A:Accession: T40856  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-572 <RAM>  
A:Cross-references: UNIPROT:Q9USP2; EMBL:AL121783; PIDN: CAB57847.1; GSPDB: GN00068; SPDB:  
A:Experimental source: strain 972h-; cosmid cille10  
C:Genetics:  
A:Gene: SPDB:SPCC11E10.05c  
A:Map position: 3

Query Match 16.1%; Score 435.5; DB 2; Length 572;  
Best Local Similarity 26.7%; Pred. No. 1.8e-26;  
Matches 144; Conservative 77; Mismatches 168; Indels 151; Gaps 22;

QY 48 KYGIVLDAGSHSTSIYIKWPAEKEN-----DTGVVHVQVEECRVKGPGRISFV 95  
DB 4 KYGIFIDAGSGSRLLIYSDYDTQSSLSDKVKVPLIETIGDGGKWSLKVQPGISSFA 63

QY 96 QKVNEIG-IYLTDCMERAREVPRSQHQTTPVYLGATAGMRLLRMESEBELADRVLDVVER 154

DB 64 NNPKHVKKHLKELLDDFAAHPKDVHKETPVFLSATAGMRLIGVDAQ---NKILSHACR 120

QY 155 SL-SNYPDPF---QGARIITGOBEGAYGWTITVYLLGKFSQKTRWFSIVPYETNNOETP 209

DB 121 YIKKNYDFDIPNCSNIRVIDKAGBGYGLATNYLLTKLEK-----DTSTV 168

QY 210 GALDGGASTQVTF-VPONQTIESPD-----NALQFRLYGKDYNYTHSFLCYGK 258

DB 169 GFLDGGASVQAFELPPSQLNKYKDSISTVHIGLQNGOOL-----EYPLFTVTLGFGA 223

QY 259 DOALMOKLAKOTQVANSNEI---LRDPCFHPGKVVNVSDLYKTCTKRPMTLPPQOPE 315

DB 224 NEAYRYLLGLLIESENGKVGNTLSDPCSLRG-----RTYDIDGIE 263

QY 316 IOGIGNYQOCHOSILEFNYSY-CPYSQCAFNGIFLPPLOGDFGAFSAFYVMKFLNLTLS 374

DB 264 FAGTGDGLKQCLKTYLLNLNKKPCMDPCNFGISIPPV--DF-ANTEFVGSEFWYTTN 320

QY 375 EKVSQ-----EKVTEMMKKFCAQPWEI-----KTSYAGVKEKYLSEYCFSGTY 418

DB 321 DVFDMGGSYHFPNFYKKVDE---YCGTEWETMLSRLYNKELTPSTDENKLEKLCFKASW 376

QY 419 ILSLLLOQ-----YHFTADSGWEIHHFIKIQSGDAGTGLGYML 456

DB 377 ALNVLHEGFDVPKSNNTSSNDAKDGLSVIPAYHSPFTSLE-----KIERTEVSWTLGQVL 430

QY 457 NLTN-----MIPAEQPLSTPLSH-----STYVP-LMWLPSLVLF 489

DB 431 LYASNOQLLAKPEYANYNDPYGKLIASGKHMRLFPNKLFIISFIFCLFLPSLVLF 490

RESULT 6  
G84442  
probable nucleoside triphosphatase [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: G84442  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, L.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: G84442  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-516 <STO>  
A:Cross-references: UNIPROT:O80612; GB:AE002093; NID:g3461821; PIDN:AAC32915.1; GSPDB:G5;  
C:Genetics:  
A:Gene: At2g02970  
A:Map position: 2  
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 15.6%; Score 421; DB 2; Length 516;  
Best Local Similarity 26.5%; Pred. No. 2.2e-25;  
Matches 136; Conservative 81; Mismatches 236; Indels 60; Gaps 15;

QY 8 NVKTPCSKNILAILGFSIIAVIALVGLTQNKALPENKVIKIVLDAGSHSTSIYIKW 67

DB 27 NSKHAASNLLTVGSIISVVLGVFLCYGISLFGSGNLRGSLRYSVVVIDGSGTGRHVFY 86

QY 68 PAEKENDTGVVHVQVEECRVK-GPGISKFPQVKQNEIGIYLTDCMERAREVPRSQHQTTPV 126

DB 87 RIESGKPVFEPRGANYASLKULHPLGUSAFADDPDGASVSLTELVEFAKGRVPKGMETBV 146

QY 127 YLGATAGMRLLRMESEBELADRVLDVVERSL--SNYPDFQCGARIITGOBEGAYGWTITN 184

DB 147 RLMTAGMRLLELPQBE---KILGVAREVLKSSGFLFRDEWASVIGSGDEGYAMVAVNF 203

QY 185 LLGKFSQKTRWFSIVPYETNNOETFGALDGGASTQVTFVPQNTQIESPDNALQFRLYGK 244

DB 204 ALGSLG-----GDPLKTTGITVELGASQAQVTFVSSEPM--PPEFSRTISFGNV 249



C.Species: *Caenorhabditis elegans*  
 C.Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C.Accession: T16696  
 R.Miller, N.  
 submitted to the EMBL Data Library, October 1995  
 A.Description: The sequence of *C. elegans* cosmid R07E4.  
 A.Reference number: Z18561  
 A.Accession: T16696  
 A.Status: preliminary; translated from GB/EMBL/DBDJ  
 A.Molecule type: DNA  
 A.Residues: 1-557 <MIL>  
 A.Cross-references: EMBL:U39652; NID:g1049390; PID:g1049394; PIDN:AAA80403.1; CESP:R07E4  
 A.Experimental source: strain Bristol N2  
 C.Genetics:  
 A.Gene: CESP:R07E4.4  
 A.Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2

Query Match	14.7%	Score 397	DB 2	Length 557
Best Local Similarity	25.0%	Pred. No. 2e-23		
Matches 133	Conservative 96	Mismatches 218	Indels 86	Gaps 21
Qy	20	ILGRSIIATVIALLAGLTONKALPENV-----KYGIVLDAGSSHTSLYIKWPAEKEN	73	
Db	9	ILVASMIFFPVIYVVEAHTSPKVLADQERSYGVICDAGSTGTRLFVNNISTDS	68	
Qy	74	D-----TGVVHQVEECRVK- <u>GP</u> GISKFSVKVNEIGIYLTDCMERAREVIPSQHOETPVYL	128	
Db	69	ELIQIEPVIYDNKPWVKISPLGSLSTFGTKPAQAAEYLRPLMELAEHRHPIPEEKRPYTPVFI	128	
Qy	129	GATAGMRLLRMESEBLADRLVDVVERSLSN-----YPPDFQAGARIITGOEGAYGWIT	181	
Db	129	FATAGMRLLIPQEVYLVIGOK--EAVLKNLRNKLPKITSMQVLKEHIRITIEGKWEGIYSWIA	186	
Qy	182	INYLKGFSQ-KTRWFSIVPVETNNQETFFGALDGGASTOVTR-VPQNQTIES-----	232	
Db	187	VNYALGKFNKTATLDFPGTSPAHARQKTVGMIDMGASAQAFELPDTDSFSSINVENIN	246	
Qy	233	----PDNALQRLYCKQYNYVTHSPFLCYGKQQAQWQ---KLAKDIQVASNEILRDPCHF	285	
Db	247	LGCREDDSL-FK-----YKLFVTFYFLGVGVNEGIRKYEHMLLSKLKOONGTIVIQDDCML	300	
Qy	286	GKKVNVVSDLYKTPTCKRFEMTLPFQOFETQGTGNYQQCHQSILELNF-----TSYC--P	339	
Db	301	NLHKTVTLLEN-----GENFVRRTGNGNMTCSNEVKVLLNPESSEVCKAE	345	
Qy	340	YSQAFNGIFLP--PLOG-DFGAPSAFYVWKFLNLTSKYSQEKVEMMKKFCQAQWEE	396	
Db	346	AAKCYFGAVAPSPISLNIEWYGFSSEYVSTHDLVGLGGQYDAENIAKKTQQYCSKRWST	405	
Qy	397	I-----KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHTADSWEHIF--IGKTQGS	449	
Db	406	IQAESKKOLYPRADEERLRTCQPKSAWITSVLHDG--FSDVK-THNKFQSVSTIATGEVQ	462	
Qy	450	WTLGYML-----NLTNMIPAEQPLSTPLSHSTYVFLMWLFSLVFTVA	492	
Db	463	WALGAMIVHMRFFPLRDSRNRLIKETHSSSESIAWPLFFLSAYFVCLFVLVCA	515	

RESULT 10  
T39109  
probable guanosine-diphosphatase - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_reviation 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T39109  
R:Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D.  
submitted to the EMBL Data Library, October 1999  
A:Reference number: Z21828  
A:Accession: T39109  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-556 <BAR>  
A:Cross-references: UNIPROT:Q9UT35; EMBL:ALJ21741; PIDN:CAB57338.1; GSPDB:GN00066; SPDB:  
A:Experimental source: strain 972h; cosmid c824

C:Genetics:  
A:Gene: SPDS:SPAC824.08  
A:Map position: 1

Query Match	14.1%	Score 381.5;	DB 2;	Length 556;
Beat Local Similarity	27.1%	Pred. No. 3.4e-22;		
Matches 121;	Conservative 71;	Mismatches 181;	Indels 73;	Gaps 17;
Qy	48	KYGIVLGDAGSSHTSLYIKWPAEKENDTGVVHQVEE--CRVKGGPGLSKFVKQKNEIGIYL	105	
Db	133	QYVLMIDAGSTGRVHVYQF-----NNCNPSPKLBEFFKMIPEGLSSSFAGDPEGAAASL	187	
Qy	106	TDCHERAREVIPSQHOETPVYLGATAGMRLRMESBELADRVLDVVVERSLN-YPPDF-	163	
Db	188	DPLLDYAMENVPEYRRCSPIAVKATAG---LRLTGESEAKALKSVQRLHENDYFPPIV	244	
Qy	164	-QGARIITGOEGAYGHWITINYLKGFSPQKTRWFSIVPYETNNQETFGALDLGGASTQVT	222	
Db	245	KDGVSIILEGSMEGIYAWITINYLGLTGGA-----THSTVAVMDLGGASTQLV	293	
Qy	223	FVPQ-----NOTIESPNALQFRUYGKDYNVYTHSFLCYCKDQALWOKLADIOVASNEIL	278	
Db	294	FEPFASDGESLDVGDKHYLDVNGEQEYLYQHSILGYGLKEA--RKLHKFVLYNNAEL	351	
Qy	279	RD-----PCFHPGYKVVNVSDLYKTPCTKPEM-----TLPPQFQFIQGIG	320	
Db	352	KESLEHLGDSSTIIHPCFLH-----LNASLTHPDSKSEASEVVVFGPSLAHLSLQCRGIA	405	
Qy	321	NYQQCHQSILEFNTSYCPVSOCAFNIGIFLPLQDGF-----AFSAFYFMVKFNLMTSE	375	
Db	406	E-----KALYKDKNCVPKPSFNGVHQPKRETFTDPSYILSYFYFDRMISLGMPS-	456	
Qy	376	KVSOEKVTEMMKKFCQAP--WEEIKTSYAGVKE-KYLSBYCFSGTYILSLLLOQYHFTAD	432	
Db	457	TFETIEDMKYLANVCSGPTYQDAPSLTDALKELKEEPWCWLDLNMWISLSVGYEIPNN	516	
Qy	433	SWBHHIFPIKIQSDAGWTLYGYNLNL	458	
Db	517	--RQLHTAKKIDNKELGWCIGASLSM	540	

RESULT 11

54859  
nucleoside triphosphatase precursor, chromatin-associated - garden pea  
C:Species: Pisum sativum (garden pea)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S65147; S48859  
R:Haieh, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.  
Plant Mol. Biol. 30, 135-147, 1996  
A>Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated, chromatin-associated nucleoside triphosphatase precursor  
A:Reference number: S65141; MUID:96197404; PMID:8616230  
A:Accession: S65147  
A:Molecule type: mRNA  
A:Residues: 1-455 <HS2>  
A:Cross-references: UNIPROT:P52914; EMBL:Z32743; NID:G5G3611; PID:CAA83655.1; EMBL:Z32743; NID:G5G3611; PID:CAA83655.1; EMBL:Z32743; NID:G5G3611; PID:CAA83655.1  
C:Superfamily: nucleoside triphosphatase chromatin-associated  
C:Keywords: nucleus

	Query Match	13.9%	Score 374.5	DB 2	Length 455
	Best Local Similarity	25.6%	Pred. No. 9.1e-22		
	Matches 120	Conservative 80	Mismatches 177	Indels 91	Gaps 19
Qy	37	LTQNKAL---	PENVKYGIVLDAGSSHTSLYIKWPAEKENDTGVVH---	QVSECRVKGGP	90
Db	29	LTSRKIFLQKEB	ISSYAVFDAGSTGSRILHVHF-----	NONLDLHLHGKVGVEYNNKITGP	84
Qy	91	ISKFVQKVEIGIYL	TDCMERAREVIPSQHOETPVYLGATAGMRLLRMESELADRVLD	150	
Db	85	LSSYANNPEQA	AKSLIPLIEQAEVDVDDLPQKTPVRLGATAGLRLNGDASE---	KILQ	141
Qy	151	VVERSLN-YPDFQ-	GARIITQBEQAGWITINYLKGKFSQKTRWFSIVPYETNNQE	207	
Db	142	SVYRDLNSNSTEN	VPDAYSIIIDGTGEGSYLWTVNYALGNLGKK-----	YTK	189



QY 412 YCFSGTYILSLLOQYHFTADSWEHIFHGKIQGSD----AGWTLLGYMLNL-----TNMI 462  
 Db 393 LCMDLIYEVTLVDG--FGLNPKHEITVIHDVQKNYLVGAAWPLGCAIDLVSSTNKI 449

RESULT 14

T23508  
 hypothetical protein K08H10.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T23508  
 R:Gardner, A.  
 submitted to the EMBL Data Library, November 1996  
 A:Reference number: Z19750  
 A:Accession: T23508  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-479 <WIL>  
 A:Cross-references: UNIPROT:Q9XU84; EMBL:Z83113; PIDN:Z83113; GSPDB:GN00023; CESP:K08H10.4  
 A:Experimental source: clone K08H10  
 C:Genetics:  
 A:Gene: CESP:K08H10.4  
 A:Map position: 5  
 A:Introns: 36/3; 83/3; 189/1; 306/2; 412/3  
 C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 12.3%; Score 332; DB 2; Length 479;  
 Best Local Similarity 26.1%; Pred. No. 2.3e-18;  
 Matches 128; Conservative 80; Mismatches 211; Indels 72; Gaps 21;

QY 18 LAILGFSSIIAVIALAVLTQNKALPENVK----YGVILDGSSHTSYIYKW---PAE 70  
 Db 8 ILLISFFSLSVTTTKYQWCHGDGVLNQHCTCRFTTIVIDAGTGTRLHLYKFHIDPAI 67  
 QY 71 KENDTGVVHVEE---CRVKGIGSKFVQKNEIGIYLTDCMERAREVIPSQHOETPY 127  
 Db 68 ASH--GMPPKVEKEIQEVK-PCLSSFAKSPSSAADSLEPLQARKEVPHFMWKEPTIT 124  
 QY 128 LGATAGMRLRMESEBELADVLVDVVERSLSNYPF--DFOGA-RIITGOEGAYGWITIN 184  
 Db 125 LKATAGLRL---PGMADDILLESVEERIFNSGFPAAPDPAVNVMPGSDGVSFTLNI 181  
 QY 185 LGKG-FSQKTRWFSIVPYETNNQETFGALDLGASQTQVTFVPPQNTIESP-----DNALQF 239  
 Db 182 LLETLTIDE---PTVGHKPAARHSAVAFDLGGSTQLTYWPNNEAVFSEHVGVERDIDF 237  
 QY 240 RLYGKDVNYVTHSFILCYGKQALWQ--KLAKDIOVASNEILRDPCHFPGYKKVNVSDLY 297  
 Db 238 --FGHHIRLFTSHFLNGLIAARLNILQLETONEIESTHQLITSCMPEGYQ-----286  
 QY 298 KTPCTKRPFMTLPFQQFEOIGNYOOCHOSILELFTNSYCPYSQCAFNGIFLPLQGD 357  
 Db 287 ----LTEWEYALKFNWINGSSSHSPESCYGTNNFVESSEI-----MHRELKGS- 332  
 QY 358 GAFSAFYFVMKFLNL-----TSEKVSQEKVTMMKKFCAQPEBIKTSYAGVKEKYLSE 411  
 Db 333 PVYLSYPPDRALNSGLVKNEGGKIELRQFKEAAEIAACREKTEIDDG-----SHWMPW 387  
 QY 412 YCFSGTYILSLLOQYHFTADSWEHIFHGKIQGSDAGWTLLGYMLNLTMIP-ARQPLST 470  
 Db 388 QCLDLITYLSLRDGYQF--EDNQPLVLAKKIKGMEVSGOGLAFATANEFOLTEGAIKT 445  
 QY 471 PLS---HSTYV 478  
 Db 446 ALUSSEPNSTV 456

RESULT 15

A40732  
 guanosine-diphosphatase (EC 3.6.1.42) - yeast (Saccharomyces cerevisiae)  
 A:Alternate names: protein YEL042w  
 C:Species: Saccharomyces cerevisiae

C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C:Accession: A40732; B40732; S30837; S50502  
 R:Abeljon, C.; Yanagisawa, K.; Mandon, E.C.; Hausler, A.; Moremen, K.; Hirschberg, C.B.; J. Cell Biol. 122, 307-323, 1993  
 A:Title: Guanosine diphosphatase is required for protein and sphingolipid glycosylation  
 A:Reference number: A40732; MUID:93308137; PMID:8391537  
 A:Accession: A40732  
 A:Molecule type: protein  
 A:Residues: 1-518 <ABE>  
 A:Cross-references: UNIPROT:P32621; EMBL:L19560; NID:G349392; PIDN:AAA34656.1; PID:G349392  
 A>Note: sequence extracted from NCBI backbone (NCBIN:134708, NCBIP:134711)  
 A:Accession: B40732

A:Molecule type: DNA  
 A:Residues: 125-144; 238-257; 276-281; 366-374; 399-412 <AB2>  
 R:Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, submitted to the EMBL Data Library, February 1993  
 A:Reference number: S30812  
 A:Accession: S30837  
 A:Molecule type: DNA  
 A:Residues: 1-518 <MUL>  
 A:Cross-references: GB:U18779; EMBL:L10830; NID:G603625; PIDN:AAB65000.1; PID:G603637  
 R:Dietrich, F.S.

submitted to the EMBL Data Library, December 1994  
 A:Description: The sequence of S. cerevisiae cosmids 8199, 8334, and 9871.  
 A:Reference number: S50491  
 A:Accession: S50502

A:Molecule type: DNA  
 A:Residues: 1-518 <DIB>  
 A:Cross-references: EMBL:U18779; NID:G603625; PIDN:AAB65000.1; PID:G603637; MIPS:YEL042w

C:Genetics:  
 A:Gene: SGD:GDAL

A:Cross-references: SGD:S0000768; MIPS:YEL042w

A:Map position: 5L

C:Function:  
 A:Description: hydrolase

C:Superfamily: nucleoside triphosphatase chromatin-associated

C:Keywords: glycoprotein; Golgi apparatus; hydrolase; transmembrane protein

F:10-24/Domain: transmembrane #status predicted <TM>

F:41,280,335/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.0%; Score 322.5; DB 2; Length 518;  
 Best Local Similarity 26.6%; Pred. No. 1.5e-17;  
 Matches 123; Conservative 72; Mismatches 195; Indels 73; Gaps 20;

QY 34 AVGLTQNKALPENVKYGVILDGSSHTSLYTKWPAEKENDTVGVVHQVEECCRVKPGGISK 93  
 Db 78 AVKQTSQTCSEEHKYVIMIDAGTSGSRVHYIKPDVCTSPPTLL---DEKFDMLFPLGSS 134  
 QY 94 FVQKNEIGI--YLTDCMERAREVIPSQHOETPVYLGATAGMRL--RMESEBELADRLVD 150  
 Db 135 F--DTDSVGAANSLDPLLLKVAMNVVPIKARSCTPVAVKATAGLRLGLDAKSKILLSAVRD 192  
 QY 151 VVERSLSNYPF---DFQGARITGOEGAYGWITINYLKGFESQKTRWFSIVPYETNQOE 207  
 Db 193 HLEK---DYPPVVGEGVSGIMGGDEGVFAWITTYNLLGNIG-----ANGPK 237  
 QY 208 --TFGALDLGASQTQVTFVPO---NOTTESPDNALQFLYKDVNVYTHSFILCYG----257  
 Db 238 LPTAAVFDLGGSTQIVPEPTFPINEXMVDSEHKFDLKFGBENTLYQFSLHLYGLKSEGR 297  
 QY 258 --KQALWQKLAKDIOVASNE-----ILRDPCHFPGYKKVNVSDLYKTPCTKRPFMTLP 310  
 Db 298 NKVNSVLVENALKDGKILKGDNTKTHQLSPLCP---KVNATNEKVLTESK-----346  
 QY 311 FQQFEIOGIG---NYQQCHOSILELFTN-TSYCPYSQCAFNGIFLPLP-----QGDFGA 359  
 Db 347 -ETTYIDFIGPDEPSGAQCREFLTDEILNKDAQCSPPCSFNGVHQPSPVLRFTKESNDIYI 405  
 QY 360 PSAPYFVMKFLNLTSSEKVSQEKVTMMKKFC--AQPBEIKTSVAGVKEKYLSE--YCFS 415  
 Db 406 PSYFYDTRPLGMPPLSTLNE-LNDLARIYCKGETWNSVFSGIAGSLDELESDFCLD 464  
 QY 416 GTYILSLLOQYHFTADSWEHIFHGKIQGSDAGWTLLGYMLNL 458

Db 465 LSFQVLLHTGYDIPLQ--RELRTGKIKANKEICWCIGASLPL 505

Search completed: September 21, 2005, 16:21:57  
Job time : 29 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2005, 13:13:33 ; Search time 91 Seconds  
(without alignments)  
2869.894 Million cell updates/sec

Title: US-09-807-660C-2  
Perfect score: 2698  
Sequence: 1 MDDTKSNVKTFCRKNILAI.....VAIIIGLLIHPKSPFWKDMV 510

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2698	100.0	510	1 ENP1_HUMAN	P49961 homo sapien
2	2096	77.7	510	1 ENP1_MOUSE	P55772 mus musculus
3	2091	77.5	510	2 Q921Q6	Q921q6 mus musculus
4	2077	77.0	539	2 Q8CDV7	Q8cdv7 mus musculus
5	2057.5	76.3	511	1 ENP1_RAT	P97687 rattus norv
6	2006	74.4	510	1 ENP1_PIG	Q9myu4 sus scrofa
7	1993	73.9	372	2 Q86VW3	Q86vw3 homo sapien
8	1982.5	73.5	513	1 ENP1_BOVIN	O18956 bos taurus
9	1693	62.8	420	2 Q8CEB1	Q8ceb1 mus musculus
10	1552	57.5	508	2 Q6DFS1	Q6dfs1 xenopus tro
11	1530	56.7	508	2 Q6GP74	Q6gp74 xenopus lae
12	1373.5	50.9	492	2 Q6DC46	Q6dc46 brachydanio
13	1063.5	39.4	497	2 Q6UQ22	Q6uq22 mus musculus
14	1029.5	38.2	493	1 ENP1_CHICK	Q93295 gallus gall
15	1014.5	37.6	493	2 Q90X66	Q90x66 gallus gall
16	1004	37.2	495	1 ENP2_RAT	O35795 rattus norv
17	1001	37.1	495	1 ENP2_MOUSE	O55026 mus musculus
18	1001	37.1	495	2 Q921R1	Q921r1 mus musculus
19	982	36.4	454	2 Q6ZM69	Q6zm69 brachydanio
20	981.5	36.4	494	1 ENP2_CHICK	P79784 gallus gall
21	981	36.4	526	2 Q6GN44	Q6gna4 xenopus lae
22	975	36.1	502	2 Q6L64	Q6l64 brachydanio
23	973.5	36.1	455	2 Q7T014	Q7t014 brachydanio
24	950	35.2	500	2 Q6NV19	Q6nv19 xenopus tro
25	942.5	34.9	529	1 ENP3_HUMAN	O75355 homo sapien
26	940	34.8	458	2 Q6UVZ0	Q6uvz0 homo sapien
27	939.5	34.8	495	1 ENP2_HUMAN	Q9y5l3 homo sapien
28	937.5	34.7	529	2 Q80Z26	Q80z26 rattus norv
29	927	34.4	529	2 Q88FW6	Q88fw6 mus muscu
30	860.5	31.9	453	2 Q6ZM68	Q6zm68 brachyd
31	843.5	31.3	452	2 Q8N6K2	Q8n6k2 homo sapien

32	698.5	25.9	544	2 Q7YTA4	Q7yta4 schistosoma
33	629.5	23.3	300	2 Q8KOL2	Q8kol2 mus musculus
34	596.5	22.1	209	2 Q8UVX9	Q8uvx9 torpedo mar
35	511.5	19.0	483	2 Q9XI62	Q9xi62 arabidopsis
36	510.5	18.9	488	2 Q6NQA8	Q6nqa8 arabidopsis
37	499	18.5	503	2 Q94AP8	Q94ap8 arabidopsis
38	499	18.5	503	2 Q8H1D8	Q8hid8 arabidopsis
39	492	18.2	537	2 Q6Z543	Q6z543 oryza sativ
40	490	18.2	336	2 Q8CCV2	Q8ccv2 mus musculus
41	488	18.1	634	2 Q6FRC2	Q6frc2 candida gla
42	486	18.0	555	2 Q94E22	Q94e22 arabidopsis
43	482.5	17.9	611	2 Q6DH30	Q6dh30 brachydanio
44	480	17.8	555	2 Q80612	Q80612 arabidopsis
45	469.5	17.4	405	2 Q9M9T7	Q9m9t7 arabidopsis

ALIGNMENTS

RESULT 1  
ENP1\_HUMAN STANDARD; PRT; 510 AA.  
AC P49961; Q9UQ09; Q9Y3Q9;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)  
DE (NTPDase1) (ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell  
activation antigen) (Ecto-apyrase) (CD39 antigen).  
GN Name=ENTPDI; Synonym=CD39;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM VASCULAR).  
RX MEDLINE=95015846; PubMed=7930580;  
RA Maliszewski C.R., Delespesse G.J.T., Schoenborn M.A., Armitage R.J.,  
RA Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K.,  
RA Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III;  
RT "The CD39 lymphoid cell activation antigen. Molecular cloning and  
structural characterization.";  
RT J. Immunol. 153:3574-3583(1994).  
RL [2]  
RP SEQUENCE FROM N.A. (ISOFORM VASCULAR).  
RX TISSUE=Umbilical vein;  
RC MEDLINE=97149443; PubMed=8996251;  
RX Robson S.C., Kacmarek E., Siegel J.B., Candinas D., Koziak K.,  
RA Millan M., Hancock W.W., Bach F.H.;  
RT "Loss of ATP diphosphohydrolase activity with endothelial cell  
activation.";  
RL J. Exp. Med. 185:153-163(1997).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND PLACENTAL II).  
RX TISSUE=Placenta;  
RC MEDLINE=93332082; PubMed=10405171; DOI=10.1016/S0014-5793(99)00751-6;  
RA Tateumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T.,  
RA Titani K., Fujimura Y., Narita N.;  
RT "The cDNA cloning of human placental ecto-ATP diphosphohydrolases I  
and II.";  
RT FEBS Lett. 453:335-340(1999).  
RL [4]  
RP SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.  
RX TISSUE=Placenta;  
RC MEDLINE=96096723; PubMed=8529670;  
RA Christoforides S., Papamarcaki T., Galaris D., Kellner R., Tsolas O.;  
RT "Purification and properties of human placental ATP  
diphosphohydrolase.";  
RL Eur. J. Biochem. 234:66-74(1995).  
RN [5]  
RP SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND  
RP 399-405 (ISOFORM PLACENTAL I).  
RC TISSUE=Placenta;

RX MEDLINE=99062444; PubMed=9846014;  
 RA Makita K., Shimoyama T., Sakurai Y., Yagi H., Matsumoto M., Narita N.,  
 RA Sakamoto Y., Saito S., Ikeda S., Suzuki M., Titani K., Fujimura Y.;  
 RT "Placental ecto-ATP diphosphohydrolase: its structural feature  
 RT distinct from CD39, localization and inhibition on shear-induced  
 RT platelet aggregation.";  
 RL Int. J. Hematol. 68:297-310(1998).  
 RN [6].  
 RP FUNCTION.  
 RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;  
 RA Kaczmarek E., Koziak K., Sevigny J., Siegel J.B., Anrather J.,  
 RA Beaudoin A.R., Bach F.H., Robson S.C.;  
 RT "Identification and characterization of CD39/vascular ATP  
 RT diphosphohydrolase.";  
 RL J. Biol. Chem. 271:33116-33122(1996).  
 RN [7].  
 RP CHARACTERIZATION.  
 RX MEDLINE=96215267; PubMed=8626624; DOI=10.1074/jbc.271.17.10391;  
 RA Wang T.F., Guidotti G.;  
 RT "CD39 is an ecto-(Ca2+, Mg2+)-ATPase.";  
 RL J. Biol. Chem. 271:9898-9901(1996).  
 RN [8].  
 RP PALMITOYLATION.  
 RX MEDLINE=20102721; PubMed=10636909; DOI=10.1074/jbc.275.3.2057;  
 RA Koziak K., Kaczmarek E., Kittel A., Sevigny J., Blusztajn J.K.,  
 RA Schulte Am Esch J. II, Inai M., Guckelberger O., Goepfert C., Qawi I.,  
 RA Robson S.C.;  
 RT "Palmitoylation targets CD39/endothelial ATP diphosphohydrolase to  
 RT caveolae.";  
 RL J. Biol. Chem. 275:2057-2062(2000).  
 CC -I- FUNCTION: In the nervous system, could hydrolyze ATP and other  
 CC nucleotides to regulate purinergic neurotransmission. Could also  
 CC be implicated in the prevention of platelet aggregation.  
 CC Hydrolyzes ATP and ADP equally well.  
 CC -I- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.  
 CC -I- COFACTOR: Requires calcium and magnesium.  
 CC -I- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -I- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=Vascular;  
 CC IsoId=P49961-1; Sequence=Displayed;  
 CC Name=Placental I;  
 CC IsoId=P49961-2; Sequence=VSP\_003607;  
 CC Name=Placental II;  
 CC IsoId=P49961-3; Sequence=VSP\_003608, VSP\_003609;  
 CC -I- TISSUE SPECIFICITY: Expressed primarily on activated lymphoid  
 CC cells. Also expressed in endothelial tissues. The vascular isoform  
 CC and the placental isoform II are present in both placenta and  
 CC umbilical vein, whereas placental isoform I is present in placenta  
 CC only.  
 CC -I- PTM: The N-terminus is blocked.  
 CC -I- MISCELLANEOUS: Optimal pH is 7.0-7.5 with ATP as substrate and  
 CC 7.5-8.0 with ADP.  
 CC -I- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.  
 CC -I- DATABASE: NAME=PROW; NOTE=CD guide CD39 entry; htm".  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd39.htm".  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL; S73813; AAB32152.1; -;  
 CC EMBL; U87967; AAB47572.1; -;  
 CC EMBL; AJ133133; CAB41886.1; -;  
 CC EMBL; AJ133134; CAB41887.1; -;  
 CC PIR; I56242; I56242.  
 CC Genew; HGNC:3363; ENTPD1.  
 CC MIM; 601752; -;.

DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0007596; P:blood coagulation; TAS.  
 DR InterPro; IPR000407; GDAL\_CD39\_NTPase.  
 DR Pfam; PF01150; GDAL\_CD39; 1.  
 DR PROSITE; PS01238; GDAL\_CD39\_NTPASE; 1.  
 KW Alternative splicing; Antigen; Calcium; Direct protein sequencing;  
 KW Glycoprotein; Hydrolase; Lipoprotein; Magnesium; Palmitate;  
 KW Transmembrane.  
 FT DOMAIN 1 16 Cytoplasmic (Potential).  
 FT TRANSMEM 17 37 Potential.  
 FT DOMAIN 38 478 Extracellular (Potential).  
 FT TRANSMEM 479 499 Potential.  
 FT DOMAIN 500 510 Cytoplasmic (Potential).  
 FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 457 457 N-linked (GlcNAc...) (Potential).  
 FT VARSPLIC 1 4 MEDT -> MKGTCKDLTSQQ (in isoform Placental  
 FT I and isoform Placental II).  
 FT VARSPLIC 272 299 /FTID=VSP\_003607.  
 FT VARSPLIC 272 299 VASNEILRDPCHFGYKVKVNVSDLYKT -> ASITQSRPA  
 FT PFTSAPPAPTSCCLFQIQ (in isoform Placental  
 FT II).  
 FT /FTID=VSP\_003608.  
 FT VARSPLIC 300 510 Missing (in isoform Placental II).  
 FT CONFLICT 57 58 SS -> G (in Ref. 5).  
 FT CONFLICT 162 162 D -> K (in Ref. 4).  
 FT CONFLICT 208 208 T -> TGET (in Ref. 5).  
 FT CONFLICT 248 248 V -> Y (in Ref. 5).  
 SQ SEQUENCE 510 AA; 57964 MW; BAD87D2499649159 CRC64;  
 Query Match 100.0%; Score 2698; DB 1; Length 510;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-195;  
 Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEDTKESNVKTCCKNLAIFGSSIIAIVALLVGLTQNKALPENVKYGVILDGSSHT 60  
 DB 1 MEDTKESNVKTCCKNLAIFGSSIIAIVALLVGLTQNKALPENVKYGVILDGSSHT 60  
 QY 61 SLVIYKWPAAKENDTGVDVHVEECRVKPGIGSKFQKVNEIGIYLTDCMERAREVIPSQ 120  
 DB 61 SLVIYKWPAAKENDTGVDVHVEECRVKPGIGSKFQKVNEIGIYLTDCMERAREVIPSQ 120  
 QY 121 HQETPVYLGATAGMRLLRMESEBELADRVLDVVVERSLSNYPDFQGARITGOEAGYGI 180  
 DB 121 HQETPVYLGATAGMRLLRMESEBELADRVLDVVVERSLSNYPDFQGARITGOEAGYGI 180  
 QY 181 TINYLLGKFSQKTRWFISIVPYETNNQETFGALDLGGASTQVTFVPQNOTIESPDNALQFR 240  
 DB 181 TINYLLGKFSQKTRWFISIVPYETNNQETFGALDLGGASTQVTFVPQNOTIESPDNALQFR 240  
 QY 241 LYGKDVNVYTHSFLCYGKQDALWQKLAKDIQVASNEILRDPCHFGYKVKVNVSDLYKTP 300  
 DB 241 LYGKDVNVYTHSFLCYGKQDALWQKLAKDIQVASNEILRDPCHFGYKVKVNVSDLYKTP 300  
 QY 301 CTKRFEMLTPFQOFIEIGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPLPQGFAG 360  
 DB 301 CTKRFEMLTPFQOFIEIGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPLPQGFAG 360  
 QY 361 SAFYFVWKFLNLTSEKVSQEKTEWKKCAQPWEEKTSYAGVKEKYLSEYCFSGTYIL 420  
 DB 361 SAFYFVWKFLNLTSEKVSQEKTEWKKCAQPWEEKTSYAGVKEKYLSEYCFSGTYIL 420  
 QY 421 SLLLOQYHFTADSWEHIFIGIKIQGSDAGWTLGYMLNLNMI PAEQPLSTPLSHSYVFL 480  
 DB 421 SLLLOQYHFTADSWEHIFIGIKIQGSDAGWTLGYMLNLNMI PAEQPLSTPLSHSYVFL 480  
 QY 481 MYLFSLVLFVTAIIIGLLIFHKPSYFWKDW 510  
 DB 481 MYLFSLVLFVTAIIIGLLIFHKPSYFWKDW 510

## RESULT 2

ENP1\_MOUSE STANDARD; PRT; 510 AA.

AC P55772; (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 44, Last annotation update)

DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)

DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell activation antigen) (Ecto-apyrase) (CD39 antigen).

GN Name=Entpdi; Synonyms=CD39;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]\_SEQUENCE FROM N.A.

RP MEDLINE=95015846; PubMed=7930580;

RX Maliszewski C.R., Delespasse G.J.T., Schoenborn M.A., Armitage R.J., Fangelow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K., Birke C., Alpert D., Friend D., Gimpel S.D., Gayle R.B. III; "The CD39 lymphoid cell activation antigen. Molecular cloning and structural characterization."; J. Immunol. 153:3574-3583(1994).

RL [2]

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvJ;

RX MEDLINE=98399871; PubMed=9730622;

RA Schoenborn M.A., Jenkins N.A., Copeland N.G., Gilbert D.J., Gayle R.B. III, Maliszewski C.R.; "Gene structure and chromosome location of mouse Cd39 coding for an ecto-apyrase."; Cytogenet. Cell Genet. 81:287-289(1998).

RL FUNCTION: In the nervous system, could hydrolyze ATP and other nucleosides to regulate purinergic neurotransmission. Could also be implicated in the prevention of platelet aggregation.

CC Hydrolyzes ATP and ADP equally well.

CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.

CC -!- COFACTOR: Requires calcium and magnesium (By similarity).

CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC

DR EMBL; AF037366; AAC92259.1; -;

DR EMBL; AF041818; AAC83203.1; -;

DR EMBL; AF041812; AAC83203.1; JOINED.

DR EMBL; AF041813; AAC83203.1; JOINED.

DR EMBL; AF041814; AAC83203.1; JOINED.

DR EMBL; AF041815; AAC83203.1; JOINED.

DR EMBL; AF041816; AAC83203.1; JOINED.

DR EMBL; AF041817; AAC83203.1; JOINED.

DR MGD; MGI:102805; Entpdi.

DR GO; GO:0005605; C:basal lamina; IDA.

DR GO; GO:0004050; P:ATPase activity; IDA.

DR GO; GO:0006200; P:ATP catabolism; IDA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IDA.

DR GO; GO:00030168; P:platelet activation; IDA.

DR GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.

DR InterPro; IPR000407; GDA1\_CD39\_NTPase.

DR Pfam; PF01150; GDA1\_CD39\_1.

DR PROSITE; PS01238; GDA1\_CD39\_NTPASE; 1.

KW Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.

FT DOMAIN 1 16 Cytoplasmic (Potential).

FT	TRANSMEM	17	37	Potential.
FT	DOMAIN	38	478	Extracellular (Potential).
FT	TRANSMEM	479	499	Potential.
FT	DOMAIN	500	510	Cytoplasmic (Potential).
FT	CARBOHYD	73	73	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	226	226	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	291	291	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	333	333	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	428	428	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	457	457	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	510 AA;	57205 MW;	8EGA6113D2E13930 CRC64;

Query Match 77.7%; Score 2096; DB 1; Length 510;

Best Local Similarity 76.0%; Pred. No. 5.4e-150;

Matches 389; Conservative 53; Mismatches 66; Indels 4; Gaps 3;

QY 1 MEDTKESNVKTFCSKNILAILGFSIIIAVIALAVLQNKALPENVKYGVILVDASSHT 60

Db 1 MEDIKDSVKRFCSKNILILIGFTSILAVIALVGLTQNKLPENVKYGVILVDASSHT 60

QY 61 SLIYKPAEKENDTGVVHVQVECRVKGPGISKFKVQKNEIGIYLTDCMERAREVIPSQ 120

Db 61 NLIYKPAEKENDTGVVQQLBECQVKGPGISKYAKTDEIGAYLAECMELSTELIPTSK 120

QY 121 HOETPVYLGATAGMRLMESEELADRLDVVERSLNYPDFQAGARIITGOEEGAYWI 180

Db 121 HHQTPVYLGATAGMRLMESEQSADVLAAVSTSLKSYPPDFQGAIIITGOEEGAYWI 180

QY 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVQNTQIESPDNALQPR 240

Db 181 TINYLLGRFTQEQSWLSLIS-DSQKQETFGALDGGASTQITFVQNSTIESPNSLQPR 239

QY 241 LYGDYNYVTHSFLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGYKVVVNSDLYKTP 300

Db 240 LYGEDYTYVTHSFLCYGKQDQALWQKLAKDIOVSSGGVLKDCFCNFGYKVVVNSLYGTP 299

QY 301 CTKRPEMTLPQQFPIQIGNYQQCHQSILELNTSYCPYSCAFNGIPLPLQSGDFGAF 360

Db 300 CTKRFEKLLPFDQFRIQGTGDEYEQCHQSILELNNSHCPYSCAFNGVPLPLHGSFGAF 359

QY 361 SAFYVPMKFLNLTSEK--VSQEKTEMKKCAQPMEEIKTSYAGVKEKYLSEYCFSGTY 418

Db 360 SAFYVPMDFFKVAKNSVISQEKMTETIKNFCSKSWEETKTSYSPVKEKYLSEYCFSGAY 419

QY 419 ILSLLQGYHTFADSWEHIFIGIQSDAGWTLGYMLNLTNMIAPQPLSLPSSHSTYV 478

Db 420 ILS-LLQGYNTDSSWEQIHFGKIKDSNAGWTLGYMLNLTNMIAPQPLSLPSSHSTYI 478

QY 479 FLMLVLSVLFTVAIIGLLIFHKPSYFWKDWY 510

Db 479 GLMWLFSLLVAVAITGLFIYKPSYFWKEAV 510

## RESULT 3

Q921Q6 PRELIMINARY; PRT; 510 AA.

AC Q921Q6;

DT 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE Entpdi protein.

GN Name=Entpdi;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C2ECH II; TISSUE=Mammary tumor;

RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,



RA	Saito R., Saïto H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA	Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA	Takawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tanaka T.,
RA	Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AK029512; BAC26486.1; -
DR	MGI; 102805; Entpd1.
DR	GO; GO:0005605; C:basal lamina; IDA.
DR	GO; GO:0016021; C:integral to membrane; TAS.
DR	GO; GO:0004050; F:apyrase activity; IDA.
DR	GO; GO:0006200; P:ATP catabolism; IDA.
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IDA.
DR	GO; GO:0030168; P:platelet activation; IDA.
DR	GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.
DR	InterPro; IPR000407; GDA1_CD39_NTPase.
DR	Pfam; PF01150; GDA1_CD39_1.
DR	PROSITE; PS01238; GDA1_CD39_NTPase; 1.
KW	Hydrolase.
SQ	SEQUENCE. 539 AA; 60590 MW; 49565788313321F4 CRC64;
Query Match 77.0%; Score 2077; DB 2; Length 539;	
Best Local Similarity 75.8%; Pred. No. 1.6e-148;	
Matches 385; Conservative 54; Mismatches 65; Indels 4; Gaps 3;	
QY.	5 KESNVTFCNKILAILGSSIIAVIALAVGLTQNKALPENVKYGVILV DAGSSHTSLYI 64
Db	34 QDSKVRKFCNKILILGTSIATLAVIALAVGLTQNKPLPENVKYGVILV DAGSSHTSLYI 93
QY	65 YKMPAEKENDTGTVHGVCEKRVKPGISKVFQKVEIGLYLTDCMERAREVTPROHQHT 124
Db	94 YKMPAEKENDTGTVVQLEECQVKPGISKYAKTQDTEIGAYLAECELMSTELIPTSKHQHT 153
QY	125 PVYLGATAGMRLRMSEBELADRVLDVVERSLNYPFPDQGARITITQGEAGYGMTTNY 184
Db	154 PVYLGATAGMRLRMSESEQADEVLAAVSTSLKSYFPDFQGAKIITQGEAGYGMTTNY 213
QY	185 LLGKFSQKTRFSPVYPYNNQETFGALDVGASTQVTPVQNTIESPDNALQRLYCK 244
Db	214 LLGRTFQEOSMLSLIS-DSQKQETFGALDVGASTQITFVPQNSTIESPENSLOFRLYGE 272
QY	245 DYNVYTHSPLCYKQDQALQKLAQIOVASNRIIDPCPHCYKVVNVSDLYKTPCTKR 304
Db	273 DTVYTHSPLCYKQDQALQKLAQIQSSGGVLDKPCPNPYKVVNVSELYGTPCTKR 332
QY	305 FEMTLFPQOFETQIGNYQQCHSILELFTNTSCYPYSQAFNGIFLPLQGDGFGAFSAFY 364
Db	333 FEKKLPFDQFRQGTGDYEQCHSILELFPNNHCPYSQAFNGVFLPLHGSFGAFSAFY 392
QY	365 FWMKFLNLTSEK--VSQEKVTEMKKFCAQPWEEIKTSYAGVKYLSYCFSGTYILSL 422
Db	393 FVMDFFKVKAKNSVISQEKWTEITKNFCSKSWETKTSYPSVKEKYLSEYCPSGAYILS- 451
QY	423 LLQGYHTADSWEHITFTGKIQSGDAGWTLGYMLNLTNMIPAEOPLSPLSHSTYVFLMV 482
Db	452 LLQGYNFTDSSWEQHFHMGKIKDSNAGWTLGYMLNLTNMIPAEQPLSPPLPHSTYVGLMV 511
QY	483 LFSVLFTVAITGLLIHFHKPSYFWMKMV 510
Db	512 LFSLLLVAVAITGLLIYKPSYFWMKEAV 539
RESULT 5	
ENP1 RAT	
ID	ENP1 RAT STANDARD; PRT; 511 AA.
AC	P97687.
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DE	Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE	(NTPDase) (Ecto-ATP diphosphohydrolase) (ATPDase)
DE	activation antigen) (Ecto-apyrase) (CD39 antigen).
GN	Name=Entpd1; Synonyms=Cd39;
OS	Rattus norvegicus (Rat).

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RP	[1] SEQUENCE FROM N.A., AND CHARACTERIZATION
RC	STRAIN=Sprague-Dawley; TISSUE=Brain, and Hippocampus;
RX	PubMed=9221928;
RA	Wang T.-F., Rosenberg P.A., Guidotti G.;
RT	"Characterization of brain ecto-apyrase: evidence for only one ecto-
RT	apyrase (CD39) gene.";
RL	Brain Res. Mol. Brain Res. 47:295-302(1997).
RN	[2] SEQUENCE FROM N.A.
RP	STRAIN=Wiistar; TISSUE=Cochlea;
RX	MEDLINE=20050856; PubMed=10581401; DOI=10.1016/S0169-328X(99)00244-2;
RA	Vlajkovic S.M., Housley G.D., Greenwood D., Thorne P.R.;
RT	"Evidence for alternative splicing of ecto-ATPase associated with
RT	termination of purinergic transmission.";
RL	Brain Res. Mol. Brain Res. 73:85-92(1999).
RN	[3] SEQUENCE OF 432-511 FROM N.A.
RP	STRAIN=Sprague-Dawley; TISSUE=Brain;
RX	MEDLINE=98031057; PubMed=9364474; DOI=10.1016/S0028-3908(97)00115-9;
RA	Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.;
RT	"An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
RT	rat brain.";
RL	Neuropharmacology 36:1189-1200(1997).
CC	- - FUNCTION: In the nervous system, could hydrolyze ATP and other
CC	nucleotides to regulate purinergic neurotransmission. Could also
CC	be implicated in the prevention of platelet aggregation.
CC	Hydrolyzes ATP and ADP equally well.
CC	- - CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC	- - COFACTOR: Requires calcium and magnesium.
CC	- - SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC	- - SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC	- - TISSUE SPECIFICITY: Expressed in primary neurons and astrocytes,
CC	kidney, liver, muscle, thymus, lung and spleen.
CC	- - PTM: N-glycosylated.
CC	- - SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; U81295; AAC53195.1; -
DR	EMBL; Y15685; CAA75730.1; -
DR	RGD; 69265; Entpd1.
DR	InterPro; IPR000407; GDA1_CD39_NTPase.
DR	Pfam; PF01150; GDA1_CD39_1.
DR	PROSITE; PS01238; GDA1_CD39_NTPase; 1.
KW	Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.
FT	DOMAIN 1 16 Cytoplasmic (Potential).
FT	TRANSMEM 17 37 Extracellular (Potential).
FT	DOMAIN 38 478 Potential.
FT	TRANSMEM 479 499 Potential.
FT	DOMAIN 500 511 Cytoplasmic (Potential).
FT	CARBOHYD 73 73 N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD 226 226 N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD 291 291 N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD 333 333 N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD 374 374 N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD 429 429 N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD 458 458 N-linked (GlcNAc. . .) (Potential).
FT	CONFLICT 332 332 F -> L (in Ref. 2).
SQ	SEQUENCE 511 AA; 57408 MW; 4CC123D3B564C193 CRC64;
Query Match 76.3%; Score 2057.5; DB 1; Length 511;	
Best Local Similarity 74.2%; Pred. No. 4.5e-147;	
Matches 380; Conservative 58; Mismatches 71; Indels 3; Gaps 3;	

```

QY 1 MEDTKESNVKTCCKNLAIFGSSIIAVIALVGLTQNKALPENVKYGVILDAGSSHT 60
DB 1 MEDIKDSKVRKFCCKNLAIFGSSIIAVIALVGLTQNKALPENVKYGVILDAGSSHT 60
QY 61 SLVIYKWPAAEKENDTGVVHVEECRVKPGISKVFQKNEIGIYLTDCMERAREVIPSQ 120
DB 61 NLYIYKWPAAEKENDTGVVHVEECRVKPGISKVFQKNEIGIYLTDCMERAREVIPSQ 120
QY 121 HQETPVYLGATAGMRLRLMESEBELADRLVDVVERSLSNYPFFDQGARITITQEGEGAYGI 180
DB 121 HQETPVYLGATAGMRLRLMESEBELADRLVDVVERSLSNYPFFDQGARITITQEGEGAYGI 180
QY 181 TYNILGKFSOKTRWESIVPYETNNQETFGALDLGGASTQVTPVPONOTIESPDNALQFR 240
DB 181 TYNILGKFSOKTRWESIVPYETNNQETFGALDLGGASTQVTPVPONOTIESPDNALQFR 240
QY 241 LYGKDYNNVYTHSPCLCYGKQDQALWQKLAKDQIVASNEILRDPFCFHPGYKKVNVVSDLYKTP 300
DB 241 LYGKDYNNVYTHSPCLCYGKQDQALWQKLAKDQIVASNEILRDPFCFHPGYKKVNVVSDLYKTP 300
QY 301 CTYKRFEMTLPFOQFETQGIQGNVQOCHQSILELENTSCYPSQCAFNGIFLPPLOQDFGAF 360
DB 301 CTYKRFEMTLPFOQFETQGIQGNVQOCHQSILELENTSCYPSQCAFNGIFLPPLOQDFGAF 360
QY 361 SAFYFVWKEL-NLTSEKV-SOEKVTMMKKFCAQWEEIKTSYAGVKEKYLSEYCFSGTY 418
DB 361 SAFYFVMDFFKWNDSVSOEKVETITKNFCSPWEEVKASPTVKEKYLSEYCFSGTY 419
QY 419 ILSLLQGYHFTADSEWHIFIKIGIQSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTTV 478
DB 419 ILSLLQGYHFTADSEWHIFIKIGIQSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTTV 478
QY 479 FLMLVLSVLFTVAITGLLIFHKPSYFWKDMV 510
DB 479 FLMLVLSVLVAMVITGLFIFSKPSYFWKEAV 511
RESULT 6
ENP1_PIG STANDARD; PRT; 510 AA.
AC QSMYU4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
DE Name=ENTPD1; Synonyms=CD39;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart endothelium;
RX MEDLINE=20325090; PubMed=10866813;
RA Lemmens R., Vandutzel L., Kittel A., Beaudoin A.R., Benrezzak O.,
RA Seigny J.;
RA "Distribution, cloning, and characterization of porcine nucleoside
RT triphosphate diphosphohydrolase-1."
RL Eur. J. Biochem. 267:4106-4114(2000).
RN [2]
RP SEQUENCE OF 202-220.
RC TISSUE=Pancreas;
RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
RA Kaczmarek E., Koziak K., Seigny J., Siegel J.B., Anrather J.,
RA Beaudoin A.R., Bach F.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
RT diphosphohydrolase."
RL J. Biol. Chem. 271:33116-33122(1996).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also

```

```

CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Highest expression found in vascular
CC endothelium, smooth muscle, spleen and lung.
CC -!- PTM: Cleaved into two polypeptides that seem to stay together by
CC noncovalent interactions.
CC -!- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ131746; CAB95871.1; -.
CC InterPro; IPR000407; GDAL_CD39_NTPase.
CC Pfam; PF01150; GDAL_CD39; 1.
CC PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
CC Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
CC Magnesium; Transmembrane.
CC CHAIN 1 510 Ectonucleoside triphosphate
CC CHAIN 1 201 diphosphohydrolase 1.
CC CHAIN 202 510 Ectonucleoside triphosphate
CC CHAIN 202 510 diphosphohydrolase 1 27 kDa subunit.
CC CHAIN 202 510 Ectonucleoside triphosphate
CC CHAIN 202 510 diphosphohydrolase 1 54 kDa subunit.
CC CHAIN 202 510 Cytoplasmic (Potential).
CC CHAIN 202 510 Potential.
CC CHAIN 202 510 Extracellular (Potential).
CC CHAIN 202 510 Potential.
CC CHAIN 202 510 Cytoplasmic (Potential).
CC CHAIN 202 510 N-linked (GlcNAc. .) (Potential).
CC CHAIN 202 510 N-linked (GlcNAc. .) (Potential).
CC CHAIN 202 510 N-linked (GlcNAc. .) (Potential).
CC CHAIN 202 510 N-linked (GlcNAc. .) (Potential).
CC CHAIN 202 510 N-linked (GlcNAc. .) (Potential).
CC CHAIN 202 510 N-linked (GlcNAc. .) (Potential).
CC CHAIN 202 510 N-linked (GlcNAc. .) (Potential).
CC CHAIN 202 510 N-linked (GlcNAc. .) (Potential).
CC CHAIN 202 510 G -> S (in Ref. 2).
CC SEQUENCE 510 AA; 57757 MW; 82F86869040D7735 CRC64;
Query Match 74.4%; Score 2006; DB 1; Length 510;
Best Local Similarity 72.0%; Pred. No. 3.5e-143;
Matches 368; Conservative 69; Mismatches 72; Indels 2; Gaps 2;
QY 1 MEDTKESNVKTCCKNLAIFGSSIIAVIALVGLTQNKALPENVKYGVILDAGSSHT 60
DB 1 MEDRESELKTCCKNLAIFGSSIIAVIALVGLTQNKALPENVKYGVILDAGSSHT 60
QY 61 SLVIYKWPAAEKENDTGVVHVEECRVKPGISKVFQKNEIGIYLTDCMERAREVIPSQ 120
DB 61 SLVIYKWPAAEKENDTGVVHVEECRVKPGISKVFQKNEIGIYLTDCMERAREVIPSQ 120
QY 121 HQETPVYLGATAGMRLRLMESEBELADRLVDVVERSLSNYPFFDQGARITITQEGEGAYGI 180
DB 121 HQETPVYLGATAGMRLRLMESEBELADRLVDVVERSLSNYPFFDQGARITITQEGEGAYGI 180
QY 181 TYNILGKFSOKTRWESIVPYETNNQETFGALDLGGASTQVTPVPONOTIESPDNALQFR 240
DB 181 TYNILGKFSOKTRWESIVPYETNNQETFGALDLGGASTQVTPVPONOTIESPDNALQFR 240
QY 241 LYGKDYNNVYTHSPCLCYGKQDQALWQKLAKDQIVASNEILRDPFCFHPGYKKVNVVSDLYKTP 300
DB 241 LYGKDYNNVYTHSPCLCYGKQDQALWQKLAKDQIVASNEILRDPFCFHPGYKKVNVVSDLYKTP 300
QY 301 CTYKRFEMTLPFOQFETQGIQGNVQOCHQSILELENTSCYPSQCAFNGIFLPPLOQDFGAF 360
DB 301 CTYKRFEMTLPFOQFETQGIQGNVQOCHQSILELENTSCYPSQCAFNGIFLPPLOQDFGAF 360

```

```
Db 300 CTRRFLTSLPFPELETQGTGDFOKCOQSIRPLNTSYCPYSRCSFDCVFLPLPQGDFAAP 359
QY 361 SAFYFVMKFLNLTSEKVS-QEKVTMMKKFCAQPWEIKTSYAGVKEKYLSEYCFSGTYI 419
Db 360 SAFYFVMKFLNLTSEKVSFQSKVTSTLEAFCSRPAELQWYFGDVKEKYLSEYCFSGTYI 419
QY 420 LSLILQGYHTADSWHEHIFIGIKQSDAGWTGLGYMLNTNMPAPQPLSTPLSHSTYVF 479
Db 420 LTLISUGYHTAETWKNHIFMGKQVSTSVGWTGLGYMLNTNMPSEPSSTRLSHSTYVF 479
QY 480 LMLVLSLVLFTVAIIGLLIFHKPSYFWKDMV 510
Db 480 LMLVLSLVLIVVILGLFVCHRPYFWKDMV 510

RESULT 7
Q86VV3 PRELIMINARY; PRT; 372 AA.
AC Q86VV3
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE ENTPI1 protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047664; AAH47664.1; -
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
SQ SEQUENCE 372 AA; 42731 MW; A8B1DE1366356EE3 CRC64;

Query Match 73.9%; Score 1993; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.3e-142; Gaps 0;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 MESEELADRVLDVRSLSNYPDFQGARITIQEGEGAGWITINYLKGFQSKTRWFSI 198
Db 1 MESEELADRVLDVRSLSNYPDFQGARITIQEGEGAGWITINYLKGFQSKTRWFSI 60
QY 199 VPEYTNNOETFGALDGGASTQVTFVQNQTIESPDNALQFLYKGVNYYTHSFLCYGK 258
|||||
```

```
Db 61 VPEYTNNOETFGALDGGASTQVTFVQNQTIESPDNALQFLYKGVNYYTHSFLCYGK 120
QY 259 DQALWQKLAKDIOVASNEILRDPCHPGYKVVVNSDLYKTCTKRFEMTLFPQQPEIQG 318
|||||
Db 121 DQALWQKLAKDIOVASNEILRDPCHPGYKVVVNSDLYKTCTKRFEMTLFPQQPEIQG 180
QY 319 IGNYOQCHQSILELENTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVS 378
Db 181 IGNYOQCHQSILELENTSYCPYSQCAFNGIFLPPLOQDFGAFSAFYFVMKFLNLTSEKVS 240
QY 379 QEKVTMMKKFCAQPWEIKTSYAGVKEKYLSEYCFSGTYIILSLLOQVHFTADSWHEH 438
|||||
Db 241 QEKVTMMKKFCAQPWEIKTSYAGVKEKYLSEYCFSGTYIILSLLOQVHFTADSWHEH 300
QY 439 FIGIKQSDAGWTGLGYMLNTNMPAEQPLSTPLSHSTYVFLMVLFSVLFTVAIIGLLI 498
|||||
Db 301 FIGIKQSDAGWTGLGYMLNTNMPAEQPLSTPLSHSTYVFLMVLFSVLFTVAIIGLLI 360
QY 499 FHKPSYFWKDMV 510
Db 361 FHKPSYFWKDMV 372

RESULT 8
ENPI_BOVIN
ID ENPI_BOVIN STANDARD; PRT; 513 AA.
AC O18956;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Econucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPdase) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
DE activation antigen) (CD39 antigen) (Ecto-apyrase).
GN Name=ENTP1; Synonyms=CD39;
OS Bos taurus (Bovine)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aortic endothelium;
RA Chang A.S., Garcia R.L., Chang S.M., Schilling W.P.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 97-103; 123-133; 136-140; 145-168 AND 459-471.
RC TISSUE=Aorta;
RX MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
RA Kaczmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J.,
RA Beaudoin A.R., Bach F.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
RT diphosphohydrolase."
RL J. Biol. Chem. 271:33116-33122 (1996).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COPACTOR: Requires calcium and magnesium.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
EMBL; AF005940; AAB62382.1; -
InterPro; IPR000407; GDA1_CD39_NTPase.
```



DR	Pfam: PF01150; GDAL CD39; 1.	
DR	PROSITE; PS01238; GDAL CD39_NTPASE; 1.	
KW	Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;	
KW	Magnesium; Transmembrane.	
FT	DOMAIN 1 16	Cytoplasmic (Potential).
FT	TRANSMEM 17 37	Potential.
FT	DOMAIN 38 481	Extracellular (Potential).
FT	TRANSMEM 482 502	Potential.
FT	DOMAIN 503 513	Cytoplasmic (Potential).
FT	CARBOHYD 73 73	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD 227 227	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD 245 245	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD 307 307	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD 336 336	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD 373 373	N-linked (GLNAC. . .) (Potential).
FT	CARBOHYD 460 460	N-linked (GLNAC. . .) (Potential).
FT	CONFLICT 97 97	K -> N (in Ref. 2).
FT	CONFLICT 101 103	INV -> CGF (in Ref. 2).
FT	CONFLICT 464 464	K -> V (in Ref. 2).
SQ	SEQUENCE 513 AA; 58113 MW; 20F998F27B6D2F96 CRC64;	
Query Match 73.5%; Score 1982.5; DB 1; Length 513;		
Best Local Similarity 70.8%; Pred. No. 2.1e-141;		
Matches 364; Conservative 73; Mismatches 72; Indels 5; Gaps 3;		
QY	1 MEDTKSNVTKFCNKILATGFSSIIANTALAVGLTQNKALPENVKYGVILDGSSHT	60
DB	1 MEDRESELKVFCSKILSLFSCIIAVIALALGLTQNKALPENVKFGVILDGSSHT	60
QY	61 SLVIYKPAEKENDTGVMHVECRVKGPGISKFVKVNEIGLYLTDICMERAREVTPRSQ	120
DB	61 SLVIYKPAEKENDTGVMHVECRVKGPGISKFVKVNEIGLYLTDICMERAREVTPRSQ	120
QY	121 HQETPVYLGATAGMRLRMSESLADRLVDLVSNSYPDFDQGIARIITGQEGAYGWI	180
DB	121 HMETPVYLGATAGMRLRMENKQADKILAAVASSISSEYPPDFDQGIARIITGQEGAYGWI	180
QY	181 TINYLGKFSQKTRFVSIVPYETNNQETFGALDGGASTQVTVFVONOTIESPDNALQPR	240
DB	181 TVNYLLGKFTQKLSWFLNPKSKDDTQETYGALDGGASTQITFVQNETTESPNNLYFR	240
QY	241 LYGKDYNVYTHSLCYGKDQALQWKLAKOIQVANSNEILRDCPFHGPYKVVVNSDYLYKTP	300
DB	241 LYGKNVSVYTHSLCYGKDQALQKALGLQ-CTNGIIEPCFHSRYMRKIKXSVLNEGF	299
QY	301 CTKRFEMT---LFPQFQFIOGNYQOCHOSILELNTSYCPYSCAFNGIFLPPLOQDF	357
DB	300 CTKRHELNSSFYPLVDIEIRGAGNFQRCRSIIQLFNTSYCPYSSCSFNGVFLPLHGQF	359
QY	358 GAFSAFYVMKFLNLTSEK-VSOEKVTEMKKCAQPWBEIKTSYAGVKKYLSEYCFSG	416
DB	360 GAFSAFYVMFLNLTSEESVSVEQLEKLEEFCAQRWEVEVQKNGEVKELYLSEYCFSG	419
QY	417 TYLSLLQGYHTFADSWEHIFGKIOGSDAGWTGLGYMLNLTNMTPAEOPLTSTPLSHST	476
DB	420 TYLVLLNGYHTFADSWKNIHFWKVRSTVDVGTGLYMLNLTNMTKIPAEPMSPPLPHST	479
QY	477 YVFLMWLFSVLVFTVAIGLLIFHKPSYFWKDMV	510
DB	480 YVFLMWLFSLLAVIIVGIWVFWKPSYFWKDMV	513
RESULT 9		
Q8CEB1	PRELIMINARY; PRT; 420 AA.	
ID	Q8CEB1	
AC	Q8CEB1	
DT	01-MAR-2003 (T-EMBLrel. 23, Created)	
DT	01-MAR-2003 (T-EMBLrel. 25, Last sequence update)	
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)	
DE	Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched	
DE	library, clone:4732419M16 product:ectonucleoside triphosphate	
DE	diphosphohydrolase 1, full insert sequence. (Fragment).	
GN	Names=Entpd1;	

OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Skin;	
RC	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;	
RX	Carninci P., Hayashizaki Y.; cDNA cloning.";	
RA	Meth. Enzymol. 303:19-44 (1999).	
RL	[2]	SEQUENCE FROM N.A.
RN	[2]	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Skin;	
RC	MEDLINE=21085860; PubMed=11217851; DOI=10.1038/350555500;	
RX	RIKEN FANTOM Consortium;	
RA	"Functional annotation of a full-length mouse cDNA collection.";	
RL	Nature 409:685-690 (2001).	
RN	[3]	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Skin;	
RC	The FANTOM Consortium;	
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;	
RA	"Analysis of the mouse transcriptome based on functional annotation of	
RT	60,770 full-length cDNAs.";	
RL	Nature 420:563-573 (2002).	
RN	[4]	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Skin;	
RC	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;	
RX	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,	
RA	Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;	
RA	"Normalization and subtraction of cap-trapper-selected cDNAs to	
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";	
RL	Genome Res. 10:1617-1630 (2000).	
RN	[5]	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Skin;	
RC	MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;	
RX	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,	
RA	Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,	
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,	
RA	Fujimoto R., Matsumoto H., Sakaguchi S., Ikegami T., Watahiki M.,	
RA	Yamawake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,	
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,	
RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;	
RT	"RIKEN integrated sequence analysis (RISA) system-384-Format	
RT	sequencing pipeline with 384 multicapillary sequencer.";	
RL	Genome Res. 10:1757-1771 (2000).	
RN	[6]	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6J; TISSUE=Skin;	
RC	Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,	
RA	Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,	
RA	Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,	
RA	Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,	
RA	Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,	
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,	
RA	Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,	
RA	Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,	
RA	Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,	
RA	Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,	
RA	Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;	
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AK028625; BAC26037.1; -.	
DR	MGD; MGI:102805; Entpd1.	
DR	GO; GO:0005605; C:basal lamina; IDA.	
DR	GO; GO:0016021; C:integral to membrane; TAS.	
DR	GO; GO:0004050; P:ATPase activity; IDA.	
DR	GO; GO:0006200; P:ATP catabolism; IDA.	
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IDA.	
DR	GO; GO:0030168; P:platelet activation; IDA.	
DR	GO; GO:0009181; P:purine ribonucleoside diphosphate catabolism; IDA.	











Search completed: September 21, 2005, 16:21:24  
Job time : 94 secs

1  
:  
6

**THIS PAGE BLANK (USPTO)**

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2005, 16:03:34 ; Search time 28 Seconds  
(without alignments)  
1359.679 Million cell updates/sec

Title: US-09-807-660C-2  
Perfect score: 2698  
Sequence: 1 MEDTKESNVKTFCSKNILAI.....VAIIIGLIFHKPSYFWKDMV 510

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A-COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B-COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A-COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B-COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS-COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2698	100.0	510	3	US-08-930-921-1
2	2698	100.0	510	4	US-09-781-796C-1
3	2650	98.2	502	4	US-09-557-800C-55
4	2650	98.2	502	4	US-09-370-625A-38
5	1171.5	43.4	282	4	US-09-949-016-7977
6	942.5	34.9	529	3	US-09-240-639-4
7	942.5	34.9	529	4	US-09-908-510A-4
8	942.5	34.9	529	4	US-09-905-744B-4
9	942.5	34.9	529	4	US-10-107-660-4
10	942.5	34.9	529	4	US-10-107-576-4
11	942.5	34.9	529	4	US-09-905-732B-4
12	942.5	34.9	529	4	US-09-923-304-4
13	942.5	34.9	529	4	US-09-949-016-6049
14	942.5	34.9	529	4	US-09-905-743B-4
15	938.5	34.8	556	4	US-09-949-016-11328
16	897	33.2	479	4	US-09-949-016-11559
17	803	29.8	153	3	US-09-240-639-13
18	803	29.8	153	4	US-09-908-510A-13
19	803	29.8	153	4	US-09-905-744B-13
20	803	29.8	153	4	US-10-107-660-13
21	803	29.8	153	4	US-10-107-576-13
22	803	29.8	153	4	US-09-905-732B-13
23	803	29.8	153	4	US-09-905-743B-13
24	604	22.4	154	3	US-09-240-639-14
25	604	22.4	154	4	US-09-908-510A-14
26	604	22.4	154	4	US-09-905-744B-14
27	604	22.4	154	4	US-10-107-660-14

28	604	22.4	154	4	US-10-107-576-14	Sequence 14, Appl
29	604	22.4	154	4	US-09-905-732B-14	Sequence 14, Appl
30	604	22.4	154	4	US-09-905-743B-14	Sequence 14, Appl
31	442.5	16.4	153	3	US-09-240-639-15	Sequence 15, Appl
32	442.5	16.4	153	4	US-09-908-510A-15	Sequence 15, Appl
33	442.5	16.4	153	4	US-09-905-744B-15	Sequence 15, Appl
34	442.5	16.4	153	4	US-10-107-660-15	Sequence 15, Appl
35	442.5	16.4	153	4	US-10-107-576-15	Sequence 15, Appl
36	442.5	16.4	153	4	US-09-905-732B-15	Sequence 15, Appl
37	442.5	16.4	153	4	US-09-905-743B-15	Sequence 15, Appl
38	427	15.8	94	4	US-09-513-999C-4273	Sequence 4273, Ap
39	427	15.8	462	4	US-09-123-112-2	Sequence 2, Appl
40	421.5	15.6	462	4	US-09-129-112-15	Sequence 15, Appl
41	417.5	15.5	150	3	US-09-240-639-16	Sequence 16, Appl
42	417.5	15.5	150	4	US-09-908-510A-16	Sequence 16, Appl
43	417.5	15.5	150	4	US-09-905-744B-16	Sequence 16, Appl
44	417.5	15.5	150	4	US-10-107-660-16	Sequence 16, Appl
45	417.5	15.5	150	4	US-10-107-576-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-930-921-1  
; Sequence 1, Application US/08930921B  
; Patent No. 6287837  
; GENERAL INFORMATION:  
; APPLICANT: BEAUDOIN, Adrien R.  
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION  
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT  
; TITLE OF INVENTION: TECHNOLOGY  
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN  
; CURRENT APPLICATION NUMBER: US/08/930,921B  
; CURRENT FILING DATE: 1998-01-02  
; EARLIER APPLICATION NUMBER: PCT/CA96/00223  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 510  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: unknown  
US-08-930-921-1

Query Match	100.0%	Score 2698;	DB 3;	Length 510;
Best Local Similarity	100.0%	Pred. No. 5.8e-277;		
Matches 510;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MEDTKESNVKTFCSKNILAIILGPSIIATAVIALLAAGLTQNKALPENVKYGVLDAGSSHT	60	
Db	1	MEDTKESNVKTFCSKNILAIILGPSIIATAVIALLAAGLTQNKALPENVKYGVLDAGSSHT	60	
Qy	61	SLYIKYKPAEKENDTGVVHVQVECRVKGPGISKVQKNEIGIYLTDCMERAREVIPSQ	120	
Db	61	SLYIKYKPAEKENDTGVVHVQVECRVKGPGISKVQKNEIGIYLTDCMERAREVIPSQ	120	
Qy	121	HOETPVYLGATAGMRLLRMESEELADRLVDVVERSLSNYPDFQGARITITQEEGAYGWI	180	
Db	121	HOETPVYLGATAGMRLLRMESEELADRLVDVVERSLSNYPDFQGARITITQEEGAYGWI	180	
Qy	181	TINYLLGKFSOKTWFISIVPYETNNQETFGALDGGASTQVTFPQNQTIESPDNALQFR	240	
Db	181	TINYLLGKFSOKTWFISIVPYETNNQETFGALDGGASTQVTFPQNQTIESPDNALQFR	240	
Qy	241	LYGKDYNVYTHSFLCYGKDQALWQKLAKDIOVASNEILRDFCFHPGKVVVNSLYKTP	300	
Db	241	LYGKDYNVYTHSFLCYGKDQALWQKLAKDIOVASNEILRDFCFHPGKVVVNSLYKTP	300	
Qy	301	CTKRFEMLTPQOPEIOGIGNYQOCHOSIILELNTSYCPYSQCAFNGIFLPPLOQDFGAF	360	

Db 301 CTRKFEMTLFPQFEIQGIGNYQOCHQSIIELENTSYCPYSQCAFNGIFLPPQLQGFAG 360  
Qy 361 SAFYFVMKFLNLTSEKVSQEKVTEMKKKCAQPWEIEKITSYAGVKSEKYLSEYCFSGTYIL 420  
Db 361 SAFYFVMKFLNLTSEKVSQEKVTEMKKKCAQPWEIEKITSYAGVKSEKYLSEYCFSGTYIL 420  
Qy 421 SLLQGYHFTADSWEHIFGKIQGSADAGWTLCGYMLNLTNMIIPAEQPLSTPLSHSYVFL 480  
Db 421 SLLQGYHFTADSWEHIFGKIQGSADAGWTLCGYMLNLTNMIIPAEQPLSTPLSHSYVFL 480  
Qy 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510  
Db 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510

## RESULT 2

US-09-781-796C-1  
; Sequence 1: Application US/09781796C  
; Patent No. 6800284  
; GENERAL INFORMATION:  
; APPLICANT: BEAUDOIN, Adrien R.  
; APPLICANT: SEVIGNY, Jean  
; APPLICANT: BACH, Fritz H.  
; APPLICANT: ROBSON, Simon  
; TITLE OF INVENTION: ATP-DIPHOSPHODIOLASES, PROCESS OF PURIFICATION  
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT  
; TITLE OF INVENTION: TECHNOLOGY  
; FILE REFERENCE: 920333.90019  
; CURRENT APPLICATION NUMBER: US/09/781.796C  
; PRIOR FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 08/419,204  
; PRIOR FILING DATE: 1995-04-10  
; PRIOR APPLICATION NUMBER: CA96/00223  
; PRIOR FILING DATE: 1996-04-10  
; PRIOR APPLICATION NUMBER: 08/930,921  
; PRIOR FILING DATE: 1998-02-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 510  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-781-796C-1

Query Match 100.0%; Score 2698; DB 4; Length 510;  
Best Local Similarity 100.0%; Pred. No. 5.8e-277;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTONKALPENVKYGVILDAGSSHT 60  
Db 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTONKALPENVKYGVILDAGSSHT 60  
Qy 61 SLVIYKWPAAEKENDTGTVHQBVECRVKGPGISKVFQKVNEIGIYLTDCMERAREVTPRSQ 120  
Db 61 SLVIYKWPAAEKENDTGTVHQBVECRVKGPGISKVFQKVNEIGIYLTDCMERAREVTPRSQ 120  
Qy 121 HQETPVYLGATAGMRLRMSEBELADRVLDVVERSLSNYPDFQGARIIITGQEGAYGWI 180  
Db 121 HQETPVYLGATAGMRLRMSEBELADRVLDVVERSLSNYPDFQGARIIITGQEGAYGWI 180  
Qy 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPQNQTIESPDNALQFR 240  
Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPQNQTIESPDNALQFR 240  
Qy 241 LYGKDYNNVYTHSFLCYGKQOALWQKLAKDIQVANSNEILRDPCHPGYKKVNVVSDLYKTP 300  
Db 241 LYGKDYNNVYTHSFLCYGKQOALWQKLAKDIQVANSNEILRDPCHPGYKKVNVVSDLYKTP 300  
Qy 301 CTRKFEMTLFPQFEIQGIGNYQOCHQSIIELENTSYCPYSQCAFNGIFLPPQLQGFAG 360  
Db 301 CTRKFEMTLFPQFEIQGIGNYQOCHQSIIELENTSYCPYSQCAFNGIFLPPQLQGFAG 360

Qy 361 SAFYFVMKFLNLTSEKVSQEKVTEMKKKCAQPWEIEKITSYAGVKSEKYLSEYCFSGTYIL 420  
Db 361 SAFYFVMKFLNLTSEKVSQEKVTEMKKKCAQPWEIEKITSYAGVKSEKYLSEYCFSGTYIL 420  
Qy 421 SLLQGYHFTADSWEHIFGKIQGSADAGWTLCGYMLNLTNMIIPAEQPLSTPLSHSYVFL 480  
Db 421 SLLQGYHFTADSWEHIFGKIQGSADAGWTLCGYMLNLTNMIIPAEQPLSTPLSHSYVFL 480  
Qy 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510  
Db 481 MVLFSVLFTVAIIGLLIFHKPSYFWKDMV 510

## RESULT 3

US-09-557-800C-55  
; Sequence 55, Application US/09557800C  
; Patent No. 6476211  
; GENERAL INFORMATION:  
; APPLICANT: Mulero, Julio  
; APPLICANT: Yeung, George  
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 28110/36457  
; CURRENT APPLICATION NUMBER: US/09/557,800C  
; CURRENT FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/481,238  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 09/370,265  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/122449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/244444  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 55  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-557-800C-55

Query Match 98.2%; Score 2650; DB 4; Length 502;  
Best Local Similarity 100.0%; Pred. No. 7e-272;  
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTONKALPENVKYGVILDAGSSHT 60  
Db 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTONKALPENVKYGVILDAGSSHT 60  
Qy 61 SLVIYKWPAAEKENDTGTVHQBVECRVKGPGISKVFQKVNEIGIYLTDCMERAREVTPRSQ 120  
Db 61 SLVIYKWPAAEKENDTGTVHQBVECRVKGPGISKVFQKVNEIGIYLTDCMERAREVTPRSQ 120  
Qy 121 HQETPVYLGATAGMRLRMSEBELADRVLDVVERSLSNYPDFQGARIIITGQEGAYGWI 180  
Db 121 HQETPVYLGATAGMRLRMSEBELADRVLDVVERSLSNYPDFQGARIIITGQEGAYGWI 180  
Qy 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPQNQTIESPDNALQFR 240  
Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPQNQTIESPDNALQFR 240  
Qy 241 LYGKDYNNVYTHSFLCYGKQOALWQKLAKDIQVANSNEILRDPCHPGYKKVNVVSDLYKTP 300  
Db 241 LYGKDYNNVYTHSFLCYGKQOALWQKLAKDIQVANSNEILRDPCHPGYKKVNVVSDLYKTP 300







```
QY 25 SIIAVIALAVGLTQNKALPENVKYIGIVLDAGSSHTSLYIKWPAEKENDTGTVVHVQVSEC 84
Db 33 SIVLVSVITVIQHKQEVLPGLKYIGIVLDAGSSRTTVVYQWPAEKENNTGVWSQTFKC 92
QY 85 RVKGPISKFVQKVNIEGIVLTDCEMERAREVTPRSQHOETPVYLGATAGMRLLRMESEL 144
Db 93 SVKSGSISSYGNPNQDVPRAFEECMQVKGVQVPSHLHGSTPIHLGATAGMRLLRQNETA 152
QY 145 ADRVLDVVERSLNSYPDFQGARITITQEBEGAYGWITINYLKGKFSQKTRWFSIVPYETN 204
Db 153 ANEVLESIQSYFKSQPFDFRGAQIISQGBEGYVGMITANYLMGNFLEKNLWHMWV--HPH 210
QY 205 NOETFGALDLGGASTQVTFVFNQNTIESPDNALQRLYKGDYNYVTHSFLCYGKQDALMQ 264
Db 211 GVETTGALDLGGASTQISFVAGERKMDLNTSDIMQVSLYGYVYVTLTHSFQCYGRNEAEKK 270
QY 265 KLAKDIQVA--SNEILRDPCHFPGYKKVNVNVDLYKTPCT--KRFEMLTLPFQOFEIQIGN 321
Db 271 FLAMLLQNSPTKHNLTNCPYPRDYSISFTMGHVFDLSLCTVDQRPESYNPNNDVITFEGTD 330
QY 322 YQQCHQSILELFTNSYC--PYSQCAFNGIFLPLQDGFAGSAPFYFVMKFLNLTSEKVSQE 380
Db 331 PSLCKEKVASIFDFKACHDQETCSPDGVYQPKIKGPFVAFAGFYTTASALNL--SGSFSLD 389
QY 381 KVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWHEHIPI 440
Db 390 TFNSSTWNFCSQNSQLPPLLKPFDEVYARSYCFSANIYIHLFVNGYKFTETWPIQHFE 449
QY 441 GKIQSDAGWTIGYMLNTNMIPAEQPL--STPLSHSTYVFLMVLFSVLFTVAIIGLLIF 499
Db 450 KEVGNSSJAMSIGYMLSLTNQIPAESPLIRLPIEBPVFV----GTLAFFTTVAALLCLAF 504
```

## RESULT 9

```
US-10-107-660-4
; Sequence 4, Application US/10107660
; Patent No. 6780977
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frieschaut, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/10/107,660
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US/09/240,639
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-660-4
```

```
Query Match 34.9%; Score 942.5; DB 4; Length 529;
Best Local Similarity 39.8%; Pred. No. 1.1e-90;
Matches 191; Conservative 90; Mismatches 186; Indels 13; Gaps 7;
```

```
QY 25 SIIAVIALAVGLTQNKALPENVKYIGIVLDAGSSHTSLYIKWPAEKENDTGTVVHVQVSEC 84
Db 33 SIVLVSVITVIQHKQEVLPGLKYIGIVLDAGSSRTTVVYQWPAEKENNTGVWSQTFKC 92
QY 85 RVKGPISKFVQKVNIEGIVLTDCEMERAREVTPRSQHOETPVYLGATAGMRLLRMESEL 144
Db 93 SVKSGSISSYGNPNQDVPRAFEECMQVKGVQVPSHLHGSTPIHLGATAGMRLLRQNETA 152
QY 145 ADRVLDVVERSLNSYPDFQGARITITQEBEGAYGWITINYLKGKFSQKTRWFSIVPYETN 204
Db 153 ANEVLESIQSYFKSQPFDFRGAQIISQGBEGYVGMITANYLMGNFLEKNLWHMWV--HPH 210
QY 205 NOETFGALDLGGASTQVTFVFNQNTIESPDNALQRLYKGDYNYVTHSFLCYGKQDALMQ 264
```

```
Db 211 GVETTGALDLGGASTQISFVAGERKMDLNTSDIMQVSLYGYVYVTLTHSFQCYGRNEAEKK 270
QY 265 KLAKDIQVA--SNEILRDPCHFPGYKKVNVNVDLYKTPCT--KRFEMLTLPFQOFEIQIGN 321
Db 271 FLAMLLQNSPTKHNLTNCPYPRDYSISFTMGHVFDLSLCTVDQRPESYNPNNDVITFEGTD 330
QY 322 YQQCHQSILELFTNSYC--PYSQCAFNGIFLPLQDGFAGSAPFYFVMKFLNLTSEKVSQE 380
Db 331 PSLCKEKVASIFDFKACHDQETCSPDGVYQPKIKGPFVAFAGFYTTASALNL--SGSFSLD 389
QY 381 KVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWHEHIPI 440
Db 390 TFNSSTWNFCSQNSQLPPLLKPFDEVYARSYCFSANIYIHLFVNGYKFTETWPIQHFE 449
QY 441 GKIQSDAGWTIGYMLNTNMIPAEQPL--STPLSHSTYVFLMVLFSVLFTVAIIGLLIF 499
Db 450 KEVGNSSJAMSIGYMLSLTNQIPAESPLIRLPIEBPVFV----GTLAFFTTVAALLCLAF 504
```

## RESULT 10

```
US-10-107-576-4
; Sequence 4, Application US/10107576
; Patent No. 6783959
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frieschaut, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120H
; CURRENT APPLICATION NUMBER: US/10/107,576
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-107-576-4
```

```
Query Match 34.9%; Score 942.5; DB 4; Length 529;
Best Local Similarity 39.8%; Pred. No. 1.1e-90;
Matches 191; Conservative 90; Mismatches 186; Indels 13; Gaps 7;
```

```
QY 25 SIIAVIALAVGLTQNKALPENVKYIGIVLDAGSSHTSLYIKWPAEKENDTGTVVHVQVSEC 84
Db 33 SIVLVSVITVIQHKQEVLPGLKYIGIVLDAGSSRTTVVYQWPAEKENNTGVWSQTFKC 92
QY 85 RVKGPISKFVQKVNIEGIVLTDCEMERAREVTPRSQHOETPVYLGATAGMRLLRMESEL 144
Db 93 SVKSGSISSYGNPNQDVPRAFEECMQVKGVQVPSHLHGSTPIHLGATAGMRLLRQNETA 152
QY 145 ADRVLDVVERSLNSYPDFQGARITITQEBEGAYGWITINYLKGKFSQKTRWFSIVPYETN 204
Db 153 ANEVLESIQSYFKSQPFDFRGAQIISQGBEGYVGMITANYLMGNFLEKNLWHMWV--HPH 210
QY 205 NOETFGALDLGGASTQVTFVFNQNTIESPDNALQRLYKGDYNYVTHSFLCYGKQDALMQ 264
Db 211 GVETTGALDLGGASTQISFVAGERKMDLNTSDIMQVSLYGYVYVTLTHSFQCYGRNEAEKK 270
QY 265 KLAKDIQVA--SNEILRDPCHFPGYKKVNVNVDLYKTPCT--KRFEMLTLPFQOFEIQIGN 321
Db 271 FLAMLLQNSPTKHNLTNCPYPRDYSISFTMGHVFDLSLCTVDQRPESYNPNNDVITFEGTD 330
QY 322 YQQCHQSILELFTNSYC--PYSQCAFNGIFLPLQDGFAGSAPFYFVMKFLNLTSEKVSQE 380
Db 331 PSLCKEKVASIFDFKACHDQETCSPDGVYQPKIKGPFVAFAGFYTTASALNL--SGSFSLD 389
QY 381 KVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTIVLSLLQGYHFTADSWHEHIPI 440
Db 390 TFNSSTWNFCSQNSQLPPLLKPFDEVYARSYCFSANIYIHLFVNGYKFTETWPIQHFE 449
```

QY 441 GKIQSDAGWTLGYMLNLTNMIAPQPL-STPLSHSTYVFLMVLFSVLFTVAIIIGLLIF 499  
Db 450 KEVGNSSIAWSLGYMLSLTNQIPAESPLRLPIEPFVF-----GTLAFTTVAALLCLAF 504

RESULT 11  
US-09-905-732B-4  
; Sequence 4, Application US/09905732B  
; Patent No. 6787328  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; FILE REFERENCE: 28110/36120B  
; CURRENT APPLICATION NUMBER: US/09/905, 732B  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-905-732B-4

Query Match 34.9%; Score 942.5; DB 4; Length 529;  
Best Local Similarity 39.8%; Pred. No. 1.1e-90;  
Matches 191; Conservative 90; Mismatches 186; Indels 13; Gaps 7;  
QY 25 SIITAVALLAVGLTQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVERC 84  
Db 33 SIIVLVSVITVQIHKQEVLPGLKYGIVLDAGSSRTTVYIQWPAKENNTGVSVSTFKC 92  
QY 85 RVKGPISGFVKQVNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEL 144  
Db 93 SVKSGISSYGNPNQDVPRAFECECMQKVGQVPSHLHGSTPIHLGATAGMRLRLQNETA 152  
QY 145 ADRVLDVVERSLNYPDFOGARIITGOBEGAYGWITINYLKGFQSKTRWFSIVPYETN 204  
Db 153 ANEVLESIQSYFKSQPFDFRGAQIIISGOBEGYGVWITANYLMGNFLEKRLWHMWV--HPH 210  
QY 205 NOETFGALDGGASTQVTFVQNPQTIESPDNALQRLYKGVNVTYTHSFLCYGKQALWQ 264  
Db 211 GVETTGALDGGASTQISFVAGERKMDLNTSDIMQVSLYGVYTYLTHSQCYGRNEAEKK 270  
QY 265 KLAQDIQVA-SNEILRDPCHFPGYKKVNVNSDLYKTPCT--KRFEMTLPPFOQFEIQIGN 321  
Db 271 FLAMLLQNSPTKNHLNTPCYPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDVITPEGTGD 330  
QY 322 YQOCHQSILELNTSYC-PYSQCAFNGIFLPPQDGFAGFAPFYVMKFLNLTSEKVSQE 380  
Db 331 PSLCKEKVASIFDFKACHDQETCSFDGVYQPKIGPFAFAGFYTTASALNL-SGSFSLD 389  
QY 381 KVTEMMKKCAQPMEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWHEIHF 440  
Db 390 TFNSSTWNPCSNWSQLPPLLKPFDEVIARSCFSANYIYHLFVNGYKFEETWPIHFE 449  
QY 441 GKIQSDAGWTLGYMLNLTNMIAPQPL-STPLSHSTYVFLMVLFSVLFTVAIIIGLLIF 499  
Db 450 KEVGNSSIAWSLGYMLSLTNQIPAESPLRLPIEPFVF-----GTLAFTTVAALLCLAF 504

RESULT 12  
US-09-923-304-4  
; Sequence 4, Application US/09923304  
; Patent No. 6797471  
; GENERAL INFORMATION:  
; APPLICANT: KATZ, RUTH  
; APPLICANT: JIANG, FENG  
; TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS  
; FILE REFERENCE: UTSC:658US  
; CURRENT APPLICATION NUMBER: US/09/923,304

; CURRENT FILING DATE: 2001-08-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-923-304-4

Query Match 34.9%; Score 942.5; DB 4; Length 529;  
Best Local Similarity 39.8%; Pred. No. 1.1e-90;  
Matches 191; Conservative 90; Mismatches 186; Indels 13; Gaps 7;  
QY 25 SIITAVALLAVGLTQNKALPENVKYGVLDAGSSHTSLYIKWPAEKENDTGVVHVERC 84  
Db 33 SIIVLVSVITVQIHKQEVLPGLKYGIVLDAGSSRTTVYIQWPAKENNTGVSVSTFKC 92  
QY 85 RVKGPISGFVKQVNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLRMESEL 144  
Db 93 SVKSGISSYGNPNQDVPRAFECECMQKVGQVPSHLHGSTPIHLGATAGMRLRLQNETA 152  
QY 145 ADRVLDVVERSLNYPDFOGARIITGOBEGAYGWITINYLKGFQSKTRWFSIVPYETN 204  
Db 153 ANEVLESIQSYFKSQPFDFRGAQIIISGOBEGYGVWITANYLMGNFLEKRLWHMWV--HPH 210  
QY 205 NOETFGALDGGASTQVTFVQNPQTIESPDNALQRLYKGVNVTYTHSFLCYGKQALWQ 264  
Db 211 GVETTGALDGGASTQISFVAGERKMDLNTSDIMQVSLYGVYTYLTHSQCYGRNEAEKK 270  
QY 265 KLAQDIQVA-SNEILRDPCHFPGYKKVNVNSDLYKTPCT--KRFEMTLPPFOQFEIQIGN 321  
Db 271 FLAMLLQNSPTKNHLNTPCYPRDYSISFTMGHVFDSLCTVDQRPESYNPNVDVITPEGTGD 330  
QY 322 YQOCHQSILELNTSYC-PYSQCAFNGIFLPPQDGFAGFAPFYVMKFLNLTSEKVSQE 380  
Db 331 PSLCKEKVASIFDFKACHDQETCSFDGVYQPKIGPFAFAGFYTTASALNL-SGSFSLD 389  
QY 381 KVTEMMKKCAQPMEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWHEIHF 440  
Db 390 TFNSSTWNPCSNWSQLPPLLKPFDEVIARSCFSANYIYHLFVNGYKFEETWPIHFE 449  
QY 441 GKIQSDAGWTLGYMLNLTNMIAPQPL-STPLSHSTYVFLMVLFSVLFTVAIIIGLLIF 499  
Db 450 KEVGNSSIAWSLGYMLSLTNQIPAESPLRLPIEPFVF-----GTLAFTTVAALLCLAF 504

RESULT 13  
US-09-949-016-6049  
; Sequence 6049, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6049  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6049  
Query Match 34.9%; Score 942.5; DB 4; Length 529;  
Best Local Similarity 39.8%; Pred. No. 1.1e-90;



Qy	381	KVTEMMKKFCAQPEEIKTSYAGVKESKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFI	440
Db	417	TFNSTWNPCSQNSQLPDLPLPKFDEVYARSYCFSANIYHLEFVNGYKFTEETWPOIHFE	476
Qy	441	GKIQSDAGWTLGYMLNLTNMIPAEQPL-STPLSHSTYVFLMVLFSVLFTVAIIIGLLIF	499
Db	477	KEVGNSSIAWSLGYMLSLTNQIPAESPLIRLPIEPPFV-----GTLAFFTRAALICLAF	531

Search completed: September 21, 2005, 16:22:30  
Job time : 30 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2005, 16:21:29 ; Search time 521 Seconds  
(without alignments)  
398.419 Million cell updates/sec

Title: US-09-807-660C-2  
Perfect score: 2698  
Sequence: 1 MEDTKESNVKTFCSKNILAI.....VAIGLLIFHKPSYFWKDMV 510

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications, AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/ECT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/ECTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2698	100.0	510	9 US-09-835-147-2	Sequence 2, Appli
2	2698	100.0	510	9 US-09-374-586-1	Sequence 1, Appli
3	2698	100.0	510	10 US-09-781-796B-1	Sequence 30, Appl
4	2698	100.0	510	16 US-10-646-308-30	Sequence 2, Appli
5	2698	100.0	511	18 US-10-922-378-2	Sequence 297, App
6	2698	100.0	511	18 US-10-934-998-297	Sequence 97, Appl
7	2677	99.2	517	18 US-10-934-998-97	Sequence 38, Appl
8	2650	98.2	502	13 US-10-092-063-38	Sequence 27, Appl
9	2358	87.4	464	9 US-09-835-147-27	Sequence 2, Appli
10	2348	87.0	439	9 US-09-374-586-2	Sequence 6, Appli
11	2348	87.0	454	9 US-09-835-147-6	

12	2348	87.0	463	9 US-09-835-147-30	Sequence 30, Appl
13	2348	87.0	473	9 US-09-835-147-29	Sequence 29, Appl
14	2348	87.0	474	9 US-09-835-147-28	Sequence 28, Appl
15	2348	87.0	476	9 US-09-835-147-3	Sequence 3, Appli
16	2348	87.0	478	9 US-09-835-147-8	Sequence 8, Appli
17	2348	87.0	487	9 US-09-835-147-26	Sequence 26, Appl
18	2297	85.1	476	9 US-09-835-147-4	Sequence 4, Appli
19	2057.5	76.3	511	17 US-10-732-923-11078	Sequence 11078, A
20	1982.5	73.5	513	17 US-10-732-923-11095	Sequence 11095, A
21	1063.5	39.4	497	20 US-11-076-982-1	Sequence 1, Appli
22	1042.5	38.6	495	9 US-09-823-356-4	Sequence 4, Appli
23	942.5	34.9	529	20 US-11-076-982-3	Sequence 3, Appli
24	942.5	34.9	529	9 US-09-923-304-4	Sequence 4, Appli
25	942.5	34.9	529	18 US-10-756-149-4804	Sequence 4804, Ap
26	940	34.8	458	13 US-10-052-586-496	Sequence 496, App
27	940	34.8	458	14 US-10-174-590-496	Sequence 496, App
28	940	34.8	458	14 US-10-176-758-496	Sequence 496, App
29	940	34.8	458	14 US-10-175-737-496	Sequence 496, App
30	940	34.8	458	14 US-10-174-581-496	Sequence 496, App
31	940	34.8	458	14 US-10-176-483-496	Sequence 496, App
32	940	34.8	458	14 US-10-176-749-496	Sequence 496, App
33	940	34.8	458	14 US-10-176-914-496	Sequence 496, App
34	940	34.8	458	14 US-10-176-915-496	Sequence 496, App
35	940	34.8	458	14 US-10-173-706-496	Sequence 496, App
36	940	34.8	458	14 US-10-175-738-496	Sequence 496, App
37	940	34.8	458	14 US-10-175-752-496	Sequence 496, App
38	940	34.8	458	14 US-10-176-482-496	Sequence 496, App
39	940	34.8	458	14 US-10-176-757-496	Sequence 496, App
40	940	34.8	458	14 US-10-176-913-496	Sequence 496, App
41	940	34.8	458	14 US-10-180-552-496	Sequence 496, App
42	940	34.8	458	14 US-10-180-557-496	Sequence 496, App
43	940	34.8	458	14 US-10-173-700-496	Sequence 496, App
44	940	34.8	458	14 US-10-174-572-496	Sequence 496, App
45	940	34.8	458	14 US-10-174-579-496	Sequence 496, App

ALIGNMENTS

RESULT 1

US-09-835-147-2

; Sequence 2, Application US/09835147

; Patent No. US20020002277A1

; GENERAL INFORMATION:

; APPLICANT: Maliszewski, Charles R.

; APPLICANT: Gayle III, Richard B.

; APPLICANT: Price, Virginia L.

; APPLICANT: Gimpel, Steven D.

; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment

; FILE REFERENCE: 2879-US

; CURRENT APPLICATION NUMBER: US/09/835,147

; CURRENT FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: US 60/104,585

; PRIOR FILING DATE: 1998-10-16

; PRIOR APPLICATION NUMBER: US 60/107,466

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: US 60/149,010

; PRIOR FILING DATE: 1999-08-13

; PRIOR APPLICATION NUMBER: PCT/US99/22955

; PRIOR FILING DATE: 1999-10-13

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 2

; LENGTH: 510

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-835-147-2

Query Match 100.0%; Score 2698; DB 9; Length 510;  
Best Local Similarity 100.0%; Pred. No. 1.3e-233;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKESNVKTFCSKNILAIIGFSSIIAVIALAVGLTQNKALPENKYGIVLDAGSSHT 60

```
Db 1 MEDTKESNVTFCCKNLAIGLGFSSIIAVIALAVGLTQNKALPENVKYGVILDAGSSHT 60
Qy 61 SLVIYKPAEKENDTGTVHGVVECRVKGPGISKFQVKNVEIGIYLTDCMERAREVIPRSQ 120
Db 61 SLVIYKPAEKENDTGTVHGVVECRVKGPGISKFQVKNVEIGIYLTDCMERAREVIPRSQ 120
Qy 121 HOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLSNYPDFQGARIIITQEGEGAYGWI 180
Db 121 HOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLSNYPDFQGARIIITQEGEGAYGWI 180
Qy 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPPQNTQIESPDNALQFR 240
Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPPQNTQIESPDNALQFR 240
Qy 241 LYGKDNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDPCHPGYKKVNVSDLYKTP 300
Db 241 LYGKDNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDPCHPGYKKVNVSDLYKTP 300
Qy 301 CTXRFEMTLPPFOQFEIQGIGNYQOCHQSILELENTSYCPYSQCAFNGIFLPLQGDGFAG 360
Db 301 CTXRFEMTLPPFOQFEIQGIGNYQOCHQSILELENTSYCPYSQCAFNGIFLPLQGDGFAG 360
Qy 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKBKYLSEYCFSGTYIL 420
Db 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKBKYLSEYCFSGTYIL 420
Qy 421 SLLQGYHFTADSWEHIFGKIQSDAGWTLYGMLNLTNMIAPAEQPLSTPLSHSHYVFL 480
Db 421 SLLQGYHFTADSWEHIFGKIQSDAGWTLYGMLNLTNMIAPAEQPLSTPLSHSHYVFL 480
Qy 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
Db 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510

RESULT 2
US-09-374-586-1
; Sequence 1, Application US/09374586
; Patent No. US20020138858A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: HOMO-SAPIEN
US-09-374-586-1

Query Match 100.0%; Score 2698; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.3e-233;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKESNVTFCCKNLAIGLGFSSIIAVIALAVGLTQNKALPENVKYGVILDAGSSHT 60
Db 1 MEDTKESNVTFCCKNLAIGLGFSSIIAVIALAVGLTQNKALPENVKYGVILDAGSSHT 60
Qy 61 SLVIYKPAEKENDTGTVHGVVECRVKGPGISKFQVKNVEIGIYLTDCMERAREVIPRSQ 120
Db 61 SLVIYKPAEKENDTGTVHGVVECRVKGPGISKFQVKNVEIGIYLTDCMERAREVIPRSQ 120
Qy 121 HOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLSNYPDFQGARIIITQEGEGAYGWI 180
Db 121 HOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLSNYPDFQGARIIITQEGEGAYGWI 180
Qy 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPPQNTQIESPDNALQFR 240
Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPPQNTQIESPDNALQFR 240
```

```
Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPPQNTQIESPDNALQFR 240
Qy 241 LYGKDNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDPCHPGYKKVNVSDLYKTP 300
Db 241 LYGKDNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDPCHPGYKKVNVSDLYKTP 300
Qy 301 CTXRFEMTLPPFOQFEIQGIGNYQOCHQSILELENTSYCPYSQCAFNGIFLPLQGDGFAG 360
Db 301 CTXRFEMTLPPFOQFEIQGIGNYQOCHQSILELENTSYCPYSQCAFNGIFLPLQGDGFAG 360
Qy 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKBKYLSEYCFSGTYIL 420
Db 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKBKYLSEYCFSGTYIL 420
Qy 421 SLLQGYHFTADSWEHIFGKIQSDAGWTLYGMLNLTNMIAPAEQPLSTPLSHSHYVFL 480
Db 421 SLLQGYHFTADSWEHIFGKIQSDAGWTLYGMLNLTNMIAPAEQPLSTPLSHSHYVFL 480
Qy 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
Db 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510

RESULT 3
US-09-781-796B-1
; Sequence 1, Application US/09781796B
; Publication No. US20030040094A1
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796B
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-796B-1

Query Match 100.0%; Score 2698; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.3e-233;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKESNVTFCCKNLAIGLGFSSIIAVIALAVGLTQNKALPENVKYGVILDAGSSHT 60
Db 1 MEDTKESNVTFCCKNLAIGLGFSSIIAVIALAVGLTQNKALPENVKYGVILDAGSSHT 60
Qy 61 SLVIYKPAEKENDTGTVHGVVECRVKGPGISKFQVKNVEIGIYLTDCMERAREVIPRSQ 120
Db 61 SLVIYKPAEKENDTGTVHGVVECRVKGPGISKFQVKNVEIGIYLTDCMERAREVIPRSQ 120
Qy 121 HOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLSNYPDFQGARIIITQEGEGAYGWI 180
Db 121 HOETPVYLGATAGMRLLRMESEBELADRVLDVVERSLSNYPDFQGARIIITQEGEGAYGWI 180
Qy 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPPQNTQIESPDNALQFR 240
Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDGGASTQVTFVPPQNTQIESPDNALQFR 240
Qy 241 LYGKDNVYTHSFLCYGKQDALWQKLAKDIOVASNEILRDPCHPGYKKVNVSDLYKTP 300
```



```
Db 241 LYGDYNYVTHSLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSOLYKTP 300
Qy 301 CTKRFEMLTPFOQFEIQIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLOQDFGAF 360
Db 301 CTKRFEMLTPFOQFEIQIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLOQDFGAF 360
Qy 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420
Db 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420
Qy 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480
Db 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480
Qy 481 MVFLSLVLTVAIIGLLIFHKPSYFWKDMV 510
Db 481 MVFLSLVLTVAIIGLLIFHKPSYFWKDMV 510

RESULT 4
US-10-646-308-30
; Sequence 30, Application US/10646308
; Publication No. US2004013692A1
; GENERAL INFORMATION:
; APPLICANT: BURTON, Paul B. J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE
; FILE REFERENCE: 3432-B
; CURRENT APPLICATION NUMBER: US/10/646,308
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: --to be assigned--
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: 60/406,418
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 30
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-646-308-30

Query Match 100.0%; Score 2698; DB 16; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.3e-233;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60
Db 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60
Qy 61 SLIYIYKPAEKENDTGVVHVQVEECRVKPGISKFGKVEIGIYLTDCMERAREVIPSQ 120
Db 61 SLIYIYKPAEKENDTGVVHVQVEECRVKPGISKFGKVEIGIYLTDCMERAREVIPSQ 120
Qy 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGOEGAYGWI 180
Db 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGOEGAYGWI 180
Qy 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQTVTFPQNTIESPNDALQFR 240
Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQTVTFPQNTIESPNDALQFR 240
Qy 241 LYGDYNYVTHSLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSOLYKTP 300
Db 241 LYGDYNYVTHSLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSOLYKTP 300
Qy 301 CTKRFEMLTPFOQFEIQIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLOQDFGAF 360
Db 301 CTKRFEMLTPFOQFEIQIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLOQDFGAF 360
Qy 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420
Db 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420
```

```
Db 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420
Qy 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480
Db 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480
Qy 481 MVFLSLVLTVAIIGLLIFHKPSYFWKDMV 510
Db 481 MVFLSLVLTVAIIGLLIFHKPSYFWKDMV 510

RESULT 5
US-10-922-378-2
; Sequence 2, Application US/10922378
; Publication No. US2005016998A1
; GENERAL INFORMATION:
; APPLICANT: ELMALEH, DAVID R.
; APPLICANT: ROBSON, SIMON C.
; TITLE OF INVENTION: CONJUGATES COMPRISING A BIODEGRADABLE POLYMER AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ELA-004.01
; CURRENT APPLICATION NUMBER: US/10/922,378
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US03/04845
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/358,303
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin ver. 3.3
; SEQ ID NO 2
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-922-378-2

Query Match 100.0%; Score 2698; DB 18; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.3e-233;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60
Db 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGIIVLDAGSSHT 60
Qy 61 SLIYIYKPAEKENDTGVVHVQVEECRVKPGISKFGKVEIGIYLTDCMERAREVIPSQ 120
Db 61 SLIYIYKPAEKENDTGVVHVQVEECRVKPGISKFGKVEIGIYLTDCMERAREVIPSQ 120
Qy 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGOEGAYGWI 180
Db 121 HOETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGOEGAYGWI 180
Qy 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQTVTFPQNTIESPNDALQFR 240
Db 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQTVTFPQNTIESPNDALQFR 240
Qy 241 LYGDYNYVTHSLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSOLYKTP 300
Db 241 LYGDYNYVTHSLCYGKQDQALWQKLAKDIOVASNEILRDPCHFGYKVVNVSOLYKTP 300
Qy 301 CTKRFEMLTPFOQFEIQIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLOQDFGAF 360
Db 301 CTKRFEMLTPFOQFEIQIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLOQDFGAF 360
Qy 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420
Db 361 SAFYFVMKFLNLTSEKVSQEKVTMMKKFCAQPWBEIKTSYAGVKEKYLSEYCFSGTYIL 420
Qy 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480
Db 421 SLLQGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIPAEQPLSTPLSHSTYVFL 480
Qy 481 MVFLSLVLTVAIIGLLIFHKPSYFWKDMV 510
```

```
Db 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
|||||
RESULT 6
US-10-934-998-297
; Sequence 297, Application US/10934998
; Publication No. US20050153917A1
; GENERAL INFORMATION:
; APPLICANT: AL-MAHMOOD, SALMAN
; APPLICANT: COLIN, SYLVIE
; APPLICANT: SCHNEIDER, CHRISTOPHE
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
; FILE REFERENCE: BMA-04-1206
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/FR03/00695
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/FR02/02717
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: FR02/04546
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: FR02/04546
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 297
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CDS protein of the sequence Genbank/S73813 (seq ID 290)
US-10-934-998-297

Query Match 100.0%; Score 2698; DB 18; Length 511;
Best Local Similarity 100.0%; Pred. No. 1.3e-233;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDTKSNVTKFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGVILDDAGSSHT 60
Db 2 MEDTKSNVTKFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGVILDDAGSSHT 61
|||
Qy 61 SLVIYKWPAAEKENDTGTVVHVQVEECRVKPGISKFVKVNEIGIYLTDCMERAREVIPSQ 120
Db 62 SLVIYKWPAAEKENDTGTVVHVQVEECRVKPGISKFVKVNEIGIYLTDCMERAREVIPSQ 121
|||
Qy 121 HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPDFQGARIIITQBEGAYGWI 180
Db 122 HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPDFQGARIIITQBEGAYGWI 181
|||
Qy 181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFR 240
Db 182 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFR 241
|||
Qy 241 LYGKDYNVYTHSFLCYGKQOALWQKLAKOIQVASNEILRDPCHPHGKVKVNVSDLYKTP 300
Db 242 LYGKDYNVYTHSFLCYGKQOALWQKLAKOIQVASNEILRDPCHPHGKVKVNVSDLYKTP 301
|||
Qy 301 CTKRFEMTLFPQOFIEIGIGNYQOCHQSILELNTSYCPYSQCAFNGIFLPPLOGDFGAF 360
Db 302 CTKRFEMTLFPQOFIEIGIGNYQOCHQSILELNTSYCPYSQCAFNGIFLPPLOGDFGAF 361
|||
Qy 361 SAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWEEKTSYAGVKSEKYLSEYCFSGTYIL 420
Db 362 SAFYFVWKFLNLTSEKVSQEKVTMMKKFCAQPWEEKTSYAGVKSEKYLSEYCFSGTYIL 421
|||
Qy 421 SLLLGQYHFTADSWEHIFHTGKIQGS DAGWTGLGYMLNLTNNMIPAEQPLSTPLSHSYVFL 480
Db 422 SLLLGQYHFTADSWEHIFHTGKIQGS DAGWTGLGYMLNLTNNMIPAEQPLSTPLSHSYVFL 481
|||
Qy 481 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 510
Db 482 MVLFSVLFTVAIIIGLLIFHKPSYFWKDMV 511
|||||

RESULT 7
US-10-934-998-97
; Sequence 97, Application US/10934998
; Publication No. US20050153917A1
; GENERAL INFORMATION:
; APPLICANT: AL-MAHMOOD, SALMAN
; APPLICANT: COLIN, SYLVIE
; APPLICANT: SCHNEIDER, CHRISTOPHE
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
; FILE REFERENCE: BMA-04-1206
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/FR03/00695
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: FR02/02717
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: FR02/04546
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CDS protein of the sequence GS-N45: 184..1737 (GS-P45)
US-10-934-998-97

Query Match 99.2%; Score 2677; DB 18; Length 517;
Best Local Similarity 100.0%; Pred. No. 1e-231;
Matches 506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGVILDDAGSSHTSLVI 64
Db 12 KESNVKTFCSKNILAILGFSSIIAVIALAVGLTQNKALPENVKYGVILDDAGSSHTSLVI 71
|||
Qy 65 YKWPAAEKENDTGTVVHVQVEECRVKPGISKFVKVNEIGIYLTDCMERAREVIPSQHOET 124
Db 72 YKWPAAEKENDTGTVVHVQVEECRVKPGISKFVKVNEIGIYLTDCMERAREVIPSQHOET 131
|||
Qy 125 PVLGATAGMRLLRMESEELADRVLDVVERSLSNYPDFQGARIIITQBEGAYGWTITNY 184
Db 132 PVLGATAGMRLLRMESEELADRVLDVVERSLSNYPDFQGARIIITQBEGAYGWTITNY 191
|||
Qy 185 LLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFRLYGK 244
Db 192 LLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQFRLYGK 251
|||
Qy 245 DYNVYTHSFLCYGKQOALWQKLAKOIQVASNEILRDPCHPHGKVKVNVSDLYKTPCTKR 304
Db 252 DYNVYTHSFLCYGKQOALWQKLAKOIQVASNEILRDPCHPHGKVKVNVSDLYKTPCTKR 311
|||
Qy 305 FEMTLFPQOFIEIGIGNYQOCHQSILELNTSYCPYSQCAFNGIFLPPLOGDFGAFSAFY 364
Db 312 FEMTLFPQOFIEIGIGNYQOCHQSILELNTSYCPYSQCAFNGIFLPPLOGDFGAFSAFY 371
|||
Qy 365 FVWKFLNLTSEKVSQEKVTMMKKFCAQPWEEKTSYAGVKSEKYLSEYCFSGTYILSLL 424
Db 372 FVWKFLNLTSEKVSQEKVTMMKKFCAQPWEEKTSYAGVKSEKYLSEYCFSGTYILSLL 431
|||
Qy 425 QGYHFTADSWEHIFHTGKIQGS DAGWTGLGYMLNLTNNMIPAEQPLSTPLSHSYVFLMVL 484
Db 432 QGYHFTADSWEHIFHTGKIQGS DAGWTGLGYMLNLTNNMIPAEQPLSTPLSHSYVFLMVL 491
|||
Qy 485 SLVLFVTVAIIIGLLIFHKPSYFWKDMV 510
Db 492 SLVLFVTVAIIIGLLIFHKPSYFWKDMV 517
|||||

RESULT 8
US-10-092-063-38
```

; Sequence 38, Application US/10092063  
; Publication No. US20020173005A1  
; GENERAL INFORMATION:  
; APPLICANT: Mulero, Julio  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES  
; FILE REFERENCE: 28110/35908  
; CURRENT APPLICATION NUMBER: US/10/092,063  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: 09/370,265  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350,836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273,447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/244,444  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/122,449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 38  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-092-063-38

Query Match 98.2%; Score 2650; DB 13; Length 502;  
Best Local Similarity 100.0%; Pred. No. 2.7e-229;  
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEDTRESNVKTCCKNIIAILGFSIIIVALLAVGLTONKALPENVKYGVLDAGSSHT	60
Db	1	MEDTRESNVKTCCKNIIAILGFSIIIVALLAVGLTONKALPENVKYGVLDAGSSHT	60
Qy	61	SLYIVKPAEKNDGTGVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPRSQ	120
Db	61	SLYIVKPAEKNDGTGVHVEECRVKPGISKFKVQKNEIGIYLTDCMERAREVIPRSQ	120
Qy	121	HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGQEEGAYGI	180
Db	121	HQETPVYLGATAGMRLRMESEELADRVLDVVERSLSNYPDFQGARIIITGQEEGAYGI	180
Qy	181	TINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQPR	240
Db	181	TINYLKGFQSKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNTIESPDNALQPR	240
Qy	241	LYGKDVNVYTHSFCLYCGKQALWQKLAKDIOVASNEILRDPCHFPGYKVVNSDLYKTP	300
Db	241	LYGKDVNVYTHSFCLYCGKQALWQKLAKDIOVASNEILRDPCHFPGYKVVNSDLYKTP	300
Qy	301	CTKREMTLPFOQFEIQIGNYQQCHQSILELFNTSYCPYSCAFNGIFLPPLOGDFGAF	360
Db	301	CTKREMTLPFOQFEIQIGNYQQCHQSILELFNTSYCPYSCAFNGIFLPPLOGDFGAF	360
Qy	361	SAFYFVMKFLNLTSEKVSQEKYTEMMKFKCAQWPBEIKTSYAGVKEKYLSEYCFSGTVIL	420
Db	361	SAFYFVMKFLNLTSEKVSQEKYTEMMKFKCAQWPBEIKTSYAGVKEKYLSEYCFSGTVIL	420
Qy	421	SLLLOGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIIPAEQPLSTPLSHSTYVFL	480
Db	421	SLLLOGYHFTADSWEHIFIGIKQSDAGWTGLGYMLNTNMIIPAEQPLSTPLSHSTYVFL	480
Qy	481	MVLFSLVLTVAIIIGLIFHKP	502
Db	481	MVLFSLVLTVAIIIGLIFHKP	502

RESULT 9

US-09-835-147-27  
; Sequence 27, Application US/09835147  
; Patent No. US20020002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Maliszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion  
; OTHER INFORMATION: construct of human CD39  
US-09-835-147-27

Query Match 87.4%; Score 2358; DB 9; Length 464;  
Best Local Similarity 97.8%; Pred. No. 4.5e-203;  
Matches 443; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy	24	SSIIATAVIALAVGLTONKALPENVKYGVLDAGSSHTSLYIYKWPBAEKENDTGVHVEE	83
Db	12	SCIALSLATVNSATONKALPENVKYGVLDAGSSHTSLYIYKWPBAEKENDTGVHVEE	71
Qy	84	CRVKGPGISKFKVQKNEIGIYLTDCMERAREVIPRSOHOETPVYLGATAGMRLRMESEE	143
Db	72	CRVKGPGISKFKVQKNEIGIYLTDCMERAREVIPRSOHOETPVYLGATAGMRLRMESEE	131
Qy	144	LADRVLDVVERSLSNYPDFQGARIIITGQEEGAYGWIITINYLKGFQSKTRWFSIVPYET	203
Db	132	LADRVLDVVERSLSNYPDFQGARIIITGQEEGAYGWIITINYLKGFQSKTRWFSIVPYET	191
Qy	204	NNQETFGALDLGGASTQVTFVPQNTIESPDNALQFRLYKDVNVYTHSFCLYCGKQALW	263
Db	192	NNQETFGALDLGGASTQVTFVPQNTIESPDNALQFRLYKDVNVYTHSFCLYCGKQALW	251
Qy	264	OKLAKDIOVASNEILRDPCHFPGYKVVNSDLYKTPCTKREMTLPFOQFEIQIGNYQ	323
Db	252	OKLAKDIOVASNEILRDPCHFPGYKVVNSDLYKTPCTKREMTLPFOQFEIQIGNYQ	311
Qy	324	QCHQSILELFNTSYCPYSCAFNGIFLPPLOGDFGAFSAFYFVMKFLNLTSEKVSQEKVT	383
Db	312	QCHQSILELFNTSYCPYSCAFNGIFLPPLOGDFGAFSAFYFVMKFLNLTSEKVSQEKVT	371
Qy	384	EMMKFKCAQWPBEIKTSYAGVKEKYLSEYCFSGTVILSLLLOGYHFTADSWEHIFIGIKI	443
Db	372	EMMKFKCAQWPBEIKTSYAGVKEKYLSEYCFSGTVILSLLLOGYHFTADSWEHIFIGIKI	431
Qy	444	QGSAGWTGLGYMLNTNMIIPAEQPLSTPLSHST	476
Db	432	QGSAGWTGLGYMLNTNMIIPAEQPLSTPLSHST	464

RESULT 10  
US-09-374-586-2  
; Sequence 2, Application US/09374586  
; Patent No. US20020138858A1  
; GENERAL INFORMATION:

```
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 0575/59167
; CURRENT APPLICATION NUMBER: US/09/374,586
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-374-586-2

Query Match      87.0%; Score 2348; DB 9; Length 439;
Best Local Similarity 100.0%; Pred. No. 3.3e-202;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKGPISKFVOK 97
Db 1 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKGPISKFVOK 60

QY 98 VNEIGIYLTDCMERAREVIPRSQHQTTPVYLGATAGVRLRMESBELADRVLDVVERSLS 157
Db 61 VNEIGIYLTDCMERAREVIPRSQHQTTPVYLGATAGVRLRMESBELADRVLDVVERSLS 120

QY 158 NYPDFQOGARIITGOEAGYGTITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGA 217
Db 121 NYPDFQOGARIITGOEAGYGTITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGA 180

QY 218 STQVTFVQNOTIESPDNALQFLRYGKDYNNVYTHSFLCYGKQDALWOKLAKDIOVASNEI 277
Db 181 STQVTFVQNOTIESPDNALQFLRYGKDYNNVYTHSFLCYGKQDALWOKLAKDIOVASNEI 240

QY 278 LRDPCHFPGYKVKVNVSDLYKTPCTKRFEMTLPPFOQFEIQIGNYQQCHQSILELFNTSY 337
Db 241 LRDPCHFPGYKVKVNVSDLYKTPCTKRFEMTLPPFOQFEIQIGNYQQCHQSILELFNTSY 300

QY 338 CPYSQAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQKVTMMKKFCAQPWEI 397
Db 301 CPYSQAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQKVTMMKKFCAQPWEI 360

QY 398 KTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFHGKIQGSDAGWTLYMLN 457
Db 361 KTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFHGKIQGSDAGWTLYMLN 420

QY 458 LTNMIPAEQPLSTPLSHST 476
Db 421 LTNMIPAEQPLSTPLSHST 439

RESULT 11
US-09-835-147-6
; Sequence 6, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; NUMBER OF SEQ ID NOS: 31
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-6

Query Match      87.0%; Score 2348; DB 9; Length 454;
Best Local Similarity 100.0%; Pred. No. 3.4e-202;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKGPISKFVOK 97
Db 16 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHQBECRVKGPISKFVOK 75

QY 98 VNEIGIYLTDCMERAREVIPRSQHQTTPVYLGATAGVRLRMESBELADRVLDVVERSLS 157
Db 76 VNEIGIYLTDCMERAREVIPRSQHQTTPVYLGATAGVRLRMESBELADRVLDVVERSLS 135

QY 158 NYPDFQOGARIITGOEAGYGTITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGA 217
Db 136 NYPDFQOGARIITGOEAGYGTITINYLKGFSQKTRWFSIVPYETNNQETFGALDLGA 195

QY 218 STQVTFVQNOTIESPDNALQFLRYGKDYNNVYTHSFLCYGKQDALWOKLAKDIOVASNEI 277
Db 196 STQVTFVQNOTIESPDNALQFLRYGKDYNNVYTHSFLCYGKQDALWOKLAKDIOVASNEI 255

QY 278 LRDPCHFPGYKVKVNVSDLYKTPCTKRFEMTLPPFOQFEIQIGNYQQCHQSILELFNTSY 337
Db 256 LRDPCHFPGYKVKVNVSDLYKTPCTKRFEMTLPPFOQFEIQIGNYQQCHQSILELFNTSY 315

QY 338 CPYSQAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQKVTMMKKFCAQPWEI 397
Db 316 CPYSQAFNGIFLPPLOQDGFAGSAFYFVMKFLNLTSEKVSQKVTMMKKFCAQPWEI 375

QY 398 KTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFHGKIQGSDAGWTLYMLN 457
Db 376 KTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFHGKIQGSDAGWTLYMLN 435

QY 458 LTNMIPAEQPLSTPLSHST 476
Db 436 LTNMIPAEQPLSTPLSHST 454

RESULT 12
US-09-835-147-30
; Sequence 30, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 463
; TYPE: PRT
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-30

Query Match      87.0%; Score 2348; DB 9; Length 463;
Best Local Similarity 100.0%; Pred. No. 3.5e-202;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVVEECRVKGPISKFVOK 97
DB 25 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVVEECRVKGPISKFVOK 84

QY 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL 157
DB 85 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL 144

QY 158 NYPDFQAGARIITQEBGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 217
DB 145 NYPDFQAGARIITQEBGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 204

QY 218 STQVTFVPQNTIESPDNALQFRLYGKDVNVYTHSFCLCYGKQALWQKLAKDIOVASNEI 277
DB 205 STQVTFVPQNTIESPDNALQFRLYGKDVNVYTHSFCLCYGKQALWQKLAKDIOVASNEI 264

QY 278 LRDPFCFHGGYKVVNSDLYKTPCTKRFEMTLFPQFQEIQIGNYQOCHQSILLELNTSY 337
DB 265 LRDPFCFHGGYKVVNSDLYKTPCTKRFEMTLFPQFQEIQIGNYQOCHQSILLELNTSY 324

QY 338 CPYSQCAFNGIFLPPLOGDFGAFSAFYFVNMKFLNLTSEKVSQKVTMMKKFCAQPWEI 397
DB 325 CPYSQCAFNGIFLPPLOGDFGAFSAFYFVNMKFLNLTSEKVSQKVTMMKKFCAQPWEI 384

QY 398 KTSVAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTLYGMLN 457
DB 385 KTSVAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTLYGMLN 444

QY 458 LTNNMPAEQPLSTPLSHST 476
DB 445 LTNNMPAEQPLSTPLSHST 463

RESULT 13
US-09-835-147-29
; Sequence 29, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39

Query Match      87.0%; Score 2348; DB 9; Length 473;
Best Local Similarity 100.0%; Pred. No. 3.7e-202;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVVEECRVKGPISKFVOK 97
DB 35 TONKALPENVKYGIIVLDAGSSHTSLYIKWPAEKENDTGVVHVVEECRVKGPISKFVOK 94

QY 98 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL 157
DB 95 VNEIGIYLTDCMERAREVIPSQHOETPVYLGATAGMRLLRMESEELADRVLDVVERSL 154

QY 158 NYPDFQAGARIITQEBGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 217
DB 155 NYPDFQAGARIITQEBGAYGWTITNYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGA 214

QY 218 STQVTFVPQNTIESPDNALQFRLYGKDVNVYTHSFCLCYGKQALWQKLAKDIOVASNEI 277
DB 215 STQVTFVPQNTIESPDNALQFRLYGKDVNVYTHSFCLCYGKQALWQKLAKDIOVASNEI 274

QY 278 LRDPFCFHGGYKVVNSDLYKTPCTKRFEMTLFPQFQEIQIGNYQOCHQSILLELNTSY 337
DB 275 LRDPFCFHGGYKVVNSDLYKTPCTKRFEMTLFPQFQEIQIGNYQOCHQSILLELNTSY 334

QY 338 CPYSQCAFNGIFLPPLOGDFGAFSAFYFVNMKFLNLTSEKVSQKVTMMKKFCAQPWEI 397
DB 335 CPYSQCAFNGIFLPPLOGDFGAFSAFYFVNMKFLNLTSEKVSQKVTMMKKFCAQPWEI 394

QY 398 KTSVAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTLYGMLN 457
DB 395 KTSVAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIFHGKIQGSDAGWTLYGMLN 454

QY 458 LTNNMPAEQPLSTPLSHST 476
DB 455 LTNNMPAEQPLSTPLSHST 473

RESULT 14
US-09-835-147-28
; Sequence 28, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-28

Query Match      87.0%; Score 2348; DB 9; Length 474;
Best Local Similarity 100.0%; Pred. No. 3.7e-202;

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2005, 16:22:35 ; Search time 6123.5 Seconds  
(without alignments)  
10801.234 Million cell updates/sec

Title: US-09-807-660C-5  
Perfect score: 1365  
Sequence: 1 gcacctacttaagttctac.....ctctctccactccacctaa 1365

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_ars.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1365	100.0	1365	6	BD228699
2	1365	100.0	1437	6	BD228700
3	1328	97.3	1464	6	BD228710
4	1319.2	96.6	1599	6	BD228698
5	1319.2	96.6	1704	9	HSU87967
6	1319.2	96.6	1818	6	AR168353
7	1319.2	96.6	1818	6	AR380930
8	1319.2	96.6	1818	6	AX828644
9	1319.2	96.6	1818	9	S73813
10	1319.2	96.6	2081	6	AX828400
11	1319.2	96.6	2081	9	HSN133133
12	1319.2	96.6	2986	6	CQ870272
13	1319.2	96.6	3236	6	CQ870276
14	1319.2	96.6	3502	6	CQ870270
15	1319.2	96.6	4411	6	AX281833
16	1305.2	95.6	3506	6	CQ870274
17	1039	76.1	1479	6	CQ769356
18	1019.8	74.7	1665	9	BC047664
19	888.4	65.1	1648	4	SSC133746

20	863	63.2	2312	10	AF037366	AF037366 Mus muscu	
21	863	63.2	2386	10	BC011278	BC011278 Mus muscu	
22	858.2	62.9	1686	10	RNU81295	U81295 Rattus norv	
23	835	61.2	2296	6	CQ870265	CQ870265 Sequence	
24	827.8	60.6	1958	4	AF005940	AF005940 Bos tauru	
25	703.2	51.5	1488	6	CQ870268	CQ870268 Sequence	
26	703.2	51.5	1815	9	HSA133134	AJ133134 Homo sapi	
c	27	640.2	46.9	704	6	AX828501	AX828501 Sequence
c	28	640.2	46.9	704	6	AX828547	AX828547 Sequence
29	541.6	39.7	2928	5	BC073267	BC073267 Xenopus l	
30	524.4	38.4	3211	5	BC076662	BC076662 Xenopus t	
31	463.2	33.9	764	6	CQ721824	CQ721824 Sequence	
32	438.8	32.1	4049	5	AJ720369	AJ720369 Gallus ga	
33	383.6	28.1	2450	5	BC078240	BC078240 Danio rer	
34	291	21.3	2783	6	CQ715235	CQ715235 Sequence	
35	291	21.3	2797	6	AR194793	AR194793 Sequence	
36	291	21.3	2797	6	AR562109	AR562109 Sequence	
37	291	21.3	2797	6	AR567207	AR567207 Sequence	
38	291	21.3	2797	6	AR567913	AR567913 Sequence	
39	291	21.3	2797	6	AX497067	AX497067 Sequence	
40	291	21.3	2797	9	AF039917	AF039917 Homo sapi	
41	291	21.3	2809	9	AF034840	AF034840 Homo sapi	
42	287.6	21.1	1494	6	CQ794578	CQ794578 Sequence	
43	287.6	21.1	1786	10	AY364442	AY364442 Mus muscu	
44	286	21.0	2338	10	BC031143	BC031143 Mus muscu	
45	275	20.1	1482	5	AF426405	AF426405 Gallus ga	

ALIGNMENTS

RESULT 1  
BD228699 1365 bp DNA linear PAT 17-JUL-2003  
LOCUS Inhibitors of platelet activation and recruitment.  
DEFINITION  
ACCESSION BD228699.1 GI:33038469  
VERSION JP 2002527096-A/2.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 1365)  
AUTHORS Maliszewski,C.R., Iii,R.B.G., Price,V.L. and Glmpe,S.D.  
TITLE Inhibitors of platelet activation and recruitment  
JOURNAL Patent: JP 2002527096-A 2 27-AUG-2002;  
IMMUNEX CORP  
COMMENT OS Artificial Sequence  
PN JP 2002527096-A/2  
PD 27-AUG-2002  
PF 13-OCT-1999 JP 2000577185  
PR 16-OCT-1998 US 60/104585,06-NOV-1998 US 60/107466 PR  
13-AUG-1999 US 60/149010  
PI CHARLES R MALISZEWSKI,RICHARD B GAYLE III,VIRGINIA L PRICE, PI  
STEVEN D GIMPEL  
PC C12N15/09,A61K38/00,A61P9/00,C07K14/705,C12N1/15,C12N1/19, PC  
C12N5/10,  
PC C12P21/02/C12N9/14,C12N15/00,A61K37/02,C12N5/00 CC  
Description of Artificial Sequence: Fusion construct of human CC  
CD39  
FH Key Location/Qualifiers  
FT CDS Location/Qualifiers  
1. .1365  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 100.0%; Score 1365; DB 6; Length 1365;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACCTACTTCAAGTTCTTACAAAGAAACACAGCTAACTAGTTCAACCCGACAAAGCA 60

Db 1 GCACCTACTTCAAGTTCTACAAAGAAAACACAGCTAACTAGTTCAACCCACAAAGCA 60  
QY 61 TTGCCAGAAAACGTTAAGTATGGATTTGCTCGATGCGGGTCTTCTCACACAAGTTTA 120  
Db 61 TTGCCAGAAAACGTTAAGTATGGATTTGCTCGATGCGGGTCTTCTCACACAAGTTTA 120  
QY 121 TACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAGGCGTGTGCATCAAGTAGAA 180  
Db 121 TACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAGGCGTGTGCATCAAGTAGAA 180  
QY 181 GAATGAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTCAGAAAAGTAAATGAAATAGGC 240  
Db 181 GAATGAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTCAGAAAAGTAAATGAAATAGGC 240  
QY 241 ATTATCTGATGATTCGATGGAAGAGCTAGGGAAGTATTCCAAGGTCCCAGCACCAA 300  
Db 241 ATTATCTGATTCGATGGAAGAGCTAGGGAAGTATTCCAAGGTCCCAGCACCAA 300  
QY 301 GAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGTGCTCAGGATGGAAAGTAA 360  
Db 301 GAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGTGCTCAGGATGGAAAGTAA 360  
QY 361 GAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCCTCAGCAACTACCCCTTTGAC 420  
Db 361 GAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCCTCAGCAACTACCCCTTTGAC 420  
QY 421 TTCAGGGTCCAGGATCATATTCTGGCCAAAGAGAAAGGTGCCTATGGCTGGATTAATATC 480  
Db 421 TTCAGGGTCCAGGATCATATTCTGGCCAAAGAGAAAGGTGCCTATGGCTGGATTAATATC 480  
QY 481 AACTATCTGTGGCCAAATTCAGTCAGAAAACAAAGTGGTTTACGATAGTCCCATATGAA 540  
Db 481 AACTATCTGTGGCCAAATTCAGTCAGAAAACAAAGTGGTTTACGATAGTCCCATATGAA 540  
QY 541 ACCAAATACAGGAAACCTTTGAGCTTTTGACCTTTGGGGAGCCTCTACACAAGTCACT 600  
Db 541 ACCAAATACAGGAAACCTTTGAGCTTTTGACCTTTGGGGAGCCTCTACACAAGTCACT 600  
QY 601 TTTGTACCCCAAAACAGACTATCGATGCCCCAGATAATGCTCTGCAATTTGCGCCTAT 660  
Db 601 TTTGTACCCCAAAACAGACTATCGATGCCCCAGATAATGCTCTGCAATTTGCGCCTAT 660  
QY 661 GGCAAGGACTACAATGCTCTACACATAGCTTCTTGTGATGGGAAGGATCAGGCACCTC 720  
Db 661 GGCAAGGACTACAATGCTCTACACATAGCTTCTTGTGATGGGAAGGATCAGGCACCTC 720  
QY 721 TGGCAGAACTGGCCCAAGGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGGACCCATGC 780  
Db 721 TGGCAGAACTGGCCCAAGGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGGACCCATGC 780  
QY 781 TTTTCATCTGGATATAGAAAGGTAGTGAACGTAAAGTGAACCTTTTCAAGACCCCTGCACC 840  
Db 781 TTTTCATCTGGATATAGAAAGGTAGTGAACGTAAAGTGAACCTTTTCAAGACCCCTGCACC 840  
QY 841 AAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAATCCAGGGTATTGGAAACTAT 900  
Db 841 AAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAATCCAGGGTATTGGAAACTAT 900  
QY 901 CAACAATGCCATCAAGAGCTCTGGAGCTCTTCAACACCAAGTTACTTGCCTTACTCCAG 960  
Db 901 CAACAATGCCATCAAGAGCTCTGGAGCTCTTCAACACCAAGTTACTTGCCTTACTCCAG 960  
QY 961 TGTGCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGATTTTGGGGCATTTTCAGCT 1020  
Db 961 TGTGCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGATTTTGGGGCATTTTCAGCT 1020  
QY 1021 TTTTACTTGTGATGAAGTTTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTG 1080  
Db 1021 TTTTACTTGTGATGAAGTTTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTG 1080  
QY 1081 ACTGAGATGATGAAAAGTTCTGTGCTCAGCCTTTGGAGGAGATAAAAACATCTTACGCT 1140

Db 1081 ACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGAGGAGATAAAAAACATCTTACGCT 1140  
QY 1141 GGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTGGTACCTACATTTCTCTCCCTC 1200  
Db 1141 GGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTGGTACCTACATTTCTCTCCCTC 1200  
QY 1201 CTTCTGCAAGGCTATCATTTTACAGCTGATTCCTGGAGCACATCCATTTCAATTTGGCAAG 1260  
Db 1201 CTTCTGCAAGGCTATCATTTTACAGCTGATTCCTGGAGCACATCCATTTCAATTTGGCAAG 1260  
QY 1261 ATCCAGGGCAGCGCGCGCTGGAGCTTTTGGGCTACATGCTGAACCTGACCAACATGATC 1320  
Db 1261 ATCCAGGGCAGCGCGCGCTGGAGCTTTTGGGCTACATGCTGAACCTGACCAACATGATC 1320  
QY 1321 CCAGCTGAGCAACCAATTGTCACACCTCTCTCCCACTCCACCTAA 1365  
Db 1321 CCAGCTGAGCAACCAATTGTCACACCTCTCTCCCACTCCACCTAA 1365  
  
RESULT 2  
BD228700  
LOCUS  
DEFINITION  
Inhibitors of platelet activation and recruitment.  
ACCESSION  
BD228700.1 GI:33038470  
VERSION  
JP 2002527096-A/3.  
KEYWORDS  
synthetic construct  
SOURCE  
ORGANISM  
REFERENCE  
1 (bases 1 to 1437)  
AUTHORS  
Maliszewski, C.R., Iii, R.B.G., Price, V.L. and Gimpe, S.D.  
TITLE  
Inhibitors of platelet activation and recruitment  
JOURNAL  
Patent: JP 2002527096-A 3 27-AUG-2002;  
IMMUNEX CORP  
COMMENT  
OS Artificial Sequence  
PN JP 2002527096-A/3  
PD 27-AUG-2002  
PF 13-OCT-1999 JP 2000577185  
PR 16-OCT-1998 US 60/104585, 06-NOV-1998 US 60/107466 PR  
13-AUG-1999 US 60/149010  
PI CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE, PI  
STEVEN D GIMPEL  
PC C12N15/09, A61K38/00, A61P9/00, C07K14/705, C12N1/15, C12N1/19, PC  
C12N5/10  
PC C12P21/02//C12N9/14, C12N15/00, A61K37/02, C12N5/00 CC  
Description of Artificial Sequence: Fusion construct of human CC  
CD39  
FH Key Location/Qualifiers  
FT CDS (1)..(1434).  
  
FEATURES  
source  
1..1437  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
  
ORIGIN  
Query Match 100.0%; Score 1365; DB 6; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GCACCTACTTCAAGTTCTACAAAGAAAACACAGCTAACTAGTTCAACCCACAAAGCA 60  
Db 73 GCACCTACTTCAAGTTCTACAAAGAAAACACAGCTAACTAGTTCAACCCACAAAGCA 132  
QY 61 TTGCCAGAAAACGTTAAGTATGGATTTGCTGGATGCGGGTCTTCTCACACAAGTTTA 120  
Db 133 TTGCCAGAAAACGTTAAGTATGGATTTGCTGGATGCGGGTCTTCTCACACAAGTTTA 192  
QY 121 TACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAGGCGTGTGCATCAAGTAGAA 180  
Db 193 TACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAGGCGTGTGCATCAAGTAGAA 252  
QY 181 GAATGAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTCAGAAAAGTAAATGAAATAGGC 240



Db 253 GAAATGAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTCAGAAAGTAAATGAAATAGGC 312  
Qy 241 ATTTACTGCTGACTGATTCGATGAAAGAGCTAGGGAAGTGATTCGAAGGTCCGAGCACCA 300  
Db 313 ATTTACTGCTGACTGATTCGATGAAAGAGCTAGGGAAGTGATTCGAAGGTCCGAGCACCA 372  
Qy 301 GAGACACCCGTTTAACTCTGGAGCCAGCGCAGGCATGCGGTTGCTCAGGATGGAAGTGA 360  
Db 373 GAGACACCCGTTTAACTCTGGAGCCAGCGCAGGCATGCGGTTGCTCAGGATGGAAGTGA 432  
Qy 361 GAGTTGGCAGACAGGGTCTGATGCTGGAGAGAGGAGCCTCAGCACTACCCCTTGAC 420  
Db 433 GAGTTGGCAGACAGGGTCTGATGCTGGAGAGAGGAGCCTCAGCACTACCCCTTGAC 492  
Qy 421 TTCCAGGGTGCCAGGATCATTAATCTGCGCAAGAGGAGGTGCTATGCGCTGGATTAATATC 480  
Db 493 TTCCAGGGTGCCAGGATCATTAATCTGCGCAAGAGGAGGTGCTATGCGCTGGATTAATATC 552  
Qy 481 AACTATCTGCTGGCAAAATTCAGTCAGAAAAACAAGGTGGTTCAGCATAGTCCCATATGAA 540  
Db 553 AACTATCTGCTGGCAAAATTCAGTCAGAAAAACAAGGTGGTTCAGCATAGTCCCATATGAA 612  
Qy 541 ACCAATATCAGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACT 600  
Db 613 ACCAATATCAGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACT 672  
Qy 601 TTGTGTACCCCAAAACAGACTATCAGTCCCGAGATAATGCTCTCAATTTTCGCTCTAT 660  
Db 673 TTGTGTACCCCAAAACAGACTATCAGTCCCGAGATAATGCTCTCAATTTTCGCTCTAT 732  
Qy 661 GCGAAGGACTACAATGTGTACACATAGCTTTCTGTGCTATGGGAAGGATCAGGCACTC 720  
Db 733 GCGAAGGACTACAATGTGTACACATAGCTTTCTGTGCTATGGGAAGGATCAGGCACTC 792  
Qy 721 TGGCAGAACTGCGCAAGGACATTCAGTTGCAAGTAATGAATTTCTCAGGAGCCCATGC 780  
Db 793 TGGCAGAACTGCGCAAGGACATTCAGTTGCAAGTAATGAATTTCTCAGGAGCCCATGC 852  
Qy 781 TTTTCATCTGGATATAAGAGGTAGTGAACGTAAAGTGACCTTTTCAAGACCCCTGCACC 840  
Db 853 TTTTCATCTGGATATAAGAGGTAGTGAACGTAAAGTGACCTTTTCAAGACCCCTGCACC 912  
Qy 841 AAGAGATTGAGATGACTCTTCCATTCAGCAGATTTGAAATCCAGGGTATTTGGAACATAT 900  
Db 913 AAGAGATTGAGATGACTCTTCCATTCAGCAGATTTGAAATCCAGGGTATTTGGAACATAT 972  
Qy 901 CAACAAATGCCATCAAGGATCCTGAGCTCTTCAACACAGTTACTGCGCTTACTCCAG 960  
Db 973 CAACAAATGCCATCAAGGATCCTGAGCTCTTCAACACAGTTACTGCGCTTACTCCAG 1032  
Qy 961 TGTGCTTTCAATGGGATTTTCTTGCCACACTCCAGGGGGATTTTGGGGCATTTTTCAGCT 1020  
Db 1033 TGTGCTTTCAATGGGATTTTCTTGCCACACTCCAGGGGGATTTTGGGGCATTTTTCAGCT 1092  
Qy 1021 TTTTACTTTGTGATGAAGTTTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAAAGGTG 1080  
Db 1093 TTTTACTTTGTGATGAAGTTTTTAACTTTGACATCAGAGAAAGTCTCTCAGGAAAAAGGTG 1152  
Qy 1081 ACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTTGGGAGGAGATAAAAACATCTTACGCT 1140  
Db 1153 ACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTTGGGAGGAGATAAAAACATCTTACGCT 1212  
Qy 1141 GGAGTAAAGGAGAGTACTCTGAGTGAATGCTTTTCTGTTGCTTACCTACTCTCTCCCTC 1200  
Db 1213 GGAGTAAAGGAGAGTACTCTGAGTGAATGCTTTTCTGTTGCTTACCTACTCTCTCCCTC 1272  
Qy 1201 CTTCTGCAAGGCTATCATTTTCAACAGCTGATTTCTGGGAGCAGATCCATTTTCAITGGCAAG 1260  
Db 1273 CTTCTGCAAGGCTATCATTTTCAACAGCTGATTTCTGGGAGCAGATCCATTTTCAITGGCAAG 1332  
Qy 1261 ATCAGGCGCAGGACCGCGCTTGGACTTTGGGCTTACATGCTGTAACCTGACCAACATGATC 1320

Db 1333 ATCCAGGCGAGCGACGCCGCTGGACTTTGGGCTACATGCTGAACTGACCAACATGATC 1392  
Qy 1321 CCAGCTGAGCAACCACTTGTCCACACCTCTCTCCCACTCCACCTAA 1365  
Db 1393 CCAGCTGAGCAACCACTTGTCCACACCTCTCTCCCACTCCACCTAA 1437  
RESULT 3  
BD228710 LOCUS BD228710 1464 bp DNA linear PAT 17-JUL-2003  
DEFINITION Inhibitors of platelet activation and recruitment.  
ACCESSION BD228710  
VERSION BD228710.1 GI:33038480  
KEYWORDS JP 2002527096-A/13.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences: artificial sequences.  
REFERENCE 1 (bases 1 to 1464)  
AUTHORS Maliszewski, C.R., Ili, R.B.G., Price, V.L. and Gimpe, S.D.  
TITLE Inhibitors of platelet activation and recruitment  
JOURNAL Patent: JP 2002527096-A 13 27-AUG-2002;  
IMMUNEX CORP  
COMMENT OS Artificial Sequence  
PN JP 2002527096-A/13  
PD 27-AUG-2002  
PF 13-OCT-1999 JP 2000577185 60/107466 PR  
PR 16-OCT-1998 US 60/104585,06-NOV-1998 US 60/107466 PR  
13-AUG-1999 US 60/149010  
PI CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE, PI  
STEVEN D GIMPEL  
PC C12N15/09, A61K38/00, C07K14/00, C07K14/705, C12N1/15, C12N1/19, PC  
C12N5/10,  
PC C12P21/02/C12N9/14, C12N15/00, A61K37/02, C12N5/00 CC  
Description of Artificial Sequence: Fusion construct of human CC  
CD39  
FH Key Location/Qualifiers  
FT CDS Location/Qualifiers  
source 1. 1464  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Query Match 97.3%; Score 1328; DB 6; Length 1464;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1334; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
Qy 11 CAAGTTCTCAAGAAAAACACAGCTAACTAGTTCAACCCAGAACAAAGCATTTGCCAGAAA 70  
Db 110 CTAGTTCAGGAGACTACAAAGATGACGATGACAAAACCCAGAACAAAGCATTTGCCAGAAA 169  
Qy 71 ACGTTAAGTATGGGATTTGCTGATGCGGGTCTTCTCACACAAGTTTATACATCTATA 130  
Db 170 ACGTTAAGTATGGGATTTGCTGATGCGGGTCTTCTCACACAAGTTTATACATCTATA 229  
Qy 131 AGTGGCCAGCAGAAAAAGGAGAAATCACACAGCGCTGGTGCATCAAGTAGAAGATCGAGGG 190  
Db 230 AGTGGCCAGCAGAAAAAGGAGAAATCACACAGCGCTGGTGCATCAAGTAGAAGATCGAGGG 289  
Qy 191 TTAAGGTCCTGGAAATCTCAAAAATTTGTTTCAGAAAGTAAATGAAATAGGCATTTTACCTGA 250  
Db 290 TTAAGGTCCTGGAAATCTCAAAAATTTGTTTCAGAAAGTAAATGAAATAGGCATTTTACCTGA 349  
Qy 251 CTGATTCGATGGAAGAGCTAGGGAAGTGATTCGAAGTCCAGGACCAAGAGACACCCG 310  
Db 350 CTGATTCGATGGAAGAGCTAGGGAAGTGATTCGAAGTCCAGGACCAAGAGACACCCG 409  
Qy 311 TTTACCTGGGAGCCAGCGCAGGCAATGCGGTTGCTCAGGATGGAAGTGAAGAGTTGGCAG 370  
Db 410 TTTACCTGGGAGCCAGCGCAGGCAATGCGGTTGCTCAGGATGGAAGTGAAGAGTTGGCAG 469  
Qy 371 ACAGGGTTCTGGATGTGGTGGAGAGGAGCCTCAGCAAACTACCCCTTTTCCAGGGTG 430

|||||  
470 ACAGGGTTCTGGATGTGGTGAGAGRGCTCAGCAACTACCCCTTTGACTCTCCAGGGTG 529  
QY 431 CCAGGATCATTTACTGSCCAAGAGAGGTCCTATGGCTGGATTACTATCAACTATCTGC 490  
Db 530 CCAGGATCATTTACTGSCCAAGAGAGGTCCTATGGCTGGATTACTATCAACTATCTGC 589  
QY 491 TGGGCAANTTCAGTCAGAAACAAGTGGTTCAGCATAGTCCCATATGAACCAATAATC 550  
Db 590 TGGGCAANTTCAGTCAGAAACAAGTGGTTCAGCATAGTCCCATATGAACCAATAATC 649  
QY 551 AGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACCTTTTGATACCCC 610  
Db 650 AGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACCTTTTGATACCCC 709  
QY 611 AAAACAGACTATCGAGTCCCCAGATAATGCTCTGCAATTCGCCCTCTATGCAAGGACT 670  
Db 710 AAAACAGACTATCGAGTCCCCAGATAATGCTCTGCAATTCGCCCTCTATGCAAGGACT 769  
QY 671 ACAATGCTACACATAGCTTTCTGCTATGCGAAGGATCAGGCACCTCTGCGCAAAAC 730  
Db 770 ACAATGCTACACATAGCTTTCTGCTATGCGAAGGATCAGGCACCTCTGCGCAAAAC 829  
QY 731 TGCCCAAGGACATTCAGGTTGCAAGTAAATGAAATTCCTCAGGGACCCATGCTTTTCATCCTG 790  
Db 830 TGCCCAAGGACATTCAGGTTGCAAGTAAATGAAATTCCTCAGGGACCCATGCTTTTCATCCTG 889  
QY 791 GATATGAAGAGTGTGAACGTAAAGTGAAGTCTTTTCAAGACCCCTCGACAAGAGATTG 850  
Db 890 GATATGAAGAGTGTGAACGTAAAGTGAAGTCTTTTCAAGACCCCTCGACAAGAGATTG 949  
QY 851 AGATGACTCTTCCATTCAGACGCTTTGAAATCCAGGGTATGGAATCTACACATGCTG 910  
Db 950 AGATGACTCTTCCATTCAGACGCTTTGAAATCCAGGGTATGGAATCTACACATGCTG 1009  
QY 911 ATCAAAGCATCTCGAGCTCTTCAAACCAAGTACTGCCCCTTACTCCAGTGTGCCCTTCA 970  
Db 1010 ATCAAAGCATCTCGAGCTCTTCAAACCAAGTACTGCCCCTTACTCCAGTGTGCCCTTCA 1069  
QY 971 ATGGGATTTTCTTGCCACCACTCCAGGGGATTTTGGGGGATTTTTCAGCTTTTACTTTG 1030  
Db 1070 ATGGGATTTTCTTGCCACCACTCCAGGGGATTTTGGGGGATTTTTCAGCTTTTACTTTG 1129  
QY 1031 TGATGAAGTTTAAATTCGACATCAGAGAACTCTCTCAGGAAAGGTGACTGAGATGA 1090  
Db 1130 TGATGAAGTTTAAATTCGACATCAGAGAACTCTCTCAGGAAAGGTGACTGAGATGA 1189  
QY 1091 TGAATAAGTTCTGTGCTCGACCTTTGGAGGAGATAAACAATCTTACGCTGGAGTAAAGG 1150  
Db 1190 TGAATAAGTTCTGTGCTCGACCTTTGGAGGAGATAAACAATCTTACGCTGGAGTAAAGG 1249  
QY 1151 AGAAGTACCTGAGTGAATACGTCTTTCTGGTACCTACATCTCTCCCTCTCTCTGCAAG 1210  
Db 1250 AGAAGTACCTGAGTGAATACGTCTTTCTGGTACCTACATCTCTCCCTCTCTCTGCAAG 1309  
QY 1211 GCTATCATTTACAGCTGATTTCTGGAGCAGATCCATTTTCATTTGGCAGATCCAGGCA 1270  
Db 1310 GCTATCATTTACAGCTGATTTCTGGAGCAGATCCATTTTCATTTGGCAGATCCAGGCA 1369  
QY 1271 GCCACGCCGCTGGACTTTTGGGCTACATGCTGAACTCTGACCAACATGATCCCACTGTAGC 1330  
Db 1370 GCCACGCCGCTGGACTTTTGGGCTACATGCTGAACTCTGACCAACATGATCCCACTGTAGC 1429  
QY 1331 AACCATTTGCCACACCTCTCTCCACTCCCACTTAA 1365  
Db 1430 AACCATTTGCCACACCTCTCTCCACTCCCACTTAA 1464

RESULT 4  
BD228698  
LOCUS  
DEFINITION Inhibitors of platelet activation and recruitment.  
ACCESSION BD228698  
PAT 17-JUL-2003

BD228698.1 GI:33038468  
JP 2002527096-A/1  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1599)  
AUTHORS Maliszewski, C.R., Iii, R.B.G., Price, V.L. and Gimpe, S.D.  
TITLE Inhibitors of platelet activation and recruitment  
JOURNAL Patent: JP 2002527096-A 1 27-AUG-2002;  
IMMUNEX CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002527096-A/1  
PD 27-AUG-2002  
PF 13-OCT-1999 JP 2000577185  
PR 16-OCT-1998 US 60/104585, 06-NOV-1998 US 60/107466 PR  
13-AUG-1999 US 60/149010  
PI CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE, PI  
STEVEN D GIMPEL  
PC C12N15/09, A61K38/00, A61P9/00, C07K14/705, C12N1/15, C12N1/19, PC  
C12N5/10,  
PC C12P21/02//C12N9/14, C12N15/00, A61K37/02, C12N5/00 CC  
Inhibitors of platelet activation and recruitment PH Key  
FEATURES  
FT CDS Location/Qualifiers  
1..1599  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 96.6%; Score 1319.2; DB 6; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAAAGTTAAAGTATGGGATTTGCTGGATCGCG 100  
Db 173 GGTGACCCAGAACAAAGCATTTGCCAGAAAAAGTTAAAGTATGGGATTTGCTGGATCGCG 232  
QY 101 GTTCTTCTCACACAAGTTTATATCATCTATAAGTGGCCAGACAGAAAAAGGAGAATGACACAG 160  
Db 233 GTTCTTCTCACACAAGTTTATATCATCTATAAGTGGCCAGACAGAAAAAGGAGAATGACACAG 292  
QY 161 GGTGTGTGTCATAGCTAGAGAATCGAGGTTAAAGTCTCGAATCTCAAAATTTGTTTC 220  
Db 293 GGTGTGTGTCATAGCTAGAGAATCGAGGTTAAAGTCTCGAATCTCAAAATTTGTTTC 352  
QY 221 AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTTGCATGGAAAGAGCTAGGGAAGTGA 280  
Db 353 AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTTGCATGGAAAGAGCTAGGGAAGTGA 412  
QY 281 TTCCAAGTCCGAGCAACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGATCGCGT 340  
Db 413 TTCCAAGTCCGAGCAACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGATCGCGT 472  
QY 341 TGCTCAGGATGGAAGTGAAGTGGCAGACAGGTTCTGGATGTGTTGGAGAGAGGCC 400  
Db 473 TGCTCAGGATGGAAGTGAAGTGGCAGACAGGTTCTGGATGTGTTGGAGAGAGGCC 532  
QY 401 TCAGCAACTACCCCTTTTGACTTCCAGGTTGCCAGGATCATTTACTGCCCAAGAGGAAGTG 460  
Db 533 TCAGCAACTACCCCTTTTGACTTCCAGGTTGCCAGGATCATTTACTGCCCAAGAGGAAGTG 592  
QY 461 CCTATGGCTGGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAAAGGTGTT 520  
Db 593 CCTATGGCTGGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAAAGGTGTT 652  
QY 521 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTTGGGG 580  
Db 653 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTTGGGG 712  
QY 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAAGACTATCGAGTCCCCAGATAATG 640

Db	713																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
----	-----	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

MEDLINE	97115858				
PUBMED	8955160				
REFERENCE	2 (bases 1 to 1704)				
AUTHORS	Robson, S.C., Kaczmarek, E., Siegel, J.B., Candinas, D., Koziak, K.,				
	Millan, M., Hancock, W. and Bach, F.H.				
TITLE	Loss of ATP diphosphohydrolase activity with endothelial cell				
	activation				
JOURNAL	J. Exp. Med. 185 (1), 153-163 (1997)				
MEDLINE	97149443				
PUBMED	8996251				
REFERENCE	3 (bases 1 to 1704)				
AUTHORS	Kaczmarek, E., Koziak, K., Sevigny, J., Siegel, J.B., Anrather, J.,				
	Beaudoin, A.R., Bach, F.H. and Robson, S.C.				
TITLE	Direct Submision				
JOURNAL	Submitted (30-JAN-1997) Medicine, Harvard University, 99 Brookline				
	Avenue, BIDMC, RN, Boston, MA 02215, USA				
FEATURES	Location/Qualifiers				
	1..1704				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/chromosome="10"				
	/cell_type="endothelial cells"				
	/tissue_type="umbilical vein"				
	31..1563				
	/note="CD39"				
	/codon_start=1				
	/product="ATP diphosphohydrolase"				
	/protein_id="AAB47572.1"				
	/db_xref="GI:1842120"				
	/translation="MEDTKEKNTVPCSKNLAILGPFSSIIAIVALLAVLTQNKALP				
	ENVKIVLDAGSSHTSLYIKPAEKENDTGVVHQVECKVKGIGIKFQKVNIEIG				
	IYLDCHMERAREVIPSQHVLTGATAGKMLLRMESEBLADRVLDVRSLSNYP				
	FDFOGARITIQEBSGAVGWITINLLGKFSOKTRWFSIVPVETNNQETFGALDLGAS				
	QTVPFQNTIESPDNALQPLRYKDYNVYTHSLCYGKQDALQKADLOVASNE				
	ILRDPCHFGPKYKVVNSDLYTCTKRFEMTLFPQPEIGNIGYQCHQSILSEFN				
	TSYCPYSCAFNGIFLPLQDGFAGSAFYFMKFLNLTSEKVSQEKYQVEMKKFCAG				
	PWEIKTYSAGVKEKLSYECSTGYTILSLLOQHYHFTADSWHEHIFTKIQGSDAGW				
	TLGYMLNLNNMIPAEQPLSTPLSHSTVFLVFLVSLVLTVAIIIGLLIFHKPSYFWD				
	MF"				
ORIGIN					
Query Match	96.6%	Score 1319.2;	DB 9;	Length 1704;	
Best Local Similarity	99.8%	Pred. No. 0;			
Matches 1321;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;	
Qy	41	GTTCAACCCAGAACAAAGCATTCGCAGAAAACGTTAGTATGGATTCGTGGATGCGG	100		
Db	137	GGTTGACCCAGAACAAAGCATTCGCAGAAAACGTTAGTATGGATTCGTGGATGCGG	196		
Qy	101	GTTCTTCTCACACAAGTTTATACATCTATAGTGGCCAGCAAGAGAGATGACACAG	160		
Db	197	GTTCTTCTCACACAAGTTTATACATCTATAGTGGCCAGCAAGAGAGATGACACAG	256		
Qy	161	GCGTGGTGCATCAAGTAGAAGATTCAGGGGTAAAGGTCCTGGAATCTCAAAAATTTGTT	220		
Db	257	GCGTGGTGCATCAAGTAGAAGATTCAGGGGTAAAGGTCCTGGAATCTCAAAAATTTGTT	316		
Qy	221	AGAAAGTAAATGAATAGGCATTTACCTGACTGATTCGATGCAAGAGAGCTAGGGAAGTGA	280		
Db	317	AGAAAGTAAATGAATAGGCATTTACCTGACTGATTCGATGCAAGAGAGCTAGGGAAGTGA	376		
Qy	281	TTCCAAGGTCCACACCAAGAGACACCGCTTTTACCTGGGAGCCACGCGCATGCCGT	340		
Db	377	TTCCAAGGTCCACACCAAGAGACACCGCTTTTACCTGGGAGCCACGCGCATGCCGT	436		
Qy	341	TGCTCAGGATGGAAGTAGAAGATTCGACACAGGGTTCTGGATGTGTGGAGAGGAGCC	400		
Db	437	TGCTCAGGATGGAAGTAGAAGATTCGACACAGGGTTCTGGATGTGTGGAGAGGAGCC	496		
Qy	401	TCAGCAACTACCCCTTTGACTCTCCAGGGTGCAGGATCATTTACTGGCCCAAGAGAGGTG	460		
Db	497	TCAGCAACTACCCCTTTGACTCTCCAGGGTGCAGGATCATTTACTGGCCCAAGAGAGGTG	556		





QY 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACATTTGTCCACACCTCTCTCCACTCCA 1360  
|||||  
Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACATTTGTCCACACCTCTCTCCACTCCA 1493  
|||||  
QY 1361 CCTA 1364  
|||||  
Db 1494 CCTA 1497  
|||||  
RESULT 8  
AX828644  
LOCUS AX828644 1818 bp DNA linear PAT 12-DEC-2003  
DEFINITION Sequence 290 from Patent WO03074073.  
ACCESSION AX828644  
VERSION AX828644.1 GI:39838595  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Al-Mahmood, S., Colin, S. and Schneider, C.  
TITLE Genes involved in regulating angiogenesis, pharmaceutical  
preparations containing same and applications thereof  
JOURNAL Patent: WO 03074073-A 290 12-SEP-2003;  
Gene Signal (FR)  
FEATURES  
source Location/Qualifiers  
1. 1818  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 96.6%; Score 1319.2; DB 6; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGATTGCTGGATGCGG 100  
|||||  
Db 174 GGTGACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGATTGCTGGATGCGG 233  
|||||  
QY 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG 160  
|||||  
Db 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG 293  
|||||  
QY 161 GCGTGTGTCATCAAGTAGAAGATGACAGGTTAAAGTCTCGAAATCTCAAAAATTTGTTT 220  
|||||  
Db 294 GCGTGTGTCATCAAGTAGAAGATGACAGGTTAAAGTCTCGAAATCTCAAAAATTTGTTT 353  
|||||  
QY 221 AGAAGTAAATGAATAGGCAATTTACCTGACTGATTTGATGGAAGAGCTTAGGGAAGTGA 280  
|||||  
Db 354 AGAAGTAAATGAATAGGCAATTTACCTGACTGATTTGATGGAAGAGCTTAGGGAAGTGA 413  
|||||  
QY 281 TTCCAAGGTCCTCAGACCAAGAGACACCCGTTTACCTGGGAGCCACGCGGATCGGT 340  
|||||  
Db 414 TTCCAAGGTCCTCAGACCAAGAGACACCCGTTTACCTGGGAGCCACGCGGATCGGT 473  
|||||  
QY 341 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTTGGTGGAGAGGACC 400  
|||||  
Db 474 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTTGGTGGAGAGGACC 533  
|||||  
QY 401 TCAGCAACTACCCCTTTGACTTTCAGGGTCCAGGATCATTTACTGGCCAGAGAGAGGTG 460  
|||||  
Db 534 TCAGCAACTACCCCTTTGACTTTCAGGGTCCAGGATCATTTACTGGCCAGAGAGAGGTG 593  
|||||  
QY 461 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAACAAGTGGT 520  
|||||  
Db 594 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAACAAGTGGT 653  
|||||  
QY 521 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGAGCTTTGGACCTTGGGG 580  
|||||  
Db 654 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGAGCTTTGGACCTTGGGG 713  
|||||

QY 581 GAGCCTCTACACAAAGTACATTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG 640  
|||||  
Db 714 GAGCCTCTACACAAAGTACATTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG 773  
|||||  
QY 641 CTCTGCAATTTCCGCTCTATAGGCAAGGACTACAATGTCTTACACACATAGCTTTCTGTGCT 700  
|||||  
Db 774 CTCTGCAATTTCCGCTCTATAGGCAAGGACTACAATGTCTTACACACATAGCTTTCTGTGCT 833  
|||||  
QY 701 ATGGGAAGGATCAGGCACATCTGGCGAAGAACTGGCCNAGGACATTCAGGTTGCAAGTAATG 760  
|||||  
Db 834 ATGGGAAGGATCAGGCACATCTGGCGAAGAACTGGCCNAGGACATTCAGGTTGCAAGTAATG 893  
|||||  
QY 761 AATTTCTCAGGACCCCATGCTTTTCTCTGGATATAAGAAAGGTAGTGAACGTAAAGTGACC 820  
|||||  
Db 894 AATTTCTCAGGACCCCATGCTTTTCTCTGGATATAAGAAAGGTAGTGAACGTAAAGTGACC 953  
|||||  
QY 821 TTTACAAGACCCCTGACCAAGAGATTGAGATGACTCTTCCATTCCAGCAGTTTGA 880  
|||||  
Db 954 TTTACAAGACCCCTGACCAAGAGATTGAGATGACTCTTCCATTCCAGCAGTTTGA 1013  
|||||  
QY 881 TCAGGGTATTGGAAACTATCAACATGCCATCAAGCATCTGGAGCTCTTCAACACCA 940  
|||||  
Db 1014 TCAGGGTATTGGAAACTATCAACATGCCATCAAGCATCTGGAGCTCTTCAACACCA 1073  
|||||  
QY 941 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGGCCACCATCCAGGGG 1000  
|||||  
Db 1074 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGGCCACCATCCAGGGG 1133  
|||||  
QY 1001 ATTTTGGGCAATTTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1060  
|||||  
Db 1134 ATTTTGGGCAATTTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1193  
|||||  
QY 1061 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAGAAAGTTCTGTGCTGAGCTTTGGAGG 1120  
|||||  
Db 1194 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAGAAAGTTCTGTGCTGAGCTTTGGAGG 1253  
|||||  
QY 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTCTG 1180  
|||||  
Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTCTG 1313  
|||||  
QY 1181 GTACCTACATTTCTCCCTCTCTTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGAGC 1240  
|||||  
Db 1314 GTACCTACATTTCTCCCTCTCTTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGAGC 1373  
|||||  
QY 1241 ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGACCGCGCTGGACTTTGGGCTACATGC 1300  
|||||  
Db 1374 ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGACCGCGCTGGACTTTGGGCTACATGC 1433  
|||||  
QY 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCACTCCA 1360  
|||||  
Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCACTCCA 1493  
|||||  
QY 1361 CCTA 1364  
|||||  
Db 1494 CCTA 1497  
|||||  
RESULT 9  
S73813  
LOCUS S73813 1818 bp mRNA linear PRI 12-APR-1995  
DEFINITION CD39=lymphoid cell activation antigen [human, B lymphoblastoid cell  
line, MP-1, mRNA, 1818 nt].  
ACCESSION S73813  
VERSION S73813.1 GI:765255  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1818)  
REFERENCE  
AUTHORS Maliszewski, C.R., Delespesse, G.J., Schoenborn, M.A., Armitage, R.J.,  
Fanslow, W.C., Nakajima, T., Baker, E., Sutherland, G.R.,

TITLE Poindexter,K., Birks,C. et,al.  
The CD39 lymphoid cell activation antigen. Molecular cloning and structural characterization  
J. Immunol. 153 (8), 3574-3583 (1994)  
MEDLINE 95015846  
PUBMED 7930580  
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gbbeg 15681] from the original journal article.  
FEATURES  
Location/Qualifiers  
1..1818  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
1..1818  
/gene="CD39"  
/note="lymphoid cell activation antigen, CD39"  
68..1600  
/gene="CD39"  
/note="guanosine diphosphatase homolog; yeast guanosine diphosphatase homolog"  
/codon\_start=1  
/product="lymphoid cell activation antigen"  
/protein\_id="AAB32152.1"  
/db\_xref="GI:745256"  
/translation="MEDIKESNVKTFCSKNILAILGFSIIAIVALLAVLTONKALP  
ENVKGI VLDAGSHSTSIYKPAEKENDTGVHQVEECRVKPGISKPVKSNIEG  
IYLDTCMERAREVIPSQHOETPVYLGATAGMRLRMESEELADRLVDVRSKNYIP  
FDFOGARIIITGEBGAYGWTINYLKGRFSIOKTRWFSIVPVETNNQETFGALDLGAS  
TOVTFVPONOTTESPDNALOPRLKYDYNVYTHSLCYKQDALWOKLAKDIOVASNE  
ILARDPCFHPGKYKYNVSDLYKTPCTKRPFEMTLPFQOPEIQIGINYQOCHOSILELFPN  
TSYCFYCAFNGLIFLPLQGDGFAPSYFVFMKFLNLTSEKVSQEKVETMMKFCFAQ  
PMEEIKTSVAGYKELSEYCFSGTYSILSLLOQYHFTADSWEHIFHTGKIQSGDAGW  
TLGYMLNLTNMIPARQPLSTPLSHSTYVFLMVLFLSLVLTVAIIIGLLIFHPKPSYFWD  
NV"

source

gene

CDS

ORIGIN

Query Match 96.6%; Score 1319.2; DB 9; Length 1818;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 41 GTTCAACCCAGAACAAAGCATTCAGAGAAACGTTAAAGTATCGGATTTGCTGGATCGG 100  
DB 174 GGTTCACCCAGAACAAAGCATTCAGAGAAACGTTAAAGTATCGGATTTGCTGGATCGG 233  
QY 101 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAGAGAGATGACACAG 160  
DB 234 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAGAGAGATGACACAG 293  
QY 161 GCGTGGTGATCAAGTAGAAGATGACAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 220  
DB 294 GCGTGGTGATCAAGTAGAAGATGACAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 353  
QY 221 AGAAGATTAATAGATAGCATTTACCTGACTGATTCGATGCAAGAGAGCTAGGAGTGA 280  
DB 354 AGAAGATTAATAGATAGCATTTACCTGACTGATTCGATGCAAGAGAGCTAGGAGTGA 413  
QY 281 TTCCAAGGTCACAGCAACAGAGACACCGGTTTACCTGGAGCCACGCGAGCATGCGGT 340  
DB 414 TTCCAAGGTCACAGCAACAGAGACACCGGTTTACCTGGAGCCACGCGAGCATGCGGT 473  
QY 341 TGCTCAGATGAAAGTAGAAGTTGGCAGACAGCGGTTCTGATGTGTGGAGAGAGCC 400  
DB 474 TGCTCAGATGAAAGTAGAAGTTGGCAGACAGCGGTTCTGATGTGTGGAGAGAGCC 533  
QY 401 TCAGCAACTACCCCTTGACTTCCAGGGTGCCAGGATCATTTACTGGCCAGAGGAGGTG 460  
DB 534 TCAGCAACTACCCCTTGACTTCCAGGGTGCCAGGATCATTTACTGGCCAGAGGAGGTG 593  
QY 461 CCTATGGCTGGATTACTTCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTG 520  
DB 594 CCTATGGCTGGATTACTTCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTG 653  
QY 521 TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGG 580

DB 654 TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTTGGAGCTTTTGGACCTTTGGGG 713  
QY 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCAGTCCCCAGATAATG 640  
DB 714 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCAGTCCCCAGATAATG 773  
QY 641 CTCTGCAATTTCCCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTTGTGTCT 700  
DB 774 CTCTGCAATTTCCCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTTGTGTCT 833  
QY 701 ATGGGAAGGATCAGGCACCTCTGGCAGAAACTGGCCCAAGAGACTTTCAGGTTGCAAGTAATG 760  
DB 834 ATGGGAAGGATCAGGCACCTCTGGCAGAAACTGGCCCAAGAGACTTTCAGGTTGCAAGTAATG 893  
QY 761 AAATTTCTCAGGGACCCATGCTTTTCACTCTGGATATAAGAAAGGTAGTGAACGTAAGTGACC 820  
DB 894 AAATTTCTCAGGGACCCATGCTTTTCACTCTGGATATAAGAAAGGTAGTGAACGTAAGTGACC 953  
QY 821 TTTTCAAGACCCCTTGCCACCAAGAGATTGAGATGACTCTTCCATTCCAGCAGTTTGAAGA 980  
DB 954 TTTTCAAGACCCCTTGCCACCAAGAGATTGAGATGACTCTTCCATTCCAGCAGTTTGAAGA 1013  
QY 881 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAAGCATCCTGAGACTTTCACACACCA 940  
DB 1014 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAAGCATCCTGAGACTTTCACACACCA 1073  
QY 941 GTTACTGCGCTTACTCCAGGTGCTCTCAATGGGATTTCTTTCGCCACCACTCCAGGGGG 1000  
DB 1074 GTTACTGCGCTTACTCCAGGTGCTCTCAATGGGATTTCTTTCGCCACCACTCCAGGGGG 1133  
QY 1001 ATTTTGGGGCAATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA 1060  
DB 1134 ATTTTGGGGCAATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA 1193  
QY 1061 AAGTCTCTCAGAAAAAGGTGATGAGATGATGAAAAAGTTCTGCTCAGCCCTTGGAGG 1120  
DB 1194 AAGTCTCTCAGAAAAAGGTGATGAGATGATGAAAAAGTTCTGCTCAGCCCTTGGAGG 1253  
QY 1121 AGATAAAACATCTTACGCTCGAGTAAAGGAGAGTACTCTGAGTGAATCTGCTTTTCTG 1180  
DB 1254 AGATAAAACATCTTACGCTCGAGTAAAGGAGAGTACTCTGAGTGAATCTGCTTTTCTG 1313  
QY 1181 GTACCTCATTTCTCTCCCTCTCTGCAAGGCTATCATTTTCAACAGCTGATTTCTGGGAGC 1240  
DB 1314 GTACCTCATTTCTCTCCCTCTCTGCAAGGCTATCATTTTCAACAGCTGATTTCTGGAGC 1373  
QY 1241 ACATCCATTTCTTGGCAAGATCCAGGCGAGGAGCCGCTGGACTTTGGGCTACATGC 1300  
DB 1374 ACATCCATTTCTTGGCAAGATCCAGGCGAGGAGCCGCTGGACTTTGGGCTACATGC 1433  
QY 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA 1360  
DB 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA 1493  
QY 1361 CCTA 1364  
DB 1494 CCTA 1497  
RESULT 10  
AX828400  
LOCUS AX828400  
DEFINITION Sequence 46 from Patent WO03074073.  
ACCESSION AX828400  
VERSION AX828400.1 GI:39838400  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Al-Mahmood,S., Colin,S. and Schneider,C.









Db 242 GTTCTTCTCACAGGTTTATACATCTATAGTGGCCAGCAGAAAGGAGATGACACAG 301  
QY 161 GCGTGTGCATCAAGTAGAAGAAATGACGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 220  
Db 302 GCGTGTGCATCAAGTAGAAGAAATGACGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 361  
QY 221 AGAAAGTAATGAANAATAGGCAATTTACTGATCTGATGTCATGGAAGAGCTAGGGAAGTGA 280  
Db 362 AGAAAGTAATGAANAATAGGCAATTTACTGATCTGATGTCATGGAAGAGCTAGGGAAGTGA 421  
QY 281 TTCCAAGGTCCTCAGCAGCAAGACACCCGTTTACTGCGAGGCCACGGCAGGATCGCGT 340  
Db 422 TTCCAAGGTCCTCAGCAGCAAGACACCCGTTTACTGCGAGGCCACGGCAGGATCGCGT 481  
QY 341 TGCTCAGGATGGAAGTAGAGTTGGCAGACAGGGTTCCTGGATGTTGGTGGAGAGAGCC 400  
Db 482 TGCTCAGGATGGAAGTAGAGTTGGCAGACAGGGTTCCTGGATGTTGGTGGAGAGAGCC 541  
QY 401 TCAGCAACTACCCCTTTGACTTCAGGGTGCAGGATCATTACTGGCCCAAGAGAGGTG 460  
Db 542 TCAGCAACTACCCCTTTGACTTCAGGGTGCAGGATCATTACTGGCCCAAGAGAGGTG 601  
QY 461 CCTATGGCTGATTTACTATCAACTATCTGCTGGGCCAAATTCAGTCAGAAAAACAAGTGTG 520  
Db 602 CCTATGGCTGATTTACTATCAACTATCTGCTGGGCCAAATTCAGTCAGAAAAACAAGTGTG 661  
QY 521 TCAGCATAGTCCCATATGAACAATAATCAGAAAACTTTGGAGCTTTGGACCTTTGGGG 580  
Db 662 TCAGCATAGTCCCATATGAACAATAATCAGAAAACTTTGGAGCTTTGGACCTTTGGGG 721  
QY 581 GAGCCTCTACAAAGTCACCTTTGTATCCCAACCAACAGACTATCGAGTCCCAAGATAATG 640  
Db 722 GAGCCTCTACAAAGTCACCTTTGTATCCCAACCAACAGACTATCGAGTCCCAAGATAATG 781  
QY 641 CTCTGCAATTTCCGCTCTATGGCAAGGACTACAAATGTCTACACACATAGCTTCTTGCT 700  
Db 782 CTCTGCAATTTCCGCTCTATGGCAAGGACTACAAATGTCTACACACATAGCTTCTTGCT 841  
QY 701 ATGGGAAGATCAGGCACCTGCGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 760  
Db 842 ATGGGAAGATCAGGCACCTGCGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 901  
QY 761 AAATTCAGGGACCCATGCTTTCATCTCGGATATAGAAAGGTAGTGAAGTGAAGTACC 820  
Db 902 AAATTCAGGGACCCATGCTTTCATCTCGGATATAGAAAGGTAGTGAAGTGAAGTACC 961  
QY 821 TTTTCAAGACCCCTGCAACAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 880  
Db 962 TTTTCAAGACCCCTGCAACAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 1021  
QY 881 TCAGGGTATTTGAAACTATCAACAATGCCATCAAAAGCATCTCGGAGCTTTCAACACCA 940  
Db 1022 TCAGGGTATTTGAAACTATCAACAATGCCATCAAAAGCATCTCGGAGCTTTCAACACCA 1081  
QY 941 GTTATGCCCTTACTCCAGTGTGCTTCAATCGGATTTTCTTGCCACCACTCCAGGGG 1000  
Db 1082 GTTATGCCCTTACTCCAGTGTGCTTCAATCGGATTTTCTTGCCACCACTCCAGGGG 1141  
QY 1001 ATTTTGGGGCATTTTCAGCTTTTACTTGTGTGATGAAGTTTAAACTTGACATCAGAGA 1060  
Db 1142 ATTTTGGGGCATTTTCAGCTTTTACTTGTGTGATGAAGTTTAAACTTGACATCAGAGA 1201  
QY 1061 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTTCTGTGCTAGCCTTTGGAGG 1120  
Db 1202 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTTCTGTGCTAGCCTTTGGAGG 1261  
QY 1121 AGATAAAAACATCTTACGCTGGAGTAAAGAGAAAGTACCTGAGTGAATACTGCTTTCTG 1180  
Db 1262 AGATAAAAACATCTTACGCTGGAGTAAAGAGAAAGTACCTGAGTGAATACTGCTTTCTG 1321  
QY 1181 GTACCTACATTTCTCCCTCTTCTGCAAGGCTATCATTTTCAACAGCTGATTTCTCGGAGC 1240

1322 GTACCTACATTTCTCCCTCTTCTGCAAGGCTATCATTTACAGCTGATTTCTCTGGAGC 1381  
QY 1241 ACATCCATTTTATTTGGCAAGATCCAGGGCAGCAGCGCGCTGGACTTTGGGCTACATGC 1300  
Db 1382 ACATCCATTTTATTTGGCAAGATCCAGGGCAGCAGCGCGCTGGACTTTGGGCTACATGC 1441  
QY 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCA 1360  
Db 1442 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCA 1501  
QY 1361 CCTA 1364  
Db 1502 CCTA 1505  
RESULT 13  
LOCUS CQ870276 3236 bp DNA linear PAT 13-SEP-2004  
DEFINITION Sequence 697 from Patent WO2004074320.  
ACCESSION CQ870276  
VERSION CQ870276.1 GI:51999880  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Morris,D.W., Morris,D.W. and Malandro,M.S.  
TITLE Novel therapeutic targets in cancer  
JOURNAL Patent: WO 2004074320-A 697 02-SEP-2004;  
Sagres Discovery, Inc. (US)  
FEATURES  
source location/Qualifiers  
1..3236  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 96.6%; Score 1319.2; DB 6; Length 3236;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAAAGTTAAGTATGGGATTTGCTGGATGCGG 100  
Db 432 GGTGACCCAGAACAAAGCATTTGCCAGAAAAAGTTAAGTATGGGATTTGCTGGATGCGG 491  
QY 101 GTTCTTCTCACAAAGTTTATACATCTATAAGTGCCAGCAGAAAAAGGAGAATGACACAG 160  
Db 492 GTTCTTCTCACAAAGTTTATACATCTATAAGTGCCAGCAGAAAAAGGAGAATGACACAG 551  
QY 161 GGTGTGTGATCAAGTAGAAGAAATGCGAGGTTTAAAGGTCCTGGAAATCTCAAAATTTGTTTC 220  
Db 552 GGTGTGTGATCAAGTAGAAGAAATGCGAGGTTTAAAGGTCCTGGAAATCTCAAAATTTGTTTC 611  
QY 221 AGAAAGTAATGAANAATAGGCAATTTACTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGA 280  
Db 612 AGAAAGTAATGAANAATAGGCAATTTACTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGA 671  
QY 281 TTCCAAGGTCCCAAGCAGCAAGAGACACCCGTTTACTCGGAGCCACGGCAGGATCCCGGT 340  
Db 672 TTCCAAGGTCCCAAGCAGCAAGAGACACCCGTTTACTCGGAGCCACGGCAGGATCCCGGT 731  
QY 341 TGCTCAGGATGGAAGTAGAGATTGGCAGACAGGGTTCCTGGATGTTGGTGGAGAGAGCC 400  
Db 732 TGCTCAGGATGGAAGTAGAGATTGGCAGACAGGGTTCCTGGATGTTGGTGGAGAGAGCC 791  
QY 401 TCAGCAACTACCCCTTTGACTTTCCAGGGTGCAGGATCATTTACTGCCCAAGAGAGAGGTG 460  
Db 792 TCAGCAACTACCCCTTTGACTTTCCAGGGTGCAGGATCATTTACTGCCCAAGAGAGAGGTG 851  
QY 461 CCTATGGCTGGAATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAAGAAAAACAAGTGTG 520  
Db 852 CCTATGGCTGGAATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAAGAAAAACAAGTGTG 911

QY	521	TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG	580
Db	912	TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG	971
QY	581	GAGCCTCTACACAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCGAGTAATG	640
Db	972	GAGCCTCTACACAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCGAGTAATG	1031
QY	641	CTCTGCAATTTGGCCTCTATGGCAAGACTACAAATGCTACACACATAGCTTCTTGCTG	700
Db	1032	CTCTGCAATTTGGCCTCTATGGCAAGACTACAAATGCTACACACATAGCTTCTTGCTG	1091
QY	701	ATGGGAAGGATCAGGCACCTCTGGCAGAAACTGCGCAAGGACATTCAGGTTGCAAGTAATG	760
Db	1092	ATGGGAAGGATCAGGCACCTCTGGCAGAAACTGCGCAAGGACATTCAGGTTGCAAGTAATG	1151
QY	761	AAATTTCTCAGGACCCCATCTTTCACTCTGGATATAAGAGGTAGTGAACTGAGTGACC	820
Db	1152	AAATTTCTCAGGACCCCATCTTTCACTCTGGATATAAGAGGTAGTGAACTGAGTGACC	1211
QY	821	TTTACAAGACCCCTCGACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA	880
Db	1212	TTTACAAGACCCCTCGACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA	1271
QY	881	TCCAGGGTATTTGGAACCTATCAACAAATGCGCATCAAGGCATCTGGAGCTTTCAACACCA	940
Db	1272	TCCAGGGTATTTGGAACCTATCAACAAATGCGCATCAAGGCATCTGGAGCTTTCAACACCA	1331
QY	941	GTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTCTTCCACCACTCCAGGGGG	1000
Db	1332	GTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTCTTCCACCACTCCAGGGGG	1391
QY	1001	ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTAACTTGACATCAGAGA	1060
Db	1392	ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTAACTTGACATCAGAGA	1451
QY	1061	AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGTTCTGTCTCAGCCTTGGGAGG	1120
Db	1452	AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGTTCTGTCTCAGCCTTGGGAGG	1511
QY	1121	AGATAAACAATCTTACGCTGAGTAAAGGAGAGTACCTGAGTGAATCTGCTTTCTG	1180
Db	1512	AGATAAACAATCTTACGCTGAGTAAAGGAGAGTACCTGAGTGAATCTGCTTTCTG	1571
QY	1181	GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTCCTGGGAGC	1240
Db	1572	GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTCCTGGGAGC	1631
QY	1241	ACATCCATTTTCAATGGCAAGATCCAGGGCAGCGACCGCGCTGGACTTTGGGCTACATGC	1300
Db	1632	ACATCCATTTTCAATGGCAAGATCCAGGGCAGCGACCGCGCTGGACTTTGGGCTACATGC	1691
QY	1301	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACTCTCTCCCACTCCA	1360
Db	1692	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACTCTCTCCCACTCCA	1751
QY	1361	CCTA 1364	
Db	1752	CCTA 1755	

RESULT 14  
LOCUS Q870270  
DEFINITION Sequence 691 from Patent WO2004074320.  
ACCESSION Q870270  
VERSION Q870270.1 GI:51999877  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE	1	Morris, D.W., Morris, D.W. and Malandro, M.S. Novel therapeutic targets in cancer Patent: WO 2004074320-A 691 02-SEP-2004; Sagres Discovery, Inc. (US)
FEATURES	source	Location/Qualifiers 1..3502 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
ORIGIN		
Query Match	96.6%;	Score 1319.2; DB 6; Length 3502;
Best Local Similarity	99.8%;	Pred. No. 0;
Matches 1321;	Conservative 0;	Mismatches 3; Indels 0; Gaps 0;
QY	41	GTTCAACCCAGAACCAAGCATTTGCCAGAAAACGTTTAAGTATGGGATTTGCTGGATGCCG 100
Db	698	GTTTGACCCAGAACCAAGCATTTGCCAGAAAACGTTTAAGTATGGGATTTGCTGGATGCCG 757
QY	101	GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGAGAAAAGGAGAAATGACACAG 160
Db	758	GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGAGAAAAGGAGAAATGACACAG 817
QY	161	GCGTGGTGCATCAAGTAGAAGATGCAAGGTTAAAGGTCCTGGAATCTCAAAAATTTGTTTC 220
Db	818	GCGTGGTGCATCAAGTAGAAGATGCAAGGTTAAAGGTCCTGGAATCTCAAAAATTTGTTTC 877
QY	221	AGAAAGTAAATGAATAGGCATTTACCTGACTGATTTGATGCTGGAAGAGCTAGGGAAGTGA 280
Db	878	AGAAAGTAAATGAATAGGCATTTACCTGACTGATTTGATGCTGGAAGAGCTAGGGAAGTGA 937
QY	281	TTCCAAGTCTCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATCGCGT 340
Db	938	TTCCAAGTCTCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATCGCGT 997
QY	341	TGCTCAGATGGAAAGTGAAGTGGCAGACAGGTTCTGATGTTGTTGGAGAGAGCC 400
Db	998	TGCTCAGATGGAAAGTGAAGTGGCAGACAGGTTCTGATGTTGTTGGAGAGAGCC 1057
QY	401	TCAGCACTACCCCTTTGACTTCCAGGGTGCAGGATCATTTACTGGCCCAAGGAGGTTG 460
Db	1058	TCAGCACTACCCCTTTGACTTCCAGGGTGCAGGATCATTTACTGGCCCAAGGAGGTTG 1117
QY	461	CCTATGGCTGATTAATCAATCTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGT 520
Db	1118	CCTATGGCTGATTAATCAATCTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGT 1177
QY	521	TCAGATAGTCCCATATGAAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 580
Db	1178	TCAGATAGTCCCATATGAAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 1237
QY	581	GAGCCTCTACACAAGTCACTTTGCTACCCCAAAACCCAGACTATCGAGTCCCGAGTAATG 640
Db	1238	GAGCCTCTACACAAGTCACTTTGCTACCCCAAAACCCAGACTATCGAGTCCCGAGTAATG 1297
QY	641	CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGCTGT 700
Db	1298	CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGCTGT 1357
QY	701	ATGGGAAGGATCAGGCACCTCTGGCAGAAACTGCGCAAGGACATTCAGGTTGCAAGTAATG 760
Db	1358	ATGGGAAGGATCAGGCACCTCTGGCAGAAACTGCGCAAGGACATTCAGGTTGCAAGTAATG 1417
QY	761	AAATTTCTCAGGACCCCATGCTTTTCATCTGGATATAAGAGGTAGTGAACTGAGTGACC 820
Db	1418	AAATTTCTCAGGACCCCATGCTTTTCATCTGGATATAAGAGGTAGTGAACTGAGTGACC 1477
QY	821	TTTACAAGACCCCTCGACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 880
Db	1478	TTTACAAGACCCCTCGACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 1537
QY	881	TCCAGGTTATTTGGAACCTATCAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACACCA 940

Db 1538 TCAGGGTATGGAACTATCAACATGCCATCAAGAGCTCTGGAGCTCTTCAACACCA 1597  
Qy 941 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACACCTCCAGGGG 1000  
Db 1598 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACACCTCCAGGGG 1657  
Qy 1001 ATTTTGGGGCATTTTCAGCTTTTACTTTGTGTGATGAAGTTTTTAAACTTTGACATCAGAGA 1060  
Db 1658 ATTTTGGGGCATTTTCAGCTTTTACTTTGTGTGATGAAGTTTTTAAACTTTGACATCAGAGA 1717  
Qy 1061 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGGAGG 1120  
Db 1718 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGGAGG 1777  
Qy 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTG 1180  
Db 1778 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTG 1837  
Qy 1181 GTACCTACATTTCTCCCTCTCTCGAAGGCTATCATTTTCAGCTGATTTCTCTGGAGC 1240  
Db 1838 GTACCTACATTTCTCCCTCTCTCGAAGGCTATCATTTTCAGCTGATTTCTCTGGAGC 1897  
Qy 1241 ACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGCGCTGGACTTTTGGGCTACATGC 1300  
Db 1898 ACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGCGCTGGACTTTTGGGCTACATGC 1957  
Qy 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1360  
Db 1958 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 2017  
Qy 1361 CCTA 1364  
Db 2018 CCTA 2021

RESULT 15  
AX281833  
LOCUS AX281833 4411 bp DNA linear PAT 02-NOV-2001  
DEFINITION Sequence 242 from Patent WO01/77389.  
ACCESSION AX281833  
VERSION AX281833.1 GI:16609084  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Shiffman,D., Somogyi,R., Lawn,R., Seilhamer,J.J., Porter,G.J.,  
Mikita,T. and Tai,J.  
TITLE Genes expressed in foam cell differentiation  
JOURNAL Patent: WO 01/77389-A 242 18-OCT-2001;  
Incyte Genomics, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..4411  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="Incyte ID No: 347965.2"

ORIGIN  
Query Match 96.6%; Score 1319.2; DB 6; Length 4411;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 41 GTTCAACCCAGAACAAAGCATTCGCCAGAAAACCGTTAAGTATGGGATTTGCTGGATCGCG 100  
Db 184 GGTTCACCCAGAACAAAGCATTCGCCAGAAAACCGTTAAGTATGGGATTTGCTGGATCGCG 243  
Qy 101 GTTCTTCTCACAAGTTTATACATCTATAAGTGGCCAGAGAAAAGGAGAATGACACAG 160  
Db 244 GTTCTTCTCACAAGTTTATACATCTATAAGTGGCCAGAGAAAAGGAGAATGACACAG 303

Qy 161 GCGTGTGTCATCAAGTAGAAGAAATCAGGGTTAAAGGTCCTCGAAATCTCAAAATTTGTTC 220  
Db 304 GCGTGTGTCATCAAGTAGAAGAAATCAGGGTTAAAGGTCCTCGAAATCTCAAAATTTGTTC 363  
Qy 221 AGAAAGTAAATGAAATAGGCATTTACTGACTGATTTGTCATGGAAGAGCTAGGGAAGTGA 280  
Db 364 AGAAAGTAAATGAAATAGGCATTTACTCTGACTGATTTGTCATGGAAGAGCTAGGGAAGTGA 423  
Qy 281 TTCCAGGCTCCAGCACCAAGAGAGACCCCGTTTACCTGGGAGCCACGGCAGGATCCGGT 340  
Db 424 TTCCAGGCTCCAGCACCAAGAGAGACCCCGTTTACCTGGGAGCCACGGCAGGATCCGGT 483  
Qy 341 TGCCTCAGGATGCAAAAGTGAAGAGTTGGCAGACAGAGGTTCTCGATGTGTGTCGAGAGAGCC 400  
Db 484 TGCCTCAGGATGCAAAAGTGAAGAGTTGGCAGACAGAGGTTCTCGATGTGTGTCGAGAGAGCC 543  
Qy 401 TCAGCAACTACCCCTTTTGAATTTCCAGGCTGTCAGGATCAATTTACCTGAGGAGGAAAGGTTG 460  
Db 544 TCAGCAACTACCCCTTTTGAATTTCCAGGCTGTCAGGATCAATTTACCTGAGGAGGAAAGGTTG 603  
Qy 461 CCTATGGCTGGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAGAAAACAAGTGTGT 520  
Db 604 CCTATGGCTGGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAGAAAACAAGTGTGT 663  
Qy 521 TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTTGGAGCTTTGGACCTTTGGGG 580  
Db 664 TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTTGGAGCTTTGGACCTTTGGGG 723  
Qy 581 GAGCCTCTACAAGAGTCACTTTTGTATCCCAAAAACAGACTATCGAGTCCCAGATAAATG 640  
Db 724 GAGCCTCTACAAGAGTCACTTTTGTATCCCAAAAACAGACTATCGAGTCCCAGATAAATG 783  
Qy 641 CTCTGCAATTTTCGCTCTATGTCAGGAGGACTACAATGTCTACACATAGCTTCTTGTGCT 700  
Db 784 CTCTGCAATTTTCGCTCTATGTCAGGAGGACTACAATGTCTACACATAGCTTCTTGTGCT 843  
Qy 701 ATGGGAAGGATCAGGCACCTCTGCGCAAAAACCTGGCCAAAGGACATTTCAAGTTGCAAGTAATG 760  
Db 844 ATGGGAAGGATCAGGCACCTCTGCGCAAAAACCTGGCCAAAGGACATTTCAAGTTGCAAGTAATG 903  
Qy 761 AAATTTCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAAGTGACC 820  
Db 904 AAATTTCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAAGTGACC 963  
Qy 821 TTTCAGAGACCCCTGCGACCAAGAGATTTGAGTGAATCTTCCATTTCCAGCAGTTTGAAG 880  
Db 964 TTTCAGAGACCCCTGCGACCAAGAGATTTGAGTGAATCTTCCATTTCCAGCAGTTTGAAG 1023  
Qy 881 TCCAGGCTATTGGAAAACCTATCAACAATGCCATCAAGGACATCCCTGGAGCTCTTCAACACCA 940  
Db 1024 TCCAGGCTATTGGAAAACCTATCAACAATGCCATCAAGGACATCCCTGGAGCTCTTCAACACCA 1083  
Qy 941 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACACCTCCAGGGGG 1000  
Db 1084 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACACCTCCAGGGGG 1143  
Qy 1001 ATTTTGGGGCATTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA 1060  
Db 1144 ATTTTGGGGCATTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA 1203  
Qy 1061 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTTCTGTCTCAGCCCTTGGGAGG 1120  
Db 1204 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTTCTGTCTCAGCCCTTGGGAGG 1263  
Qy 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTG 1180  
Db 1264 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTG 1323  
Qy 1181 GTACCTTACATTTCTCCCTCTCTTCTGCAAGGCTATCATTTTCAGCTGATTTCTCTGGAGC 1240  
Db 1324 GTACCTTACATTTCTCCCTCTCTTCTGCAAGGCTATCATTTTCAGCTGATTTCTCTGGAGC 1383  
Qy 1241 ACATCCATTTTCATTTGGCAAGATCCAGGGCAGGGAACGCCGGCTGGACTTTTGGGCTACATGC 1300

Accession	Sequence	Length
Db	ACATCCATTTCTATTGGCAAGATCAGGGCAGCAGCCGGCTGGACTTTGGGTACATGC	1443
Qy	TGAACCTGACCACCATGATCCAGCTGAGCAACCATTTGTCCACACTCTCTCCCACTCCA	1360
Db	TGAACCTGACCACCATGATCCAGCTGAGCAACCATTTGTCCACACTCTCTCCCACTCCA	1503
Qy	CCTA	1364
Db	CCTA	1507

Search completed: September 21, 2005, 20:35:06  
Job time : 6130.5 secs

**THIS PAGE BLANK (USPTO)**

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2005, 16:22:05 ; Search time 785.776 Seconds  
(without alignments)  
10283.394 Million cell updates/sec

Title: US-09-807-660C-5  
Perfect score: 1365  
Sequence: 1 gcactacttcaagtctac.....ctctctccactccacctaa 1365

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1365	100.0	1365	3 AD00206	Aad00206 Human sol
2	1365	100.0	1365	3 AD00201	Aad00201 Fusion co
3	1365	100.0	1437	3 AD00207	Aad00207 Human sol
4	1365	100.0	1437	3 AD00202	Aad00202 Coding re
5	1328	97.3	1464	3 AD00209	Aad00209 Human sol
6	1328	97.3	1464	3 AD00204	Aad00204 Coding re
7	1319.2	96.6	1599	3 AD00205	Aad00205 Human sol
8	1319.2	96.6	1599	3 AD00200	Aad00200 Human sol
9	1319.2	96.6	1599	12 ADL24294	Adl24294 Human CD3
10	1319.2	96.6	1704	3 AAA96069	Aaa96069 Human ATP
11	1319.2	96.6	1704	10 ADJ57261	Adj57261 Human CD3
12	1319.2	96.6	1818	2 AAT38516	Aat38516 Human lym
13	1319.2	96.6	1818	2 AAT33966	Aat33966 DNA codin
14	1319.2	96.6	1818	11 ADI32149	Adi32149 Human cDN
15	1319.2	96.6	1818	12 ADK60414	Adk60414 Angiogene
16	1319.2	96.6	1818	12 ADK60715	Adk60715 Angiogene
17	1319.2	96.6	1818	12 ADP73338	Adp73338 CD39 lym
18	1319.2	96.6	2080	11 ADN95840	Adn95840 Human BEC
19	1319.2	96.6	2081	6 ABK83558	Abk83558 Human cDN
20	1319.2	96.6	2081	12 ADK60471	Adk60471 Angiogene

21	1319.2	96.6	2081	12 ADK60772	Adk60772 Angiogene
22	1319.2	96.6	2081	12 ADP73094	Adp73094 Angiogene
23	1319.2	96.6	2986	13 ABD32956	Abd32956 Human can
24	1319.2	96.6	3236	13 ABD32958	Abd32958 Human can
25	1319.2	96.6	3502	13 ABD32955	Abd32955 Human can
26	1319.2	96.6	4411	6 AAS94987	Aas94987 Human DNA
27	1305.2	95.6	3506	13 ABD32957	Abd32957 Human can
28	1287.4	94.3	3244	13 ACN42028	Acn42028 Human dia
29	1119.4	82.0	3165	13 ACN42029	Acn42029 Human dia
30	1039	76.1	1479	10 ADI62639	Adi62639 Human apo
31	835	61.2	2296	13 ABD32952	Abd32952 Mouse can
32	703.2	51.5	1488	13 ABD32954	Abd32954 Human can
C 33	640.2	46.9	704	12 ADK60271	Adk60271 Antisense
C 34	640.2	46.9	704	12 ADK60572	Adk60572 Antisense
C 35	640.2	46.9	704	12 ADP73195	Adp73195 Angiogene
C 36	640.2	46.9	6164	12 ADK60317	Adk60317 Angiogene
C 37	640.2	46.9	6164	12 ADK60618	Adk60618 Angiogene
C 38	640.2	46.9	6164	12 ADP73241	Adp73241 Angiogene
39	414	30.3	475	9 ACH37444	Ach37444 Human end
40	379	27.8	484	9 ACH35840	Ach35840 Human end
41	291	21.3	2797	3 AAA96067	Aaa96067 Human ect
42	291	21.3	2797	6 AAD31694	Aad31694 Human CD3
43	291	21.3	2797	6 ABK10350	Abk10350 DNA encod
44	291	21.3	2797	12 ADQ99443	Adq99443 Human CD3
45	291	21.3	2797	13 ADR69172	Adr69172 Human CD3

ALIGNMENTS

RESULT 1

AAD00206

ID AAD00206 standard; DNA; 1365 BP.

XX AC AAD00206;

XX DT 17-AUG-2000 (first entry)

XX DE Human soluble CD39 and IL2 N-terminus comprising fusion DNA construct.

KW Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT CDS 1..1365

FT FT /\*tag= a /product= "Fusion protein of human Interleukin 2 (IL2) N-terminus and human soluble CD39 protein"

FT FT misc\_feature 1..45

FT FT /\*tag= b /note= "N-terminus of mature human interleukin 2 (IL2) "

FT FT misc\_feature 46..1362

FT FT /\*tag= c /note= "Coding region of human soluble CD39 (solCD39) "

XX WO200023459-A1.

XX PD 27-APR-2000.

XX PF 13-OCT-1999; 99WO-US022955.

XX PR 16-OCT-1998; 98US-0104595P.

XX PR 06-NOV-1998; 98US-0107466P.

XX PR 13-AUG-1999; 99US-0149010P.





KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;  
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;  
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;  
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;  
KW occlusion; reocclusion; stenosis; restenosis; antitanginal; cardiant;  
KW cerebroprotective; antiarteriosclerotic; vasotrophic; anticoagulant;  
KW coronary ischaemia; vascular occlusion; ss.  
OS Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX 1..1365  
XX CDS /tag= a  
XX /product= "Human soluble CD39 protein"  
XX  
XX WO200023094-A2.  
XX  
XX 27-APR-2000.  
XX  
XX 13-OCT-1999; 99WO-US023641.  
XX  
XX 16-OCT-1998; 98US-0104585P.  
XX 06-NOV-1998; 98US-0107466P.  
XX 13-AUG-1999; 99US-0149010P.  
XX  
XX (IMV ) IMMUNEX CORP.  
XX (CORR ) CORNELL RES FOUND INC.  
XX  
XX Maliszewski CR, Gayle RB, Marcus AJ;  
XX  
XX WPI; 2000-339518/29.  
XX P-PSDB; AAY70890.  
XX  
XX Inhibiting platelet activation and recruitment, useful for treating a  
XX mammal suffering from unstable angina, myocardial infarction, stroke,  
XX coronary artery disease or injury, comprises administering soluble CD39  
XX polypeptides.  
XX  
XX Claim 10; Page 93-95; 118pp; English.  
XX  
XX The present cDNA sequence is a fusion construct encoding sol(soluble)CD39  
XX having apyrase activity. Fusion of 12 amino acids from the N-terminus of  
XX mature human IL2 to the solCD39 coding region results in high levels of  
XX both expression and activity in the supernatants of transfected cells.  
XX This is used in the treatment of unstable angina, myocardial infarction,  
XX stroke, coronary artery disease or injury, atherosclerosis, peripheral  
XX vascular occlusion, preclampsia, embolism, platelet-associated ischaemic  
XX disorder including lung ischaemia, coronary ischaemia and cerebral  
XX ischaemia, a thrombotic disorder including coronary artery thrombosis,  
XX cerebral artery thrombosis, intracardiac thrombosis, peripheral artery  
XX thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous  
XX thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.  
XX Soluble CD39 is also useful for preventing thrombus formation or  
XX reformation, occlusion, reocclusion, stenosis or restenosis of blood  
XX vessels or stroke  
XX  
XX Sequence 1365 BP; 394 A; 317 C; 319 G; 335 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 1365; DB 3; Length 1365;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
XX Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 GCACCTACTTCAAGTTCTACAAGAAACACAGCTAAGTTCAACCCAGAACAAAGCA 60  
XX  
XX 1 GCACCTACTTCAAGTTCTACAAGAAACACAGCTAAGTTCAACCCAGAACAAAGCA 60  
XX  
XX 61 TTGCGAGAAAACGTTTAAGTATGGGATGTGCTGGATGCGGGTTCTTCTCACAAAGTTTA 120  
XX  
XX 61 TTGCGAGAAAACGTTTAAGTATGGGATGTGCTGGATGCGGGTTCTTCTCACAAAGTTTA 120  
XX  
XX 121 TACATCTATAGTGGCCAGCAGAAAGAGATGACACAGGGGTGGTGCATCAAGTAGAA 180  
XX  
XX 121 TACATCTATAGTGGCCAGCAGAAAGAGATGACACAGGGGTGGTGCATCAAGTAGAA 180

QY 181 GAATCAGGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTCAGAAAGTAAATGAAATAGGC 240  
DB 181 GAATCAGGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTCAGAAAGTAAATGAAATAGGC 240  
QY 241 ATTTACCTGACTGATGTGATGGAAGAGACTAGGGAAGTGTATCCAAAGTCCAGACCCAA 300  
DB 241 ATTTACCTGACTGATGTGATGGAAGAGACTAGGGAAGTGTATCCAAAGTCCAGACCCAA 300  
QY 301 GAGACACCCGTTTACCTGGGAGCCACGCGCATGCGGTGCTCAGATGGAAGTGA 360  
DB 301 GAGACACCCGTTTACCTGGGAGCCACGCGCATGCGGTGCTCAGATGGAAGTGA 360  
QY 361 GAGTTGGCAGACAGGGTTCTGGATGTGTTGGAGAGAGCCTCAGCAACTACCCCTTTGAC 420  
DB 361 GAGTTGGCAGACAGGGTTCTGGATGTGTTGGAGAGAGCCTCAGCAACTACCCCTTTGAC 420  
QY 421 TTCCAGGGTGCAGGATCATTTACTGGCCAAAGAGAGGTGCTATGGCTGGATTAATATC 480  
DB 421 TTCCAGGGTGCAGGATCATTTACTGGCCAAAGAGAGGTGCTATGGCTGGATTAATATC 480  
QY 481 AACTATCTGCTGGGCAAAATTCAGTCAGAAACAAAGTGTGTTTCAGCATAGTCCCATATGAA 540  
DB 481 AACTATCTGCTGGGCAAAATTCAGTCAGAAACAAAGTGTGTTTCAGCATAGTCCCATATGAA 540  
QY 541 ACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAACTCACT 600  
DB 541 ACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAACTCACT 600  
QY 601 TTTGTACCCCAAAACCCAGACTATCGAGTCCCAAGATAATGCTCTGCAATTTGCGCTCTAT 660  
DB 601 TTTGTACCCCAAAACCCAGACTATCGAGTCCCAAGATAATGCTCTGCAATTTGCGCTCTAT 660  
QY 661 GGCAGAGACTACAATGCTACACATAGCTTTGCTGCTATGGGAAGATCAGGACCTC 720  
DB 661 GGCAGAGACTACAATGCTACACATAGCTTTGCTGCTATGGGAAGATCAGGACCTC 720  
QY 721 TGGCAGAACTGGCCAAAGGACATTCAGGTTTCAAGTAAATGAAATTTCTCAGGAGACCCATGC 780  
DB 721 TGGCAGAACTGGCCAAAGGACATTCAGGTTTCAAGTAAATGAAATTTCTCAGGAGACCCATGC 780  
QY 781 TTTCACTCTGATATAGAAGGTAGTGAACGTAGTGACCTTTTACAAGACCCCTTGACCC 840  
DB 781 TTTCACTCTGATATAGAAGGTAGTGAACGTAGTGACCTTTTACAAGACCCCTTGACCC 840  
QY 841 AAGAGATTGAGATGACTCTTCCATTCAGAGTTTGAATCCAGGGTATTTGGAAACTAT 900  
DB 841 AAGAGATTGAGATGACTCTTCCATTCAGAGTTTGAATCCAGGGTATTTGGAAACTAT 900  
QY 901 CAACAATGCCATCAAGCATCCTCGAGCTTTCAACACACAGTACTGCGCTTACTCCAG 960  
DB 901 CAACAATGCCATCAAGCATCCTCGAGCTTTCAACACACAGTACTGCGCTTACTCCAG 960  
QY 961 TGTGCTTCAATGGGATTTTCTGCCACCACTCCAGGGGATTTTGGGGCATTTTTCAGCT 1020  
DB 961 TGTGCTTCAATGGGATTTTCTGCCACCACTCCAGGGGATTTTGGGGCATTTTTCAGCT 1020  
QY 1021 TTTTACTTTGTGATGAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTG 1080  
DB 1021 TTTTACTTTGTGATGAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTG 1080  
QY 1081 ACTGAGATGATGAAAAAGTTTCTGTGCTCAGCCTTTGGGAGGAGATAAAAACATCTTACGCT 1140  
DB 1081 ACTGAGATGATGAAAAAGTTTCTGTGCTCAGCCTTTGGGAGGAGATAAAAACATCTTACGCT 1140  
QY 1141 GGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTTGTTACTCACTTCTCTCCCTC 1200  
DB 1141 GGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTTGTTACTCACTTCTCTCCCTC 1200  
QY 1201 CTTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGGGAGCATCCATTTTCAATTTGGCAAG 1260  
DB 1201 CTTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGGGAGCATCCATTTTCAATTTGGCAAG 1260

QY 1261 ATCCAGGCGACGACCGCGCTGGACTTTGGGTACATGCTGAACCTGACCAACATGATC 1320  
 DB |||||||  
 QY 1261 ATCCAGGCGACGACCGCGCTGGACTTTGGGTACATGCTGAACCTGACCAACATGATC 1320  
 DB |||||||  
 QY 1321 CCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCACCTAA 1365  
 DB |||||||  
 QY 1321 CCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCACCTAA 1365  
 DB |||||||

RESULT 3  
 AAD00207  
 ID AAD00207 standard; DNA; 1437 BP.  
 XX  
 AC AAD00207;  
 XX  
 DT 17-AUG-2000 (first entry)  
 XX  
 DE Human soluble CD39 fusion DNA construct, pIL2LsolCD39.  
 XX  
 KW Soluble CD39; human; apyrase activity; platelet activation;  
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
 KW atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism;  
 KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;  
 KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;  
 KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;  
 KW antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant;  
 KW cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1437  
 FT /\*tag= a  
 FT /product= "Fusion protein of pIL2LsolCD39"  
 FT sig\_peptide 1..72  
 FT /\*tag= b  
 FT /note= "Human interleukin 2 (hIL2) leader sequence"  
 FT misc\_feature 73..108  
 FT /\*tag= c  
 FT /product= "Mature human interleukin 2 N-terminal end"  
 FT misc\_feature 109..117  
 FT /\*tag= d  
 FT /note= "Linker sequence"  
 FT misc\_feature 118..1434  
 FT /\*tag= e  
 FT /note= "Coding region of human soluble CD39 (solCD39)"  
 XX  
 WO200023459-A1.  
 XX  
 PD 27-APR-2000.  
 XX  
 PF 13-OCT-1999; 99WO-US022955.  
 XX  
 PR 16-OCT-1998; 98US-0104585P.  
 PR 06-NOV-1998; 98US-0107466P.  
 PR 13-AUG-1999; 99US-0149010P.  
 XX  
 PA (IMMUNEX ) IMMUNEX CORP.  
 XX  
 PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;  
 XX  
 DR WPI; 2000-339644/29.  
 DR P-PSDB; AAY70914.  
 XX  
 PT New soluble CD39 polypeptides having apyrase activity, useful for  
 PT inhibiting angiogenesis and treating unstable angina, myocardial  
 PT infarction, stroke, coronary artery disease or injury.  
 XX  
 PS Claim 15a; Page 97-99; 122pp; English.  
 XX  
 CC The present DNA sequence is a fusion construct pIL2LsolCD39, comprising  
 CC leader peptide of human interleukin 2 (hIL2), 12 amino acids from the

CC mature N-terminus of hIL2 and soluble CD39 (solCD39) coding region,  
 CC having apyrase activity. This produces high levels of solCD39 expression  
 CC and activity in the transfected cells. Soluble CD39 is constructed by  
 CC removing the N- and C-terminal transmembrane domains. It retains the  
 CC capacity to metabolise ATP and ADP at relevant concentrations and the  
 CC ability to block and reverse ADP-induced platelet activation and  
 CC recruitment, including platelet aggregation. Soluble CD39 polypeptides  
 CC are useful for inhibiting angiogenesis. It is useful for the treatment of  
 CC unstable angina, myocardial infarction, stroke, coronary artery disease  
 CC or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia,  
 CC embolism, platelet-associated ischaemic disorders including lung,  
 CC coronary and cerebral ischaemia, thrombotic disorders including coronary,  
 CC peripheral and cerebral artery thrombosis, intracardiac and venous  
 CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary  
 CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful  
 CC for preventing thrombus formation or reformation, occlusion, reocclusion,  
 CC stenosis or restenosis of blood vessels or stroke  
 XX  
 SQ Sequence 1437 BP; 411 A; 336 C; 335 G; 355 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1365; DB 3; Length 1437;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCACCTACTTCAAGTTCTACAAAGAAACACACAGCTAACTAGTTCAACCCAGAACAAAGCA 60  
 DB 73 GCACCTACTTCAAGTTCTACAAAGAAACACACAGCTAACTAGTTCAACCCAGAACAAAGCA 132  
 QY 61 TTGCCAGAAACCGTTAAAGTATGGGATTTGCTGGATGCGGGTTCTTCTCACAAAGTTTA 120  
 DB 133 TTGCCAGAAACCGTTAAAGTATGGGATTTGCTGGATGCGGGTTCTTCTCACAAAGTTTA 192  
 QY 121 TACATCTATAGTGGCGCAGAGAAAGGAGATGACACAGGGCGTGGTCATCAAGTAGAA 180  
 DB 193 TACATCTATAGTGGCGCAGAGAAAGGAGATGACACAGGGCGTGGTCATCAAGTAGAA 252  
 QY 181 GAATCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTGAGAAAGTAAATGAAATAGC 240  
 DB 253 GAATCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTGAGAAAGTAAATGAAATAGC 312  
 QY 241 ATTTACCTGACTGATTTGCAATGGAAGAGCTAGGAAAGTGAATTCAGAGTCCAGACCA 300  
 DB 313 ATTTACCTGACTGATTTGCAATGGAAGAGCTAGGAAAGTGAATTCAGAGTCCAGACCA 372  
 QY 301 GAGACACCGTTTACCTGGAGCCACGCGAGCATGCGGTGCTCAGGATGAAAGTGA 360  
 DB 373 GAGACACCGTTTACCTGGAGCCACGCGAGCATGCGGTGCTCAGGATGAAAGTGA 432  
 QY 361 GAGTTGGCAGACAGGGGTTCTGGATGTGGTGGAGAGAGCCTCAGCAACTACCCCTTTGAC 420  
 DB 433 GAGTTGGCAGACAGGGGTTCTGGATGTGGTGGAGAGAGCCTCAGCAACTACCCCTTTGAC 492  
 QY 421 TTCCAGGGTGCAGGATCAATTACTGCCCAAGAGAGTGCCTATGGCTGGATTACTATC 480  
 DB 493 TTCCAGGGTGCAGGATCAATTACTGCCCAAGAGAGTGCCTATGGCTGGATTACTATC 552  
 QY 481 AACTATCTCTGGGCAGAAATTCAGTCAGAAAAAAGAGTGGTTCAGCATAGTCCCATATGA 540  
 DB 553 AACTATCTCTGGGCAGAAATTCAGTCAGAAAAAAGAGTGGTTCAGCATAGTCCCATATGA 612  
 QY 541 ACCAATAATCAGGAAACCTTTTGGAGCTTTGGACCTTTGGGGAGCCCTCTACACAAGTCACT 600  
 DB 613 ACCAATAATCAGGAAACCTTTTGGAGCTTTGGAGCTTTGGGGAGCCCTCTACACAAGTCACT 672  
 QY 601 TTTGTACCCCAAAAACAGACTATCGAGTATCGAGTCCCGAGATAATGCTCTGCAATTTGCGCTTAT 660  
 DB 673 TTTGTACCCCAAAAACAGACTATCGAGTATCGAGTCCCGAGATAATGCTCTGCAATTTGCGCTTAT 732  
 QY 661 GCGAAGGACTACAATGCTCTACACATAGCTTCTTGCTATGGGAGGATCAGGCACTC 720  
 DB 733 GCGAAGGACTACAATGCTCTACACATAGCTTCTTGCTATGGGAGGATCAGGCACTC 792  
 QY 721 TGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAAATGAAATTTCTCAGGGACCCATGC 780

Db 793 TGGCAGAAATGTCGCCAAGGACATTCAGGTTGCAAGTAATGAAATCTCTCAGGAGCCCATGC 852  
Qy 781 TTTTCATCTCTGGATATAAGAAGGTAGTGAACGTAAAGTGAAGTCTTTACAAGACCCCTGCACC 840  
Db 853 TTTTCATCTCTGGATATAAGAAGGTAGTGAACGTAAAGTGAAGTCTTTACAAGACCCCTGCACC 912  
Qy 841 AAGAGATTGAGATGATCTCTTCATTCACAGAGTTTGAATCCAGGGTATTCGAAACTAT 900  
Db 913 AAGAGATTGAGATGATCTCTTCATTCACAGAGTTTGAATCCAGGGTATTCGAAACTAT 972  
Qy 901 CAACATGCGCATCAAGCATCTGGAGCTCTTCAACACCCAGTACTGCCCTTACTCCGAG 960  
Db 973 CAACATGCGCATCAAGCATCTGGAGCTCTTCAACACCCAGTACTGCCCTTACTCCGAG 1032  
Qy 961 TGTGCTCTTCAATGGGATTTCTTGGCCACCATCTCCAGGGGATTTTGGGGCATTTTCAGCT 1020  
Db 1033 TGTGCTCTTCAATGGGATTTCTTGGCCACCATCTCCAGGGGATTTTGGGGCATTTTCAGCT 1092  
Qy 1021 TTTTACTTTTGTGATGAAGTTTAACTTTGAACATCAGAGAAAGTCTCTCAGGAAAAGTG 1080  
Db 1093 TTTTACTTTTGTGATGAAGTTTAACTTTGAACATCAGAGAAAGTCTCTCAGGAAAAGTG 1152  
Qy 1081 ACTGAGATGATCAAAAGTTCTGTGCTCAGCCTTGGAGGAGATATAAACATCTTACGCT 1140  
Db 1153 ACTGAGATGATCAAAAGTTCTGTGCTCAGCCTTGGAGGAGATATAAACATCTTACGCT 1212  
Qy 1141 GGAGTAAAGGAGAAGTACCTGAGTGAATCTCTTCTGCTGACCTTGGAGGAGATATAAACATCTTACGCT 1200  
Db 1213 GGAGTAAAGGAGAAGTACCTGAGTGAATCTCTTCTGCTGACCTTGGAGGAGATATAAACATCTTACGCT 1272  
Qy 1201 CTTCTGCAAGGCTATCATTTACAGCTGATTCCTGGAGGACATCATTTTTCATTTGGCAAG 1260  
Db 1273 CTTCTGCAAGGCTATCATTTACAGCTGATTCCTGGAGGACATCATTTTTCATTTGGCAAG 1332  
Qy 1261 ATCCAGGCGAGCGCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAAGATGATC 1320  
Db 1333 ATCCAGGCGAGCGCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAAGATGATC 1392  
Qy 1321 CCAGCTGAGCAACCATTTGCCACACTCTCTCCCACTCCACTAA 1365  
Db 1393 CCAGCTGAGCAACCATTTGCCACACTCTCTCCCACTCCACTAA 1437

RESULT 4

AAD00202

ID AAD00202 standard; DNA; 1437 BP.

AC AAD00202;

XX

XX 17-AUG-2000 (first entry)

XX

XX Coding region of pIL2Lsol CD39.

XX Soluble CD39; ADP-induced platelet activation; platelet aggregation;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;  
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;  
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;  
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;  
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;  
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;  
KW occlusion; reocclusion; stenosis; restenosis; antiangiogenic; cardiant;  
KW cerebroprotective; antiarteriosclerotic; vasotrophic; anticoagulant;  
KW coronary ischaemia; vascular occlusion; ss.

OS Homo sapiens.

XX Location/Qualifiers

XX 1. 1437

FT CDS

FT /product= a

FT sig\_peptide 1. .72

FT /tag= b  
FT /note= "human IL2 leader sequence"  
FT 73. .108  
FT /tag= c  
FT /product= "Mature human IL2 protein"  
FT 109. .117  
FT /tag= c  
FT /note= "a three amino acid linker"  
FT 118. .1434  
FT /tag= d  
FT /product= "Soluble CD39 protein"

XX WO200023094-A2.

PN 27-APR-2000.

XX 13-OCT-1999; 99WO-US023641.

XX 16-OCT-1998; 98US-0104585P.

PR 06-NOV-1998; 98US-0107466P.

PR 13-AUG-1999; 99US-0149010P.

XX (IMV ) IMMUNEX CORP.

PA (CORR ) CORNELL RES FOUND INC.

XX Maliszewski CR, Gayle RB, Marcus AJ;

PI WPI; 2000-339518/29.

XX P-PSDB; AAY70891.

XX Inhibiting platelet activation and recruitment, useful for treating a  
PT mammal suffering from unstable angina, myocardial infarction, stroke,  
PT coronary artery disease or injury, comprises administering soluble CD39  
PT polypeptides.

PS Claim 11; Page 97-99; 118pp; English.

XX The present sequence is coding region of pIL2solCD39, a fusion construct  
CC encoding sol(soluble)CD39 having apyrase activity. Fusion of 12 amino  
CC acids from the N-terminus of mature human IL2 to the solCD39 coding  
CC region results in high levels of both expression and activity in the  
CC supernatants of transfected cells. This is used in the treatment of  
CC unstable angina, myocardial infarction, stroke, coronary artery disease  
CC or injury, atherosclerosis, peripheral vascular occlusion, pre-eclampsia,  
CC embolism, platelet-associated ischaemic disorder including lung  
CC ischaemia, coronary ischaemia and cerebral ischaemia, thrombotic disorder  
CC including coronary artery thrombosis, cerebral artery thrombosis,  
CC intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis,  
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary  
CC embolism (PE), transient ischaemic attack. Soluble CD39 is also useful  
CC for preventing thrombus formation or reformation, occlusion, reocclusion,  
CC stenosis or restenosis of blood vessels or stroke

XX Sequence 1437 BP; 411 A; 336 C; 335 G; 355 T; 0 U; 0 Other;

Qy Query Match 100.0%; Score 1365; DB 3; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACCTACTTCAAGTTCTTACAGAAAACACAGCTAATAGTTCAACCCAGAACAAAGCA 60

Db 73 GCACCTACTTCAAGTTCTTACAGAAAACACAGCTAATAGTTCAACCCAGAACAAAGCA 132

Qy 61 TTGCCAGAAAACGTTTAAGTATGGATGCTGCTGATCGGGTCTTCTTCACACAGTTTA 120

Db 133 TTGCCAGAAAACGTTTAAGTATGGATGCTGCTGATCGGGTCTTCTTCACACAGTTTA 192

Qy 121 TACATCTATAAGTGGCCAGCAGAAAAGAGAAATACACAGCGCTGGTGCATCAAGTAGAA 180

Db 193 TACATCTATAAGTGGCCAGCAGAAAAGAGAAATACACAGCGCTGGTGCATCAAGTAGAA 252

Qy 181 GAATGCAGGGTTAAAGTCTCTGGAATCTCAAAATTTCTTCAGAAAAGTAAATAGGC 240

Db 253 GAATGCAGGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTCAGAAAAGTAAATGAAATAGGC 1312

Qy 241 ATTTACTGACTGATTTGCATGGAAAGAGCTAGGAAAGTGTATTCCAAGGTCCACGACCAA 300

Db 313 ATTTACTGACTGATTTGCATGGAAAGAGCTAGGAAAGTGTATTCCAAGGTCCACGACCAA 372

Qy 301 GAGACACCCGTTTACCTGGGAGCCAGCGAGGATCGGTTGCTCAGGATGGAAGTGAA 360

Db 373 GAGACACCCGTTTACCTGGGAGCCAGCGAGGATCGGTTGCTCAGGATGGAAGTGAA 432

Qy 361 GAGTTGGCAGACAGGGTTCTGGATGTGTGGAGAGGAGCCCTCAGCAACTACCCCTTTTGAC 420

Db 433 GAGTTGGCAGACAGGGTTCTGGATGTGTGGAGAGGAGCCCTCAGCAACTACCCCTTTTGAC 492

Qy 421 TTCCAGGGTGCAGGATCATTTACTGGCCAAAGAGAGGTGCCTATGGCTGGATTACTATTC 480

Db 493 TTCCAGGGTGCAGGATCATTTACTGGCCAAAGAGAGGTGCCTATGGCTGGATTACTATTC 552

Qy 481 AACTATCTGCTGGGCAAAATTCAGTCAAGAAACAAGGTGGTTTCAGCATAGTCCCATATGAA 540

Db 553 AACTATCTGCTGGGCAAAATTCAGTCAAGAAACAAGGTGGTTTCAGCATAGTCCCATATGAA 612

Qy 541 ACCAATAATCAGAAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTCTACACAAGTCACT 600

Db 613 ACCAATAATCAGAAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTCTACACAAGTCACT 672

Qy 601 TTTGTACCCCAAAACAGACTATCGAGTCCCGAGATAATGCTCTGCAATTTTGGCCTCTAT 660

Db 673 TTTGTACCCCAAAACAGACTATCGAGTCCCGAGATAATGCTCTGCAATTTTGGCCTCTAT 732

Qy 661 GGCAGGACTACAAATGTCACACATAGTCTTCTGTGCTATGGGAAGGATCAGGCACATC 720

Db 733 GGCAGGACTACAAATGTCACACATAGTCTTCTGTGCTATGGGAAGGATCAGGCACATC 792

Qy 721 TGCAGAAAATCGCCCAAGGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGGACCCATGC 780

Db 793 TGCAGAAAATCGCCCAAGGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGGACCCATGC 852

Qy 781 TTTTCATCTGGATATAGAAGGTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840

Db 853 TTTTCATCTGGATATAGAAGGTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 912

Qy 841 AACAGATTTGAGATGACTCTTCATTCACAGCAGTTTGAATCCAGGGTATTTGGAAGTAT 900

Db 913 AACAGATTTGAGATGACTCTTCATTCACAGCAGTTTGAATCCAGGGTATTTGGAAGTAT 972

Qy 901 CAACAATGCCATCAAAAGCATCTCGAGCTCTTCAACACCAAGTTACTGCCCTTACTCCAG 960

Db 973 CAACAATGCCATCAAAAGCATCTCGAGCTCTTCAACACCAAGTTACTGCCCTTACTCCAG 1032

Qy 961 TGTGCCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGATTTTGGGGCATTTTCAGCT 1020

Db 1033 TGTGCCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGATTTTGGGGCATTTTCAGCT 1092

Qy 1021 TTTTACTTTGTGATGAAGTTTTTAACTTGACATCAGAGAACTCTCTCAGGAAAAGGTG 1080

Db 1093 TTTTACTTTGTGATGAAGTTTTTAACTTGACATCAGAGAACTCTCTCAGGAAAAGGTG 1152

Qy 1081 ACTGAGATGATGAAAAGTTTCTGTGCTCAGCCCTGGGAGAGATAAAAACATCTTACGCT 1140

Db 1153 ACTGAGATGATGAAAAGTTTCTGTGCTCAGCCCTGGGAGAGATAAAAACATCTTACGCT 1212

Qy 1141 GGAGTAAAGAGAAAGTACCTGAGTGAATATCTGCTTTTCTGGTACCTACATTTCTCCCTC 1200

Db 1213 GGAGTAAAGAGAAAGTACCTGAGTGAATATCTGCTTTTCTGGTACCTACATTTCTCCCTC 1272

Qy 1201 CTTCTCGAAGCTATCATTTTCAGCTGATTTCTCTGGAGCACATCATTTTCATTTGCAAG 1260

Db 1273 CTTCTCGAAGCTATCATTTTCAGCTGATTTCTCTGGAGCACATCATTTTCATTTGCAAG 1332

Qy 1261 ATCCAGGGCAGCGCCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1320

Db 1333 ATCCAGGGCAGCGCCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1392

Qy 1321 CCAGCTGAGCAACCATTTGCCACACCTCTCTCCCACTCCACCTAA 1365

Db 1393 CCAGCTGAGCAACCATTTGCCACACCTCTCTCCCACTCCACCTAA 1437

RESULT 5

AAD00209

ID AAD00209 standard; DNA; 1464 BP.

XX

XX AAD00209;

XX

DT 17-AUG-2000 (first entry)

XX

DE Human soluble CD39 fusion DNA construct, pIL2LFlagSolCD39.

XX

KW Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antilanginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.

XX

OS Homo sapiens.

OS Synthetic.

XX

PH Key

FT CDS

FT Location/Qualifiers

FT 1..1464

FT /tag= a

FT /product= "Fusion protein of pIL2LFlagSolCD39"

FT 1..72

FT /tag= b

FT /note= "Human interleukin 2 (hIL2) leader sequence"

FT 73..108

FT /tag= c

FT /product= "Mature human interleukin 2 N-terminal end"

FT 109..120

FT /tag= d

FT /note= "Linker sequence"

FT 121..144

FT /tag= e

FT /note= "FLAG tag sequence"

FT 145..1461

FT /tag= e

FT /note= "Coding region of human soluble CD39 (solCD39)"

FT

PN WO20023459-A1.

XX

XX 27-APR-2000.

XX

PF 13-OCT-1999; 99WO-US022955.

XX

PR 16-OCT-1998; 98US-0104585P.

PR 06-NOV-1998; 98US-0107466P.

PR 13-AUG-1999; 99US-0149010P.

XX

XX (IMMV ) IMMUNEX CORP.

PA

XX

PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;

XX

XX WPI; 2000-339644/29.

DR P-PSDB; AAY70921.

XX

XX New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury.

PT

PT

XX

PS Example 9; Page 107-109; 122pp; English.

XX

XX The present DNA sequence is a fusion construct pIL2LFlagSolCD39, comprising the leader peptide of human interleukin 2 (hIL2), 12 amino

CC acids from the mature N-terminus of hIL2, a linker, FLAG tag sequence and  
CC soluble CD39 (solCD39) coding region, that has apyrase activity. This  
CC produces high levels of solCD39 expression and activity in the  
CC transfected cells. Soluble CD39 is constructed by removing the N- and C-  
CC terminal transmembrane domains. It retains the capacity to metabolize ATP  
CC and ADP at relevant concentrations and the ability to block and reverse  
CC ADP-induced platelet activation and recruitment, including platelet  
CC aggregation. Soluble CD39 polypeptides are useful for inhibiting  
CC angiogenesis. It is useful for the treatment of unstable angina,  
CC myocardial infarction, stroke, coronary artery disease or injury,  
CC atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism,  
CC platelet-associated ischaemic disorders including lung, coronary and  
CC cerebral ischaemia, thrombotic disorders including coronary, peripheral  
CC and cerebral artery thrombosis, intracardiac and venous thrombosis,  
CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and  
CC transient ischaemic attack. Soluble CD39 is also useful for preventing  
CC thrombus formation or reformation, occlusion, reocclusion, stenosis or  
CC restenosis of blood vessels or stroke  
XX  
SQ Sequence 1464 BP; 424 A; 340 C; 342 G; 358 T; 0 U; 0 Other;

Query Match 97.3%; Score 1328; DB 3; Length 1464;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1334; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 11 CAAGTTCTTCAAGAAGAAACACACAGCTTAACCTAGTTTCAACCAGAACAAAGCAATGCCAGAAA 70  
DB 110 CTAGTTCAGGAGACTACAAGATGACGATGACAAAACCCAGAACAAAGCATTTGCCAGAAA 169  
QY 71 AGCTTAAGTATGGGATTTGCTGGATGGCGGTTCTTCTCACACAAGTTTATACATCTATA 130  
DB 170 AGCTTAAGTATGGGATTTGCTGGATGGCGGTTCTTCTCACACAAGTTTATACATCTATA 229  
QY 131 AGTGGCCAGCAGAAAAGAGAGATGACACAGCGGTGGTGCATCAAGTAGAAGAAATCCAGGG 190  
DB 230 AGTGGCCAGCAGAAAAGAGAGATGACACAGCGGTGGTGCATCAAGTAGAAGAAATCCAGGG 289  
QY 191 TTAAAGGTCCTGGAATCTCAAAATTTGTTTCAAGAAAGTAAATGAATAGGCATTTCACCTGA 250  
DB 290 TTAAAGGTCCTGGAATCTCAAAATTTGTTTCAAGAAAGTAAATGAATAGGCATTTCACCTGA 349  
QY 251 CTGATTGATGAAAGAGCTAGGAAGTGATTTCAAGGTCCAGACCAAGACAGACCCGG 310  
DB 350 CTGATTGATGAAAGAGCTAGGAAGTGATTTCAAGGTCCAGACCAAGACAGACCCGG 409  
QY 311 TTACTCTGGAGCCAGCGGAGCATGCGTCTCAGGATGGAAGTGAAGATTTGGCAG 370  
DB 410 TTACTCTGGAGCCAGCGGAGCATGCGTCTCAGGATGGAAGTGAAGATTTGGCAG 469  
QY 371 ACAGGGTTCTGGATGTGGTGGAGAGAGCCTCAGCAACTACCCCTTTTGACTTTCCAGGGTG 430  
DB 470 ACAGGGTTCTGGATGTGGTGGAGAGAGCCTCAGCAACTACCCCTTTTGACTTTCCAGGGTG 529  
QY 431 CCAGGATCATTTACTGCCAAGGAGAGGTGCTTATGGCTGGATTAATCAATCATCTGC 490  
DB 530 CCAGGATCATTTACTGCCAAGGAGAGGTGCTTATGGCTGGATTAATCAATCATCTGC 589  
QY 491 TGGGCAAAATTCAGTCAGAAAACAAGTGTTCAGCATAGTCCCATATGAACCAATATC 550  
DB 590 TGGGCAAAATTCAGTCAGAAAACAAGTGTTCAGCATAGTCCCATATGAACCAATATC 649  
QY 551 AGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCGCTTACACAAAGTCACTTTTGATCCCC 610  
DB 650 AGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCGCTTACACAAAGTCACTTTTGATCCCC 709  
QY 611 AAACCCAGCATTCAGTCCAGTCCCAAGATATGCTCTGCAATTTGCGCTCTATGGCAAGGACT 670  
DB 710 AAACCCAGCATTCAGTCCAGTCCCAAGATATGCTCTGCAATTTGCGCTCTATGGCAAGGACT 769  
QY 671 ACAATGTCTACACATAGCTTTCTGTGCTATGGGAAGGATCAGGCACTCTGGCAGAAC 730  
DB 770 ACAATGTCTACACATAGCTTTCTGTGCTATGGGAAGGATCAGGCACTCTGGCAGAAC 829

QY 731 TGGCCAAGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGAGCCCATGCTTTTCATCTCTG 790  
DB 830 TGGCCAAGGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGAGCCCATGCTTTTCATCTCTG 889  
QY 791 GATATAAGAGGTAGTGAACGTAACTTACAAAGACCCCTTGCACCAAGAGATTG 850  
DB 890 GATATAAGAGGTAGTGAACGTAACTTACAAAGACCCCTTGCACCAAGAGATTG 949  
QY 851 AGATGACTCTTTCATTTCCAGCAGGTTTGAATCCAGGGTATTGGAACTATCAACAATGCC 910  
DB 950 AGATGACTCTTTCATTTCCAGCAGGTTTGAATCCAGGGTATTGGAACTATCAACAATGCC 1009  
QY 911 ATCAAGCATCTCGAGCTCTTCAACACAGTTACTTGCCTTTACTCCAGTGTGCTTCA 970  
DB 1010 ATCAAGCATCTCGAGCTCTTCAACACAGTTACTTGCCTTTACTCCAGTGTGCTTCA 1069  
QY 971 ATGGGATTTCTTGGCCACACTCCAGGGGGATTTTGGGGCATTTTCAGCTTTTACTTTG 1030  
DB 1070 ATGGGATTTCTTGGCCACACTCCAGGGGGATTTTGGGGCATTTTTCAGCTTTTACTTTG 1129  
QY 1031 TGATGAAGTTTAACTTTGACATCAGAGAAAGTCTCTCAGGAAAAGGTGACTGAGATGA 1090  
DB 1130 TGATGAAGTTTAACTTTGACATCAGAGAAAGTCTCTCAGGAAAAGGTGACTGAGATGA 1189  
QY 1091 TGAAGAAAGTTCTGTGCTCAGCCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGG 1150  
DB 1190 TGAAGAAAGTTCTGTGCTCAGCCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGG 1249  
QY 1151 AGNAGTACTCAGTGAATACTGCTTTTCTGGTACTTACATCTCTCTCCCTCTCTGCAAG 1210  
DB 1250 AGAAGTACTCAGTGAATACTGCTTTTCTGGTACTTACATCTCTCTCCCTCTCTGCAAG 1309  
QY 1211 GCTATCATTTTCAACAGCTGATTTCTGGGAGCAGATCCATTTTATTGGCAAGATCCAGGGCA 1270  
DB 1310 GCTATCATTTTCAACAGCTGATTTCTGGGAGCAGATCCATTTTATTGGCAAGATCCAGGGCA 1369  
QY 1271 CGCAGCGCGGTGAGCTTTGGGCTACATGCTGAACCTGACCAACATGATCCAGCTGAGC 1330  
DB 1370 CGCAGCGCGGTGAGCTTTGGGCTACATGCTGAACCTGACCAACATGATCCAGCTGAGC 1429  
QY 1331 AACCATTTGTCCACACCTCTCTCCCACTCCACTAA 1365  
DB 1430 AACCATTTGTCCACACCTCTCTCCCACTCCACTAA 1464  
RESULT 6  
AAD00204  
ID AAD00204 standard; DNA; 1464 BP.  
XX  
AC AAD00204;  
XX  
DT 17-AUG-2000 (first entry)  
XX  
DE Coding region of soluble CD39 expression plasmid.  
XX  
KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism;  
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;  
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;  
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;  
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;  
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;  
KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiatic;  
KW cerebroprotective; antiarteriosclerotic; vasotrophic; anticoagulant;  
KW coronary ischaemia; vascular occlusion; solCD39 expression plasmid; ss.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 1..1464  
FT /\*tag= b  
FT /product= "SolCD39 expression plasmid protein"

```

FT sig_peptide 1..72
FT /tag= a
FT /notes= "hul12 leader sequence"
FT mat_peptide 73..108
FT /tag= c
FT /product= "Mature human IL2"
FT misc_feature 109..120
FT /tag= d
FT /label= linker
FT misc_feature 121..144
FT /tag= e
FT /note= "Flag tag"
FT mat_peptide 145..1461
FT /tag= f
FT /product= "Sol CD39"
XX
XX WO200023094-A2.
XX
XX 27-APR-2000.
XX
XX 13-OCT-1999; 99WO-US023641.
XX
XX 16-OCT-1998; 98US-0104585P.
XX
XX 06-NOV-1998; 98US-0107466P.
XX
XX 13-AUG-1999; 99US-0149010P.
XX
XX (IMV ) IMMUNEX CORP.
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Maliszewski CR, Gayle RB, Marcus AJ;
XX
XX WPI; 2000-339518/29.
XX P-PSDB; AAY70898.
XX
XX Inhibiting platelet activation and recruitment, useful for treating a
XX mammal suffering from unstable angina, myocardial infarction, stroke,
XX coronary artery disease or injury, comprises administering soluble CD39
XX polypeptides.
XX
XX Example 9; Page 107-109; 118pp; English.
XX
XX The present sequence is the coding region of soluble CD39(solCD39)
XX expression plasmid. This was used for the transient expression of solCD39
XX protein in mammalian expression systems. SolCD39 is used in the treatment
XX of unstable angina, myocardial infarction, stroke, coronary artery
XX disease or injury, atherosclerosis, peripheral vascular occlusion,
XX preeclampsia, embolism, platelet-associated ischaemic disorder including
XX lung ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic
XX disorder including coronary artery thrombosis, cerebral artery
XX thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous
XX thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT),
XX pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also
XX useful for preventing thrombus formation or reformation, occlusion,
XX reocclusion, stenosis or restenosis of blood vessels or stroke
XX
XX Sequence 1464 BP; 424 A; 340 C; 342 G; 358 T; 0 U; 0 Other;
XX
XX Query Match 97.3%; Score 1328; DB 3; Length 1464;
XX Best Local Similarity 98.5%; Pred. No. 0;
XX Matches 1334; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
XX
XX 11 CAAGTTCTCAAGAAACACACGCTACTAGTTCAACCCAGAACAAAGCAATTGCCAGAAA 70
XX |||||
XX 110 CTAGTTTCAGGAGACTACAAGATGACGATGACAAAACCCAGAACAAAGCAATTGCCAGAAA 169
XX
XX 71 ACGTTAAGTATGGATTGTCTCGATCGGGTTCTTCTCACACAAAGTTTATACATCTATA 130
XX |||||
XX 170 ACGTTAAGTATGGATTGTCTCGATCGGGTTCTTCTCACAAAGTTTATACATCTATA 229
XX |||||
XX 131 AGTGGCCAGCAGAAAAGGAATGACACAGGCGTGGTGTCATCAAGTAGAAGAAATGCAGGG 190
XX |||||
XX 230 AGTGGCCAGCAGAAAAGGAATGACACAGGCGTGGTGTCATCAAGTAGAAGAAATGCAGGG 289
XX |||||

```

---

```

191 TTAAGGTCCTGGAATCTCAAAATTTGTTCAAGAAAGTAAATGAAATAGGCAATTTACCTGA 250
192 |||||
193 |||||
194 |||||
195 |||||
196 |||||
197 |||||
198 |||||
199 |||||
200 TTAAGGTCCTGGAATCTCAAAATTTGTTCAAGAAAGTAAATGAAATAGGCAATTTACCTGA 349
201 |||||
202 |||||
203 |||||
204 |||||
205 |||||
206 |||||
207 |||||
208 |||||
209 |||||
210 CTGATTGTCATGGAAGAGCTAGGGAAGTGAATTCGAAGTCCAGCAACCAAGAGACACCCG 310
211 |||||
212 |||||
213 |||||
214 |||||
215 |||||
216 |||||
217 |||||
218 |||||
219 |||||
220 CTGATTGTCATGGAAGAGCTAGGGAAGTGAATTCGAAGTCCAGCAACCAAGAGACACCCG 409
221 |||||
222 |||||
223 |||||
224 |||||
225 |||||
226 |||||
227 |||||
228 |||||
229 |||||
230 TTTTACCTGGAGCCACGGCAGCATCGGTTCTCAGGATGGAAGTGAAGAGTTGGCAG 370
231 |||||
232 |||||
233 |||||
234 |||||
235 |||||
236 |||||
237 |||||
238 |||||
239 |||||
240 TTTTACCTGGAGCCACGGCAGCATCGGTTCTCAGGATGGAAGTGAAGAGTTGGCAG 469
241 |||||
242 |||||
243 |||||
244 |||||
245 |||||
246 |||||
247 |||||
248 |||||
249 |||||
250 ACAGGTTCTGGATGTGTGGAGAGAGCCTCAGCAACTACCCCTTTGACTTCCAGGGTG 430
251 |||||
252 |||||
253 |||||
254 |||||
255 |||||
256 |||||
257 |||||
258 |||||
259 |||||
260 ACAGGTTCTGGATGTGTGGAGAGAGCCTCAGCAACTACCCCTTTGACTTCCAGGGTG 529
261 |||||
262 |||||
263 |||||
264 |||||
265 |||||
266 |||||
267 |||||
268 |||||
269 |||||
270 CCAGGATCAATTACTGGCCAAAGAGAGTGCCCTATGGCTGGATTACTATCAACTATCTGC 490
271 |||||
272 |||||
273 |||||
274 |||||
275 |||||
276 |||||
277 |||||
278 |||||
279 |||||
280 CCAGGATCAATTACTGGCCAAAGAGAGTGCCCTATGGCTGGATTACTATCAACTATCTGC 589
281 |||||
282 |||||
283 |||||
284 |||||
285 |||||
286 |||||
287 |||||
288 |||||
289 |||||
290 TGGGCAAAATTCAGTCAGAAAACAAGGTGGTTCCAGCATAGTCCCATATGAAAACCAATAATC 550
291 |||||
292 |||||
293 |||||
294 |||||
295 |||||
296 |||||
297 |||||
298 |||||
299 |||||
300 TGGGCAAAATTCAGTCAGAAAACAAGGTGGTTCCAGCATAGTCCCATATGAAAACCAATAATC 649
301 |||||
302 |||||
303 |||||
304 |||||
305 |||||
306 |||||
307 |||||
308 |||||
309 |||||
310 AGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTTACACAAAGTCACCTTTGTACCCC 610
311 |||||
312 |||||
313 |||||
314 |||||
315 |||||
316 |||||
317 |||||
318 |||||
319 |||||
320 AGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTTACACAAAGTCACCTTTGTACCCC 709
321 |||||
322 |||||
323 |||||
324 |||||
325 |||||
326 |||||
327 |||||
328 |||||
329 |||||
330 AAAACCAAGTATCGAGTCCCAGATAATGCTCTGCAATTTTCGCTCTATGCAAGGACT 670
331 |||||
332 |||||
333 |||||
334 |||||
335 |||||
336 |||||
337 |||||
338 |||||
339 |||||
340 AAAACCAAGTATCGAGTCCCAGATAATGCTCTGCAATTTTCGCTCTATGCAAGGACT 769
341 |||||
342 |||||
343 |||||
344 |||||
345 |||||
346 |||||
347 |||||
348 |||||
349 |||||
350 ACAATGCTACACATAGCTTTCTGTGCTATGGGAAGGATCAGGCACCTCTGCAGAAAC 730
351 |||||
352 |||||
353 |||||
354 |||||
355 |||||
356 |||||
357 |||||
358 |||||
359 |||||
360 ACAATGCTACACATAGCTTTCTGTGCTATGGGAAGGATCAGGCACCTCTGCAGAAAC 829
361 |||||
362 |||||
363 |||||
364 |||||
365 |||||
366 |||||
367 |||||
368 |||||
369 |||||
370 TGGCCAAAGACATTCAGGTTGCAAGTAAATGAAATTTCTCAGGAGCCCATCTTTTCATCTG 790
371 |||||
372 |||||
373 |||||
374 |||||
375 |||||
376 |||||
377 |||||
378 |||||
379 |||||
380 TGGCCAAAGACATTCAGGTTGCAAGTAAATGAAATTTCTCAGGAGCCCATCTTTTCATCTG 889
381 |||||
382 |||||
383 |||||
384 |||||
385 |||||
386 |||||
387 |||||
388 |||||
389 |||||
390 GATATAAGAGGTAGTGAAACGTAAGTGACCTTTTACAAGACCCCTGCACCAAGAGATTG 850
391 |||||
392 |||||
393 |||||
394 |||||
395 |||||
396 |||||
397 |||||
398 |||||
399 |||||
400 GATATAAGAGGTAGTGAAACGTAAGTGACCTTTTACAAGACCCCTGCACCAAGAGATTG 949
401 |||||
402 |||||
403 |||||
404 |||||
405 |||||
406 |||||
407 |||||
408 |||||
409 |||||
410 AGATGACTCTTCATTCAGCAGATTGAAATCCAGGTTATGGAACTATCAACATGCC 910
411 |||||
412 |||||
413 |||||
414 |||||
415 |||||
416 |||||
417 |||||
418 |||||
419 |||||
420 AGATGACTCTTCATTCAGCAGATTGAAATCCAGGTTATGGAACTATCAACATGCC 1009
421 |||||
422 |||||
423 |||||
424 |||||
425 |||||
426 |||||
427 |||||
428 |||||
429 |||||
430 ATCAAAGCATCTGGAGCTCTTCAACACCAAGTTACTGCCCCTTACTCCAGTGTGCCCTTCA 970
431 |||||
432 |||||
433 |||||
434 |||||
435 |||||
436 |||||
437 |||||
438 |||||
439 |||||
440 ATCAAAGCATCTGGAGCTCTTCAACACCAAGTTACTGCCCCTTACTCCAGTGTGCCCTTCA 1069
441 |||||
442 |||||
443 |||||
444 |||||
445 |||||
446 |||||
447 |||||
448 |||||
449 |||||
450 ATGGGATTTTCTTGCCACCACCTCCAGGGGGATTTTGGGGCATTTTCAGCTTTTACTTTG 1030
451 |||||
452 |||||
453 |||||
454 |||||
455 |||||
456 |||||
457 |||||
458 |||||
459 |||||
460 ATGGGATTTTCTTGCCACCACCTCCAGGGGGATTTTGGGGCATTTTTCAGCTTTTACTTTG 1129
461 |||||
462 |||||
463 |||||
464 |||||
465 |||||
466 |||||
467 |||||
468 |||||
469 |||||
470 TGATGAAGTTTAAACTTGACATCAGAAAAGTCTCTCAGGAAAAGGTGACTGAGATGA 1090
471 |||||
472 |||||
473 |||||
474 |||||
475 |||||
476 |||||
477 |||||
478 |||||
479 |||||
480 TGATGAAGTTTAAACTTGACATCAGAAAAGTCTCTCAGGAAAAGGTGACTGAGATGA 1189
481 |||||
482 |||||
483 |||||
484 |||||
485 |||||
486 |||||
487 |||||
488 |||||
489 |||||
490 TCAAAAAGTTCTGTGCTCAGCCCTTGGGAGGAGATAAAAACATCTTACGCTGGAGTAAAGG 1150
491 |||||
492 |||||
493 |||||
494 |||||
495 |||||
496 |||||
497 |||||
498 |||||
499 |||||
500 TGAAGAAGTTCTGTGCTCAGCCCTTGGGAGGAGATAAAAACATCTTACGCTGGAGTAAAGG 1249
501 |||||
502 |||||
503 |||||
504 |||||
505 |||||
506 |||||
507 |||||
508 |||||
509 |||||
510 AGAAGTACCTGAGTGAATCTGCTTTCTGGTACCTTACATTTCTCCCTCCTTCTCAAG 1310
511 |||||
512 |||||
513 |||||
514 |||||
515 |||||
516 |||||
517 |||||
518 |||||
519 |||||
520 AGAAGTACCTGAGTGAATCTGCTTTTCTGGTACCTTACATTTCTCCCTCCTTCTCAAG 1309
521 |||||
522 |||||
523 |||||
524 |||||
525 |||||
526 |||||
527 |||||
528 |||||
529 |||||
530 GCTATCATTTACAGCTGATTCCTGGGAGCATCCATTTTCATTTGGCAGATCCAGGGCA 1270
531 |||||
532 |||||
533 |||||
534 |||||
535 |||||
536 |||||
537 |||||
538 |||||
539 |||||
540 GCTATCATTTACAGCTGATTCCTGGGAGCATCCATTTTCATTTGGCAGATCCAGGGCA 1369
541 |||||

```

QY 1271 GCGAGCGCGCTGGACTTTGGGCTACATGCTGACCTGACCAACATGATCCAGCTGAGC 1330  
Db |||||||  
1370 GCGAGCGCGCTGGACTTTGGGCTACATGCTGACCTGACCAACATGATCCAGCTGAGC 1429  
QY 1331 AACCATTTGTCACACACCTCTCTCCACTCCACACTAA 1365  
Db |||||||  
1430 AACCATTTGTCACACACCTCTCTCCACTCCACACTAA 1464

RESULT 7

AAD00205

ID AAD00205 standard; cDNA; 1599 BP.

XX

AC AAD00205;

DT 17-AUG-2000 (first entry)

XX

DE Human soluble CD39 protein encoding cDNA.

XX

KW Soluble CD39; human; apyrase activity; platelet activation; inhibitor;  
unstable angina; myocardial infarction; stroke; coronary artery disease;  
atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;  
platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;  
coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;  
thrombus formation; occlusion; stenosis; restenosis; angiogenesis;  
antithrombotic; cerebroprotective; antiarteriosclerotic; anticoagulant;  
cardiac; vasotropic; thrombolytic; ss.

KW

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 67..1599

FT /\*tag= a

FT /product= "Human soluble CD39 protein"

FT /note= "Cell surface molecule"

XX

PN WO200023459-A1.

XX

PD 27-APR-2000.

XX

PF 13-OCT-1999; 99WO-US022955.

XX

PR 16-OCT-1999; 98US-0104585P.

PR

PR 06-NOV-1999; 98US-0107466P.

PR

PR 13-AUG-1999; 99US-0149010P.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;

PI

DR WPI; 2000-339644/29.

DR

DR P-PSDB; AAY70910.

XX

XX New soluble CD39 polypeptides having apyrase activity, useful for

PT inhibiting angiogenesis and treating unstable angina, myocardial

PT infarction, stroke, coronary artery disease or injury.

PS

PS Example 9; Page 85-87; 122pp; English.

XX

CC The present sequence is the cDNA encoding the human soluble CD39 protein,  
a cell surface molecule, having apyrase activity. It is derived from a  
human B cell line cDNA library, referred to as MP-1. Soluble CD39 is  
constructed by removing the N- and C-terminal transmembrane domains. It  
retains the capacity to metabolise ATP and ADP at relevant concentrations  
and the ability to block and reverse ADP-induced platelet activation and  
recruitment, including platelet aggregation. Soluble CD39 polypeptides  
are useful for inhibiting angiogenesis. It is useful for the treatment of  
unstable angina, myocardial infarction, stroke, coronary artery disease  
or injury, atherosclerosis, peripheral vascular occlusion, pre-eclampsia,  
embolism, platelet-associated ischaemic disorders including lung,  
coronary and cerebral ischaemia, thrombotic disorders including coronary,  
peripheral and cerebral artery thrombosis, intracardiac and venous  
thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary

CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful  
CC for preventing thrombus formation or reformation, occlusion, reocclusion,  
CC stenosis or restenosis of blood vessels or stroke

XX  
SQ Sequence 1599 BP; 446 A; 366 C; 382 G; 405 T; 0 U; 0 Other;

Query Match 96.6%; Score 1319.2; DB 3; Length 1599;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 41 GTTCAACCCAGAACCAAGCATTTGCCAGAAAAAGCTTAAAGTATGCGATTTGCTGGATGCCG 100

Db |||||||

173 GGTGACCCAGAACCAAGCATTTGCCAGAAAAAGCTTAAAGTATGCGATTTGCTGGATGCCG 232

QY 101 GTTCTTCTCACACAAGTTTATATCATCTATAAGTGGCCAGACAGAAAGAGAAATGACACAG 160

Db |||||||

233 GTTCTTCTCACACAAGTTTATATCATCTATAAGTGGCCAGACAGAAAGAGAAATGACACAG 292

QY 161 GCGTGGTGCATCAAGTAGAAGATGCAAGGTTTAAAGTCTCTGGAATCTCAAAATTTGTTTC 220

Db |||||||

293 GCGTGGTGCATCAAGTAGAAGATGCAAGGTTTAAAGTCTCTGGAATCTCAAAATTTGTTTC 352

QY 221 AGAAGTAATCAATAGATGCGATTTTACCTGACTGATTGCAATGCAAGAGCTAGGAGATGA 280

Db |||||||

353 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTGCAATGCAAGAGCTAGGAGATGA 412

QY 281 TTCCAAGGTCCAGACCAAGAGACACCCGTTTACCTGGGAGCCAGCGAGGATCGCGT 340

Db |||||||

413 TTCCAAGGTCCAGACCAAGAGACACCCGTTTACCTGGGAGCCAGCGAGGATCGCGT 472

QY 341 TGCTCAGATGGAAAGTGAAGATGGGAGACAGAGGTTCTGATGTGTGGAGAGAGCC 400

Db |||||||

473 TGCTCAGATGGAAAGTGAAGATGGGAGACAGAGGTTCTGATGTGTGGAGAGAGCC 532

QY 401 TCAGCACTACCCCTTTGACTTCCAGGTCGACAGATCATTTACTGCGCCAGAGGAGGTG 460

Db |||||||

533 TCAGCACTACCCCTTTGACTTCCAGGTCGACAGATCATTTACTGCGCCAGAGGAGGTG 592

QY 461 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGT 520

Db |||||||

593 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGT 652

QY 521 TCAGCATAGTCCCATATGAAAACCAATATAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 580

Db |||||||

653 TCAGCATAGTCCCATATGAAAACCAATATAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 712

QY 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATATG 640

Db |||||||

713 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATATG 772

QY 641 CTCTGCAATTTTCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTTGTGCT 700

Db |||||||

773 CTCTGCAATTTTCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTTGTGCT 832

QY 701 ATGGGAAGATCAGGCACTCTGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATG 760

Db |||||||

833 ATGGGAAGATCAGGCACTCTGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATG 892

QY 761 AAATTTCTCAGGGACCCATGCTTTTCATCTGATATAGAAAGGTAGTGAACGTAAAGTACC 820

Db |||||||

893 AAATTTCTCAGGGACCCATGCTTTTCATCTGATATAGAAAGGTAGTGAACGTAAAGTACC 952

QY 821 TTTTCAAGACCCCTGCACCAAGAGATTGAGATGACTCTTCCATTTCCAGCAGATTTGAAA 880

Db |||||||

953 TTTTCAAGACCCCTGCACCAAGAGATTGAGATGACTCTTCCATTTCCAGCAGATTTGAAA 1012

QY 881 TCCAGGATTTGGAAACTATCAACAATGCCATCAAAAGCATCCTGGAGCTTTTCAACACCA 940

Db |||||||

1013 TCCAGGATTTGGAAACTATCAACAATGCCATCAAAAGCATCCTGGAGCTTTTCAACACCA 1072

QY 941 GTTACTGCCCTTACTCCAGTGTCCCTCAATGGATTTTCTTGGCACCACCTCCAGGGGG 1000

Db |||||||

1073 GTTACTGCCCTTACTCCAGTGTCCCTCAATGGATTTTCTTGGCACCACCTCCAGGGGG 1132



QY 1001 ATTTGGGGCATTTTTCAGCTTTTACTTTTGTGATGAAGCTTTTAAACTTTGACATCAGAGA 1060  
DB 1133 ATTTGGGGCATTTTTCAGCTTTTACTTTTGTGATGAAGCTTTTAAACTTTGACATCAGAGA 1192  
QY 1061 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCTTGGGAGG 1120  
DB 1193 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCTTGGGAGG 1252  
QY 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1180  
DB 1253 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1312  
QY 1181 GTRACCTACATCTCTCCCTCTCTCTGCAAGGCTATCATTTTCAGCTGATTTCTGGGAGC 1240  
DB 1313 GTRACCTACATCTCTCCCTCTCTCTGCAAGGCTATCATTTTCAGCTGATTTCTGGGAGC 1372  
QY 1241 ACATCATTTTCATTTGCAAGATCCAGGCGAGCGCGCTGGACTTTGGGCTACATGC 1300  
DB 1373 ACATCATTTTCATTTGCAAGATCCAGGCGAGCGCGCTGGACTTTGGGCTACATGC 1432  
QY 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGCCACCTCTCTCCCACTCCA 1360  
DB 1433 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGCCACCTCTCTCCCACTCCA 1492  
QY 1361 CCTA 1364  
DB 1493 CCTA 1496

RESULT 8  
AAD00200  
ID AAD00200 standard; cDNA; 1599 BP.  
XX  
AC AAD00200;  
XX  
DT 17-AUG-2000 (first entry)  
XX  
DE Human soluble CD39 cDNA.  
KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;  
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;  
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;  
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;  
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;  
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;  
KW occlusion; reocclusion; stenosis; restenosis; antidiabetic; cardiant;  
KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;  
KW coronary ischaemia; vascular occlusion; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 67..1599  
FT /\*tag= a  
FT /product= "Soluble CD39 protein"  
XX  
PN WO200023094-A2.  
XX  
PD 27-APR-2000.  
XX  
PF 13-OCT-1999; 99WO-US023641.  
XX  
PR 16-OCT-1998; 98US-0104585P.  
PR 06-NOV-1998; 98US-0107466P.  
PR 13-AUG-1999; 99US-0149010P.  
XX  
XX (IMMV ) IMMUNEX CORP.  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Maliszewski CR, Gayle RB, Marcus AJ;

Query Match 96.6%; Score 1319.2; DB 3; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAACGTTTAAAGTATCGGATTTGCTGGATCGCG 100  
DB 173 GGTTCACCCAGAACAAAGCATTTGCCAGAAACGTTTAAAGTATCGGATTTGCTGGATCGCG 232  
QY 101 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGACAGAAAGGAGATGACACAG 160  
DB 233 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGACAGAAAGGAGATGACACAG 292  
QY 161 GGTGGTGCATCAAGTAGAAGATGAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 220  
DB 293 GGTGGTGCATCAAGTAGAAGATGAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 352  
QY 221 AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTTGCATGGAAGAGAGTGGGAAGTGA 280  
DB 353 AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTTGCATGGAAGAGAGTGGGAAGTGA 412  
QY 281 TTCCAAGGTCCAGCACCAGACACCCGTTTACTTGGGACCCAGCGCATCGCGT 340  
DB 413 TTCCAAGGTCCAGCACCAGACACCCGTTTACTTGGGACCCAGCGCATCGCGT 472  
QY 341 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGAGGTTCTCGATGTGGTGGAGAGAGCC 400  
DB 473 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGAGGTTCTCGATGTGGTGGAGAGAGCC 532  
QY 401 TCAGCAACTACCCCTTTTGAATTTCCAGGGTGCAGAGATCAATTAAGTCCCAAGAGGAGGTTG 460  
DB 533 TCAGCAACTACCCCTTTTGAATTTCCAGGGTGCAGAGATCAATTAAGTCCCAAGAGGAGGTTG 592  
QY 461 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAACAAAGGTGGT 520  
DB 593 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAACAAAGGTGGT 652  
QY 521 TCAGCATAGTCCATATGAACCAATATCAAGAAACCTTTTGAGCTTTGGACCTTTGGGG 580  
DB 653 TCAGCATAGTCCATATGAACCAATATCAAGAAACCTTTTGAGCTTTGGACCTTTGGGG 712  
QY 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 640  
DB 713 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 772



QY 641 CTCTGCAATTTGGCTCTATGGCAAGGACTACAAATGCTTACACACATAGCTTCTTGCT 700  
Db |||||  
QY 773 CTCTGCAATTTGGCTCTATGGCAAGGACTACAAATGCTTACACACATAGCTTCTTGCT 832  
Db |||||  
QY 701 ATGGGAAGGATCAGGCACCTCTGSCAGAAATGSCCAAGGACATTCAGGTTGCAAGTAATG 760  
Db |||||  
QY 833 ATGGGAAGGATCAGGCACCTCTGSCAGAAATGSCCAAGGACATTCAGGTTGCAAGTAATG 892  
Db |||||  
QY 761 AAATTTCTCAGGACCCATCTTTTCATCTCGATATAGGAAGGTAGTGAACGTAAGTGACC 820  
Db |||||  
QY 893 AAATTTCTCAGGACCCATCTTTTCATCTCGATATAGGAAGGTAGTGAACGTAAGTGACC 952  
Db |||||  
QY 821 TTATACAGACCCCTGSCACCAAGAGATTTGAGATGACTCTTCATTTCCAGCATTTGAAA 880  
Db |||||  
QY 953 TTATACAGACCCCTGSCACCAAGAGATTTGAGATGACTCTTCATTTCCAGCATTTGAAA 1012  
Db |||||  
QY 881 TCCAGGGTATTCGAACTATCAACATGCAATGCAATCAAGCATCTGAGGCTCTTCAACCA 940  
Db |||||  
QY 1013 TCCAGGGTATTCGAACTATCAACATGCAATGCAATCAAGCATCTGAGGCTCTTCAACCA 1072  
Db |||||  
QY 941 GTTACTGCCCTTACTCCCACTGTCCTTCAATGGGATTTCTTGCCACCACTCCAGGGGG 1000  
Db |||||  
QY 1073 GTTACTGCCCTTACTCCCACTGTCCTTCAATGGGATTTCTTGCCACCACTCCAGGGGG 1132  
Db |||||  
QY 1001 ATTTTGGGCAATTTTCAGCTTTTACTTTTGTGATGAAGTTTAACTTGACATCAGAGA 1060  
Db |||||  
QY 1133 ATTTTGGGCAATTTTCAGCTTTTACTTTTGTGATGAAGTTTAACTTGACATCAGAGA 1192  
Db |||||  
QY 1061 AGTCTCTCAGGAAAGGTGCTGAGATGATGAAAAGTTCTGCTCAGCCCTGGGAGG 1120  
Db |||||  
QY 1193 AGTCTCTCAGGAAAGGTGCTGAGATGATGAAAAGTTCTGCTCAGCCCTGGGAGG 1252  
Db |||||  
QY 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACTGAGTGAATACTGCTTTTCTG 1180  
Db |||||  
QY 1253 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACTGAGTGAATACTGCTTTTCTG 1312  
Db |||||  
QY 1181 GTACTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTACAGCTGATTTCTCGGAGC 1240  
Db |||||  
QY 1313 GTACTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTACAGCTGATTTCTCGGAGC 1372  
Db |||||  
QY 1241 ACATCCATTTCAATGGCAAGTCCAGGCGAGCGAGCGCGCTGGACTTTGGGCTACATGC 1300  
Db |||||  
QY 1373 ACATCCATTTCAATGGCAAGTCCAGGCGAGCGAGCGCGCTGGACTTTGGGCTACATGC 1432  
Db |||||  
QY 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGCCACACTCTCTCCCACTCCA 1360  
Db |||||  
QY 1433 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGCCACACTCTCTCCCACTCCA 1492  
Db |||||  
QY 1361 CCTA 1364  
Db |||||  
QY 1493 CCTA 1496  
Db |||||

RESULT 9

ADL24294  
ID ADL24294 standard; DNA; 1599 BP.  
XX  
AC ADL24294;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human CD39 coding sequence.  
XX  
KW ds: gene; cardiovascular disease; IL-17; interleukin; IL-18; 4-1BB; CD30;  
KW OX40; antagonist.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 67..1599  
FT /\*tag= a  
FT /product= "CD39"

XX WO2004019866-A2.  
XX 11-MAR-2004.  
XX 21-AUG-2003; 2003WO-US026354.  
XX 28-AUG-2002; 2002US-0406418P.  
XX 12-AUG-2003; 2003US-0494457P.  
XX (IMMV ) IMMUNEX CORP.  
XX Burton PB, Deisher TA;  
XX WPI; 2004-239107/22.  
XX P-PSDB; ADL24295.  
XX Use of IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists, for treating a  
XX cardiovascular disease, e.g. chronic immune myocarditis, congestive heart  
XX failure, aneurysm, angina, embolism, restenosis, ischemia or  
XX thrombocytopenic purpura.  
XX Disclosure; Page 130-132; 135pp; English.  
XX The present invention relates to a method of treating cardiovascular  
XX disease in a subject, comprising administering an IL-17, IL-18, 4-1BB,  
XX CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40  
XX antagonists are useful for treating cardiovascular disorders, e.g.  
XX (chronic immune) myocarditis, congestive heart failure, aneurysms,  
XX angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. The  
XX present sequence is a coding sequence used in the exemplification of the  
XX invention.  
XX Sequence 1599 BP; 446 A; 366 C; 382 G; 405 T; 0 U; 0 Other;  
Query Match 96.6%; Score 1319.2; DB 12; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 41 GTTCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGCTGGATCGG 100  
Db |||||  
QY 173 GTTGACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGCTGGATCGG 232  
Db |||||  
QY 101 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGACAGAAAGAGATGACACAG 160  
Db |||||  
QY 233 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGACAGAAAGAGATGACACAG 292  
Db |||||  
QY 161 GCGTGGTGCAATCAAGTAGAAGATGCGGGTTAAAGGTCCTGGAAATCTCAAAATTTGTT 220  
Db |||||  
QY 293 GCGTGGTGCAATCAAGTAGAAGATGCGGGTTAAAGGTCCTGGAAATCTCAAAATTTGTT 352  
Db |||||  
QY 221 AGAAGTAAATGAATAGGCAATTTACCTGACTGATTCATCGAAGAGAGCTAGGGAAGTGA 280  
Db |||||  
QY 353 AGAAGTAAATGAATAGGCAATTTACCTGACTGATTCATCGAAGAGAGCTAGGGAAGTGA 412  
Db |||||  
QY 281 TTCCAAGGTCCTCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGCGAGCATGCCGT 340  
Db |||||  
QY 413 TTCCAAGGTCCTCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGCGAGCATGCCGT 472  
Db |||||  
QY 341 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGGAGCC 400  
Db |||||  
QY 473 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGGAGCC 532  
Db |||||  
QY 401 TCAGCACTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGGCCACAGAGGAGTG 460  
Db |||||  
QY 533 TCAGCACTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGGCCACAGAGGAGTG 592  
Db |||||  
QY 461 CCTATGGCTGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGG 520  
Db |||||  
QY 593 CCTATGGCTGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGG 652  
Db |||||  
QY 521 TCAGCATAGTCCCATATGAAACCAATTAATCAGGAAACCTTTGGAGCTTTGACCTTGGGG 580  
Db |||||

Db 653 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 712  
Qy 581 GAGCCTCTACAAAGTACATTTTGTACCCCAAAACAGACTATCGAGTCCCGAGATAATG 640  
Db 713 GAGCCTCTACAAAGTACATTTTGTACCCCAAAACAGACTATCGAGTCCCGAGATAATG 772  
Qy 641 CTCTGCAATTTCCCTCTATGGCAAGACTTACAAATGTCTACACACATAGTCTTCTGTGCT 700  
Db 773 CTCTGCAATTTCCCTCTATGGCAAGACTTACAAATGTCTACACACATAGTCTTCTGTGCT 832  
Qy 701 ATCGGAAGGATCAGGACCTCTGCGCAAACTTGCCCAAGGACATTCAGGTTGCAAGTAATG 760  
Db 833 ATCGGAAGGATCAGGACCTCTGCGCAAACTTGCCCAAGGACATTCAGGTTGCAAGTAATG 892  
Qy 761 AAATTTCTCAGGACCCATGCTTTTCATCTCGGATATGAAGGTAGTGAAGTGAAGTACC 820  
Db 893 AAATTTCTCAGGACCCATGCTTTTCATCTCGGATATGAAGGTAGTGAAGTGAAGTACC 952  
Qy 821 TTTTACAAGACCCCTCTGACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGA 880  
Db 953 TTTTACAAGACCCCTCTGACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGA 1012  
Qy 881 TCAGGGTATTTGAAACTATCAACAATGCCATCAAAAGCATCTCGGAGCTTTCAACACCA 940  
Db 1013 TCAGGGTATTTGAAACTATCAACAATGCCATCAAAAGCATCTCGGAGCTTTCAACACCA 1072  
Qy 941 GTTACTGCCCTTACTCCAGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGG 1000  
Db 1073 GTTACTGCCCTTACTCCAGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGG 1132  
Qy 1001 ATTTTGGGGCATTTTCAGCTTTTCTTCTGTGATGAAGTTTTPAAACTTTGACATCAGAGA 1060  
Db 1133 ATTTTGGGGCATTTTCAGCTTTTCTTCTGTGATGAAGTTTTPAAACTTTGACATCAGAGA 1192  
Qy 1061 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTTCTGTCTCAGCCTTTGGAGG 1120  
Db 1193 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTTCTGTCTCAGCCTTTGGAGG 1252  
Qy 1121 AGATAAACAATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1180  
Db 1253 AGATAAACAATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1312  
Qy 1181 GTACCTACATTTCTCCTCTCTGCAAGGCTATCATTTTCAGCTGATTTCTCTGGGAGC 1240  
Db 1313 GTACCTACATTTCTCCTCTCTGCAAGGCTATCATTTTCAGCTGATTTCTCTGGGAGC 1372  
Qy 1241 ACATCCATTTTCATTTGGCAAGATCCAGGCGACGACCGCGCTGGACTTTGGGCTACATGC 1300  
Db 1373 ACATCCATTTTCATTTGGCAAGATCCAGGCGACGACCGCGCTGGACTTTGGGCTACATGC 1432  
Qy 1301 TGAACCTGACCAATGATCCGAGCTGAGCAACCATTTGTCACACCTCTCTCCACTCCA 1360  
Db 1433 TGAACCTGACCAATGATCCGAGCTGAGCAACCATTTGTCACACCTCTCTCCACTCCA 1492  
Qy 1361 CCTA 1364  
Db 1493 CCTA 1496

RESULT 10  
AAA96069  
ID AAA96069 standard; DNA; 1704 BP.  
XX  
AC  
XX  
XX  
29-JAN-2001 (first entry)  
XX  
DE Human ATP diphosphohydrolase coding sequence.  
XX  
KW Drug resistance; ATP gradient; chemotherapeutic; antibiotic; herbicide;  
XX human; ATP diphosphohydrolase; ds.  
XX  
OS Homo sapiens.

XX WO200052144-A1.  
PN  
XX  
PD 08-SEP-2000.  
XX  
PF 28-FEB-2000; 2000WO-US005315.  
XX  
PR 03-MAR-1999; 99US-00261825.  
XX  
PA (TEXA ) UNIV TEXAS.  
XX  
PI Thomas CE, Windsor JB, Roux SJ, Lloyd AM, Hurley L;  
XX  
XX WPI; 2000-587306/55.  
DR  
XX Increasing or decreasing drug resistance in target bacteria, yeast, plant  
PT or mammalian cells comprises altering ATP gradient across biological  
PT membrane of target cell.  
XX  
XX Claim 14; Page: 85pp; English.  
XX  
CC The present invention relates to a method for increasing or decreasing  
CC drug resistance in target bacteria, yeast, plant or mammalian cells by  
CC altering the ATP gradient across the biological membrane of the target  
CC cell. The method is useful for modulating drug resistance of cells. It is  
CC useful for increasing the sensitivity of cells to chemotherapeutic and  
CC antibiotic agents and increasing resistance to herbicides. The present  
CC sequence is human ATP diphosphohydrolase coding sequence. This sequence  
CC encodes was used in the present invention to modulate drug resistance.  
CC Note: The present sequence is not shown in the specification, but is  
CC referred to via its GenBank accession number  
XX  
SQ Sequence 1704 BP; 468 A; 392 C; 403 G; 441 T; 0 U; 0 Other;

Query Match 96.6%; Score 1319.2; DB 3; Length 1704;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGCTGGATCGG 100  
Db 137 GGTTCACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGCTGGATCGG 196  
Qy 101 GTTCTTCTCACACAAGTTTATACATCTATACTTAAGTGGCCAGACAAAAGGAGAATGACACAG 160  
Db 197 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAAAAGGAGAATGACACAG 256  
Qy 161 GCGTGGTGATCAAGTAGAAGAAAGTAAAGGTTCTGGAATCTCAAAAATTTGTTTC 220  
Db 257 GCGTGGTGATCAAGTAGAAGAAAGTAAAGGTTCTGGAATCTCAAAAATTTGTTTC 316  
Qy 221 AGAAGTAGAATGAATAGGCAATTTACCTGACATTTGATGAGAAAGAGCTAGGGAAGTCA 280  
Db 317 AGAAGTAGAATGAATAGGCAATTTACCTGACATTTGATGAGAAAGAGCTAGGGAAGTCA 376  
Qy 281 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATCGCGT 340  
Db 377 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATCGCGT 436  
Qy 341 TGCTCAGGATGGAAGTAGAAGTTGGCAGACAGGGTTCTGATGTGTGGAGAGAGGCC 400  
Db 437 TGCTCAGGATGGAAGTAGAAGTTGGCAGACAGGGTTCTGATGTGTGGAGAGAGGCC 496  
Qy 401 TCAGCAACTACCCCTTTGACTTTCCAGGGTGCCAGGATCATTTACTGCCCAAGAGGAGGTG 460  
Db 497 TCAGCAACTACCCCTTTGACTTTCCAGGGTGCCAGGATCATTTACTGCCCAAGAGGAGGTG 556  
Qy 461 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 520  
Db 557 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 616  
Qy 521 TCAGCATAGTCCCATATGAAACAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 580  
Db 617 TCAGCATAGTCCCATATGAAACAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 676

Qy	581	GAGCCTCTACAAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG	640
Db	677	GAGCCTCTACAAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG	736
Qy	641	CTCTGCAATTTTCGCCTCTATGGCAAGGACTCAATGTCTACACACATAGCTTTCTTGCT	700
Db	737	CTCTGCAATTTTCGCCTCTATGGCAAGGACTCAATGTCTACACACATAGCTTTCTTGCT	796
Qy	701	ATGGGAAGGATCAGGCACCTCTGGCAGAAACCTGGCCCAAGGACATTCAGTTCGCAAGTAATG	760
Db	797	ATGGGAAGGATCAGGCACCTCTGGCAGAAACCTGGCCCAAGGACATTCAGTTCGCAAGTAATG	856
Qy	761	AAATTTCTCAGGGACCCATGCTTTTCATCTCGGATATAAGAAAGTAGTGAACCTAAAGTGACC	820
Db	857	AAATTTCTCAGGGACCCATGCTTTTCATCTCGGATATAAGAAAGTAGTGAACCTAAAGTGACC	916
Qy	821	TTTACAAAGACCCCTGCACCAAGAGATTGAGATGACTCTTCCATTTCCAGCAGTTTGAAGA	880
Db	917	TTTACAAAGACCCCTGCACCAAGAGATTGAGATGACTCTTCCATTTCCAGCAGTTTGAAGA	976
Qy	881	TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAAGCATCCTCGAGCTTTCAACACCA	940
Db	977	TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAAGCATCCTCGAGCTTTCAACACCA	1036
Qy	941	GTTACTGCCCTTACTCCCAAGTGTGCCTTCAATGGGATTTTCTGCCACCACTCCAGGGGG	1000
Db	1037	GTTACTGCCCTTACTCCCAAGTGTGCCTTCAATGGGATTTTCTGCCACCACTCCAGGGGG	1096
Qy	1001	ATTTTGGGGCAATTTTCAGCTTTTACTTTGTGATGAAGTATTTTAACTTGACATCAGAGA	1060
Db	1097	ATTTTGGGGCAATTTTCAGCTTTTACTTTGTGATGAAGTATTTTAACTTGACATCAGAGA	1156
Qy	1061	AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTTGGGAGG	1120
Db	1157	AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTTGGGAGG	1216
Qy	1121	AGATAAAAAACATTTACGCTGGAGTAAAGGAAGTAGCTGAGTGAATATCTGCTTTTCTG	1180
Db	1217	AGATAAAAAACATTTACGCTGGAGTAAAGGAAGTAGCTGAGTGAATATCTGCTTTTCTG	1276
Qy	1181	GTACTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTCTGGGAGC	1240
Db	1277	GTACTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTCTGGGAGC	1336
Qy	1241	ACATCCATTTTCATTTGGCAAGATTCAGGGCAGCGAGCGGGCTGGACTTTGGGGCTACATGC	1300
Db	1337	ACATCCATTTTCATTTGGCAAGATTCAGGGCAGCGAGCGGGCTGGACTTTGGGGCTACATGC	1396
Qy	1301	TGAACCTTGACCAACATGATCCCACTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA	1360
Db	1397	TGAACCTTGACCAACATGATCCCACTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA	1456
Qy	1361	CCTA 1364	
Db	1457	CCTA 1460	

RESULT 11  
ADJ57261  
ID ADJ57261 standard; DNA; 1704 BP.  
XX  
XX AC ADJ57261;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Human CD39 polypeptide encoding DNA.  
XX  
XX CD39; nucleoside diphosphate; thrombolytic; anticoagulant;  
KW cardiovascular; cytosolic; antibacterial; immunosuppressive; vasotropic;  
KW cardiant; antianginal; antierosclerotic; gynaecological;  
KW cerebroprotective; cancer; human; apyrase; gene; ds.  
XX  
XX

OS	Homo sapiens.	
XX		
XX	Key	Location/Qualifiers
XX	CDS	31..1563
FT	FT	/*tag= a
FT	FT	/product= "CD39"
XX		
FN	WO2003070823-A2.	
XX		
XX	28-AUG-2003.	
PD		
XX		
XX	19-FEB-2003; 2003WO-US004845.	
PF		
XX		
PR	20-FEB-2002; 2002US-0358303P.	
XX		
PA	(GEO ) GEN HOSPITAL CORP.	
PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.	
XX		
XX	Elmalch DR, Robson SC, Papisov MI;	
FI		
XX	WPI; 2003-778966/73.	
DR	P-PSDB; ADJ57262.	
DR		
XX		
XX	New enzyme polymer conjugate used for treating abnormal levels of	
PT	extracellular nucleotides or platelet aggregation, graft transplant,	
PT	cardiovascular disease, cancer and sepsis.	
PT		
XX		
PS	Disclosure; SEQ ID NO 1; 82pp; English.	
XX		
CC	The invention relates to a conjugate (I) comprising an enzyme and a	
CC	biodegradable polymer, where (i) enzymatic activity of the enzyme is	
CC	higher relative to that of the enzyme in the absence of the biodegradable	
CC	polymer, or (ii) the half life of the enzyme is longer than that of the	
CC	enzyme in the absence of the polymer. The enzymatic activity (i) is at	
CC	least 10 (preferably at least 100) times higher in the presence of the	
CC	polymer. The enzyme is a multimeric, soluble and/or extracellular enzyme,	
CC	preferably an apyrase, especially a soluble form of CD39 and catalyzes	
CC	hydrolysis of nucleoside diphosphate. The conjugate can be used to treat	
CC	diseases relating to abnormal levels of extracellular nucleotides or	
CC	abnormal aggregation of platelets, particularly cardiovascular disease,	
CC	cancer, sepsis or a disease related to graft transplant. (I) is also used	
CC	for treating coronary artery disease or injury following myocardial	
CC	infarction, unstable angina, atherosclerosis, pre-eclampsia, embolism,	
CC	platelet associated ischaemic disorders including lung, coronary and	
CC	cerebral ischaemia, reocclusion following thrombosis, thrombotic	
CC	disorders, and thrombosis and coagulopathies associated with exposure to	
CC	a foreign or injured tissue surface, in combination with angioplasty,	
CC	carotid endarterectomy, anastomosis of vascular grafts and chronic	
CC	cardiovascular diseases. The present sequence represents a DNA encoding a	
CC	human CD39 polypeptide.	
XX		
SQ	Sequence 1704 BP; 468 A; 392 C; 403 G; 441 T; 0 U; 0 Other;	

	Query Match	96.8%	Score 1319.2	DB 10	Length 1704
	Best Local Similarity	99.8%	Pred. No. 0		
	Matches 1321	Conservative 0	Mismatches 3	Indels 0	Gaps 0
Qy	41	GTTCACCCAGAACAAAGACATCCAGAAAAACGTTAAGTATGGGATTTGCTGGATCGCG	100		
Db	137	GGTGTGACCCAGAACAAAGACATTCGCAGAAAACGTTAAGTATGGGATTTGCTGGATCGCG	196		
Qy	101	GTTCCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGGAGAATGACACAG	160		
Db	197	GTTCCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGGAGAATGACACAG	256		
Qy	161	GCGTGGTGGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTCGAACTCTCAAAATTTGTTTC	220		
Db	257	GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTCGNAATCTCAAAATTTGTTTC	316		
Qy	221	AGAAAGTAAATGAAATAGGCATTTTACCTGACTCATTTGGCATGGAAAAGCTAGGGAAGTGA	280		
Db	317	AGAAAGTAAATGAAATAGGCATTTTACCTGACTCATTTGGCATGGAAAAGCTAGGGAAGTGA	376		

QY 281 TTCCAGGTCCTCCAGCACCAGAGACACCCGTTTACCTGGAGGCCACGGCAGGCATCGCGT 340  
DB |||||  
377 TTCCAGGTCCTCCAGCACCAGAGACACCCGTTTACCTGGAGGCCACGGCAGGCATCGCGT 436  
QY 341 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGGTTCTGGATGTGGTGGAGAGAGCC 400  
DB |||||  
437 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGGTTCTGGATGTGGTGGAGAGAGCC 496  
QY 401 TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGCGCAAGAGAGAGTG 460  
DB |||||  
497 TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGCGCAAGAGAGAGTG 556  
QY 461 CCTATGGCTGGATTACTATCAACTATCTGTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 520  
DB |||||  
557 CCTATGGCTGGATTACTATCAACTATCTGTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 616  
QY 521 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 580  
DB |||||  
617 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 676  
QY 581 GAGCCTCTACACAAGTCACCTTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATG 640  
DB |||||  
677 GAGCCTCTACACAAGTCACCTTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATG 736  
QY 641 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTCTGTGTCT 700  
DB |||||  
737 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTCTGTGTCT 796  
QY 701 ATGGGAAGGATCAGGCACCTCTGCGAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATG 760  
DB |||||  
797 ATGGGAAGGATCAGGCACCTCTGCGAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATG 856  
QY 761 AAATTTCTCAGGAGCCCATGCTTTCATCTCGATATGAAGAGTAGTGAAGTAGCC 820  
DB |||||  
857 AAATTTCTCAGGAGCCCATGCTTTCATCTCGATATGAAGAGTAGTGAAGTAGCC 916  
QY 821 TTTTACAGACCCCTGACCAAGAGATTTGAGATGACTCTTCATTTCCAGCAGTTTGAAA 880  
DB |||||  
917 TTTTACAGACCCCTGACCAAGAGATTTGAGATGACTCTTCATTTCCAGCAGTTTGAAA 976  
QY 881 TCAGGAGTATTTGAAACTATCAACAATGCCATCAAAAGCATCTCGAGCTTTCAACACCA 940  
DB |||||  
977 TCAGGAGTATTTGAAACTATCAACAATGCCATCAAAAGCATCTCGAGCTTTCAACACCA 1036  
QY 941 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGCACACACTCCAGGGG 1000  
DB |||||  
1037 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGCACACACTCCAGGGG 1096  
QY 1001 ATTTTGGGGCATTTTCAAGCTTTTACTTTCTGTGATGAAGTTTAAACTTGACATCAGAGA 1060  
DB |||||  
1097 ATTTTGGGGCATTTTCAAGCTTTTACTTTTGTGATGAAGTTTAAACTTGACATCAGAGA 1156  
QY 1061 AAGTCTCTCAGGAAAGGAGTGAAGTATGAAGAAAGTTTCTGTCTCAGCCTTTGGAGG 1120  
DB |||||  
1157 AAGTCTCTCAGGAAAGGAGTGAAGTATGAAGAAAGTTTCTGTCTCAGCCTTTGGAGG 1216  
QY 1121 AGATAAAACATCTTACGCTGGAGTAAAGAGAAAGTACCTGAGTGAATCTGCTTTCTG 1180  
DB |||||  
1217 AGATAAAACATCTTACGCTGGAGTAAAGAGAAAGTACCTGAGTGAATCTGCTTTCTG 1276  
QY 1181 GTACCTACATTTCTCCCTCTTCTGCAAGGCTATCATTTTCAGAGCTGATTCTCTGGAGC 1240  
DB |||||  
1277 GTACCTACATTTCTCCCTCTTCTGCAAGGCTATCATTTTCAGAGCTGATTCTCTGGAGC 1336  
QY 1241 ACATCCATTTTCAITGGCAAGATCCAGGGCAGCGCCGCTGGACTTTGGGTACATGC 1300  
DB |||||  
1337 ACATCCATTTTCAITGGCAAGATCCAGGGCAGCGCCGCTGGACTTTGGGTACATGC 1396  
QY 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCATCCA 1360  
DB |||||  
1397 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCATCCA 1456  
QY 1361 CCTA 1364

Db 1457 CCTA 1460  
|||  
RESULT 12  
AAT38516  
ID AAT38516 standard; DNA; 1818 BP.  
XX  
AC AAT38516;  
XX  
DT 29-DEC-1996 (first entry)  
XX  
DE Human lymphoid cell activation antigen CD39.  
XX  
KW ATP diphosphohydrolase; ATPase; bovine aorta; pig pancreas; apyrase;  
KW CD39; lymphoid cell activation antigen; enzyme; platelet aggregation;  
KW thrombogenicity; anti-haemostatic; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 68..1600  
FT /\*tag= a  
XX  
PN WO9632471-A2.  
XX  
PD 17-OCT-1996.  
XX  
PF 10-APR-1996; 96WO-CA000223.  
XX  
PR 10-APR-1995; 95US-00419204.  
XX  
PA (UYSH ) UNIV SHERBROOKE.  
XX  
PI Beaudoin AR, Sevigny J;  
XX  
DR WPI; 1996-477122/47.  
DR P-PSDB; AAW04334.  
XX  
PT Isolated ATP di:phospho:hydrolase enzymes - have anti-haemostatic  
PT activity, useful for reducing platelet aggregation and thrombogenicity.  
XX  
PS Claim 18; Page 44-45; 60pp; English.  
XX  
CC The bovine aorta (AAW04335 to AAW04338 and AAW04340) and porcine  
CC pancreatic (AAW04339) ATPases have been partially sequenced. The  
CC sequences have been found to be highly homologous to a human lymphoid  
CC cell activation antigen designated CD39 (Maliszewski et al. (1994). J.  
CC Immunol.: 3574-3583). The complete sequences of the ATPases types I and  
CC II have not been obtained yet. Assuming that the CD39 gene product is an  
CC ATPase type II, the use of CD39 in the reduction of platelet aggregation  
CC and of thrombogenicity may be contemplated, as well as a process of  
CC making ATPases using the CD39 sequence (AAT38516)  
XX  
SQ Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;  
Query Match 96.6%; Score 1319.2; DB 2; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAACGTTTAAGTATCGGATTTGCTGGATGCGG 100  
DB |||||  
174 GGTTCACCCAGAACAAAGCATTTGCCAGAAACGTTTAAGTATCGGATTTGCTGGATGCGG 233  
QY 101 GTTCTTCTCACACAAGTTTATACATCTATACTGCTGCCAGCAGAAAAAGGAGATGACACAG 160  
DB |||||  
234 GTTCTTCTCACACAAGTTTATACATCTATACTGCTGCCAGCAGAAAAAGGAGATGACACAG 293  
QY 161 GGTGGTGCATCAAGTCAGAGAAATCGAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 220  
DB |||||  
294 GGTGGTGCATCAAGTCAGAGAAATCGAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 353  
QY 221 AGAAAGTAAATGAAATAGGCATTTTACCTGACTGTTGATGGAAGAGCTAGGGAAGTGA 280

Db 354 AGAAGTAATGAAATAGGACATTTACCTGACTGATTTGCATGGAAAGAGCTAGGGAAGTGA 413  
Qy 281 TTCCAAAGGTCCAGCACCAGAGACACCCGTTTACCTCTGGGAGCCACGGCAGGCGATGCGGT 340  
Db 414 TTCCAAAGGTCCAGCACCAGAGACACCCGTTTACCTCTGGGAGCCACGGCAGGCGATGCGGT 473  
Qy 341 TGTCTAGGATGGAAGTGAAGAGTTGGCAGACAGAGGTTCTGATGTGTGGAGAGAGCC 400  
Db 474 TGTCTAGGATGGAAGTGAAGAGTTGGCAGACAGAGGTTCTGATGTGTGGAGAGAGCC 533  
Qy 401 TCAGCAACTACCCCTTTGACTTCCAGGTTCCAGGTCAGGATCAATTAATGAGGAGAGTGTG 460  
Db 534 TCAGCAACTACCCCTTTGACTTCCAGGTTCCAGGTCAGGATCAATTAATGAGGAGAGTGTG 593  
Qy 461 CCTATGGCTGGATTAATCACTATCTCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGTGT 520  
Db 594 CCTATGGCTGGATTAATCACTATCTCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGTGT 653  
Qy 521 TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 580  
Db 654 TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 713  
Qy 581 GAGCCTCTACAAAGTCACTTTTGTACCCCAAAACAGACTATCAGTCCCCAGATAATG 640  
Db 714 GAGCCTCTACAAAGTCACTTTTGTACCCCAAAACAGACTATCAGTCCCCAGATAATG 773  
Qy 641 CTCTGCAATTTGCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 700  
Db 774 CTCTGCAATTTGCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 833  
Qy 701 ATGGGAAGGATCAGGACCTCTGGCAGAAACCTGGCCAAAGGACATTCAGGTTGCAAGTAATG 760  
Db 834 ATGGGAAGGATCAGGACCTCTGGCAGAAACCTGGCCAAAGGACATTCAGGTTGCAAGTAATG 893  
Qy 761 AAATTTCTCAGGACCCATGCTTTTCATCTGGATATAAGAGTAGTGAACGTAGTGACC 820  
Db 894 AAATTTCTCAGGACCCATGCTTTTCATCTGGATATAAGAGTAGTGAACGTAGTGACC 953  
Qy 821 TTTTAAAGACCCCTGCACCAAGAGATTGAGATGACTTCTTCCATTCCAGCAGATTTGAAA 880  
Db 954 TTTTAAAGACCCCTGCACCAAGAGATTGAGATGACTTCTTCCATTCCAGCAGATTTGAAA 1013  
Qy 881 TCCAGGGTATTGGAACCTATCAACAAATGCCATCAAGCATCTGGAGCTCTTCAACACCA 940  
Db 1014 TCCAGGGTATTGGAACCTATCAACAAATGCCATCAAGCATCTGGAGCTCTTCAACACCA 1073  
Qy 941 GTTACTGCGCTTACTCCAGTGCTGCTTCAATGGGATTTTCTTGCCACCATCTCCAGGGGG 1000  
Db 1074 GTTACTGCGCTTACTCCAGTGCTGCTTCAATGGGATTTTCTTGCCACCATCTCCAGGGGG 1133  
Qy 1001 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTAACTTGACATCAGAGA 1060  
Db 1134 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTAACTTGACATCAGAGA 1193  
Qy 1061 AAGTCTCTCAGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGGCTTTGGGAGG 1120  
Db 1194 AAGTCTCTCAGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGGCTTTGGGAGG 1253  
Qy 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACGTCTTTTCTG 1180  
Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACGTCTTTTCTG 1313  
Qy 1181 GTACCTACATCTCTCCCTCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTTGGGAGC 1240  
Db 1314 GTACCTACATCTCTCCCTCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTTGGGAGC 1373  
Qy 1241 ACATCCATTTTCAATGGCAAGATCCAGGGCAGCGCGGTGGACTTTGGGCTACATGC 1300  
Db 1374 ACATCCATTTTCAATGGCAAGATCCAGGGCAGCGCGGTGGACTTTGGGCTACATGC 1433  
Qy 1301 TGAACCTGACCAACATGATGCCAGTGAGCAACCAATGTTCCACACTCTCTCTCCCACTCCA 1360

Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCCACACCTCTCTCTCCCACTCCA 1493  
Qy 1361 CCTA 1364  
Db 1494 CCTA 1497  
RESULT 13  
AAT33966  
ID AAT33966 standard; DNA; 1818 BP.  
XX AAT33966;  
AC AAT33966;  
XX 29-MAY-1997 (first entry)  
XX DNA coding for human CD39 protein.  
XX Human; lymphocyte activation marker; gene therapy;  
KW ATP diphosphohydrolase; transgenic animal; pig; porcine; graft; donor;  
KW transplantation; endothelial cell; prosthetic device;  
KW platelet aggregation; inhibition; intravascular; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 68..1600  
CDS /\*tag= a  
FT /EC number= "3.6.1.5"  
FT /note= "CD39 protein has ATP diphosphohydrolase activity"  
XX WO9630532-A1.  
XX 03-OCT-1996.  
XX 22-MAR-1996; 96WO-EP001270.  
XX 24-MAR-1995; 95US-00410371.  
PR 12-FEB-1996; 96US-00600383.  
XX (SANO ) SANDOZ LTD.  
PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.  
XX Bach FH, Robson S;  
FI WPI; 1996-455377/45.  
DR P-PSDB; AAW04264.  
XX Gene therapy of inflammatory or immunological stimulation of platelet aggregation - using CD39 protein with ATP di:phospho:hydrolase activity, useful for preventing or alleviating thrombotic condition in mammalian subject.  
XX Claim 3; Page 38; 65pp; English.  
XX Non-human transgenic or somatic recombinant mammals, whose cells contain a heterologous DNA encoding a polypeptide (especially human CD39 protein) having ATP-diphosphohydrolase activity under cellular activating conditions is claimed. In particular the animal is a pig and its cells (or tissues or organs) can be used for transplantation. DNA coding for human CD39 is also useful for genetically modifying a mammalian cell to render it less susceptible to an inflammatory or immunological stimulus and platelet aggregation. The modified cells can be used to prevent or alleviate a thrombotic condition. The present sequence encodes human CD39 protein and was disclosed in J.Immunol. 153 (8) (1994) 3574-3584  
SQ Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;  
Query Match 96.6%; Score 1319.2; DB 2; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAACGTTAAGATGGAATGTGCTGATGCGG 100

Db 174 GGTGACCAGAAACAAAGCATTCGCCAGAAAAACGTTAAGTATGGATTGTGCTGGATGCGG 233  
 Qy 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGGAGATGACACAG 160  
 Db 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGGAGATGACACAG 293  
 Qy 161 GCGTGGTGCATCAAGTAGAAGATGAGAGGTAAAGGTCCTGGAATCTCMAAATTTGTTTC 220  
 Db 294 GCGTGGTGCATCAAGTAGAAGATGAGAGGTAAAGGTCCTGGAATCTCMAAATTTGTTTC 353  
 Qy 221 AGAAAGTAAATGAATAGGCAITTTACCTGACTGATTTGCATGGAAGAGCTAGGGAAGTGA 280  
 Db 354 AGAAAGTAAATGAATAGGCAITTTACCTGACTGATTTGCATGGAAGAGCTAGGGAAGTGA 413  
 Qy 281 TTCCAAGGTCCAGACACCAAGAGACACCCGTTTACCTGGAGGCCAGCGGATGCGGT 340  
 Db 414 TTCCAAGGTCCAGACACCAAGAGACACCCGTTTACCTGGAGGCCAGCGGATGCGGT 473  
 Qy 341 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCC 400  
 Db 474 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCC 533  
 Qy 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAAGTCCCAAGAGGAAAGTGG 460  
 Db 534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAAGTCCCAAGAGGAAAGTGG 593  
 Qy 461 CCTATGGCTGGATTAATCAACTATCTGCTGGGCAATTCAGTCAGAAAAAAGGTGGT 520  
 Db 594 CCTATGGCTGGATTAATCAACTATCTGCTGGGCAATTCAGTCAGAAAAAAGGTGGT 653  
 Qy 521 TCAGCATAGTCCCATATGAACCAATAATCAGAGAAACCTTTGAGCTTTGGACCTTTGGGG 580  
 Db 654 TCAGCATAGTCCCATATGAACCAATAATCAGAGAAACCTTTGAGCTTTGGACCTTTGGGG 713  
 Qy 581 GAGCCTCTACACAAGTCACATTTTGTATCCCAACCAAGAGCTATCGAGTCCCCAGATAATG 640  
 Db 714 GAGCCTCTACACAAGTCACATTTTGTATCCCAACCAAGAGCTATCGAGTCCCCAGATAATG 773  
 Qy 641 CTCTGCATTTGGCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTTCTGTGCT 700  
 Db 774 CTCTGCATTTGGCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTTCTGTGCT 833  
 Qy 701 ATGGGAAGGATCAGGCACTCTGCAGAAACTGCGCAAGGACATTCAGGTTCGCAAGTAATG 760  
 Db 834 ATGGGAAGGATCAGGCACTCTGCAGAAACTGCGCAAGGACATTCAGGTTCGCAAGTAATG 893  
 Qy 761 AAATTTCTCAGGGACCCATGCTTTTCATCTGGATATAAGAGGTAGTGAACGTAAAGTGACC 820  
 Db 894 AAATTTCTCAGGGACCCATGCTTTTCATCTGGATATAAGAGGTAGTGAACGTAAAGTGACC 953  
 Qy 821 TTTTCAAGACCCCTGACCAAGAGATTTGAGATGACTTTCATTTCCAGCAGTTTGA 880  
 Db 954 TTTTCAAGACCCCTGACCAAGAGATTTGAGATGACTTTCATTTCCAGCAGTTTGA 1013  
 Qy 881 TCCAGGGTATTTGAAACTATCAACAATGCCATCAAGAGCTCTGGAGCTTCAACACCA 940  
 Db 1014 TCCAGGGTATTTGAAACTATCAACAATGCCATCAAGAGCTCTGGAGCTTCAACACCA 1073  
 Qy 941 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTCCACCACTCCAGGGG 1000  
 Db 1074 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTCCACCACTCCAGGGG 1133  
 Qy 1001 ATTTTGGGGATTTTACGCTTTTACTTTGTGATGAAGTTTTTAACTTGACATCAGAGA 1060  
 Db 1134 ATTTTGGGGATTTTACGCTTTTACTTTGTGATGAAGTTTTTAACTTGACATCAGAGA 1193  
 Qy 1061 AAGTCTCTCAGGAAAAAGGTGACCTGAGATGATGAAAAGTTCTGTGCTCAGCCCTTGGAGG 1120  
 Db 1194 AAGTCTCTCAGGAAAAAGGTGACCTGAGATGATGAAAAGTTCTGTGCTCAGCCCTTGGAGG 1253  
 Qy 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTCTG 1180  
 Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTCTG 1313

Qy 1181 GTACCTACATTTCTCCCTCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTCTGGAGC 1240  
 Db 1314 GTACCTACATTTCTCCCTCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTCTGGAGC 1373  
 Qy 1241 ACATCCATTTTCAATTTGGCAAGATCCAGGGCAGCGAGCCGGCTGGACTTTGGGCTACATGC 1300  
 Db 1374 ACATCCATTTTCAATTTGGCAAGATCCAGGGCAGCGAGCCGGCTGGACTTTGGGCTACATGC 1433  
 Qy 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACTCTCTCTCCACTCCA 1360  
 Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACTCTCTCTCCACTCCA 1493  
 Qy 1361 CCTA 1364  
 Db 1494 CCTA 1497  
 RESULT 14  
 ADI32149  
 ID ADI32149 standard; cDNA; 1818 BP.  
 XX  
 AC ADI32149;  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Human cDNA #1475.  
 XX  
 KW Human; gene; ss; immunological response; immunopathological condition;  
 KW Crohn's disease; asthma; ulcerative colitis; hyper eosinophilia;  
 KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;  
 KW acute monocytic leukemia; antiinflammatory; antiasthmatic; antiulcer;  
 KW osteopathic; antiarthritic; antirheumatic; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6607879-B1.  
 XX  
 PD 19-AUG-2003.  
 XX  
 PF 09-FEB-1998; 98US-00023655.  
 XX  
 PR 09-FEB-1998; 98US-00023655.  
 XX  
 PA (INCY-) INCYTE CORP.  
 XX  
 PI Cocks BG, Stuart SG, Seilhamer JJ;  
 XX  
 DR WPI; 2003-895307/82.  
 XX  
 PS A competition comprising a plurality of cDNAs, useful for detecting  
 XX altered expression of genes in an immunological response or for  
 XX diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma  
 XX or osteoarthritis.  
 XX  
 Claim 1; SEQ ID NO 1475; 50pp; English.  
 XX  
 CC The invention relates to a composition comprising a plurality of cDNAs  
 CC for detecting the altered expression of genes in an immunological  
 CC response. The invention also relates to a method of diagnosing or  
 CC monitoring the treatment of an immunopathological condition in a sample,  
 CC comprising obtaining nucleic acids from a sample, contacting the nucleic  
 CC acids of the sample with an array comprising the plurality of cDNAs under  
 CC conditions to form one or more hybridisation complexes, detecting the  
 CC hybridisation complexes and comparing the levels of the detected  
 CC hybridisation complexes with the level of hybridisation complexes  
 CC detected in a non-diseased sample, where an altered level of the detected  
 CC hybridisation complexes correlates with the presence of an  
 CC immunopathological condition. Also disclosed are an expression profile  
 CC comprising a microarray and a plurality of detectable complexes and a  
 CC method for identifying a plurality of polynucleotide probes. The cDNAs  
 CC are useful as hybridisable array elements in a microarray for monitoring  
 CC the expression of target polynucleotides. The microarray can be used in

CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,  
CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,  
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukemia, and in  
CC identifying agents for the treatment of the diseases. The microarray may  
CC also be used in drug discovery and development, toxicological and  
CC carcinogenicity studies, forensics or pharmacogenomics. The composition  
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or  
CC genomic fragments. This sequence represents a human cDNA of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification but was obtained in electronic format directly  
CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;

Query Match 96.6%; Score 1319.2; DB 11; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 41 GTTCAACCCAGAACAAAGCAATTCGCCAGAAACGTTAAAGTATGGGATTTGGATGGCG 100  
DB 174 GGTTCACCCAGAACAAAGCAATTCGCCAGAAACGTTAAAGTATGGGATTTGGATGGCG 233  
QY 101 GTTCTTCTCACACAGATTATACATCTATAAGTGGCCAGCAAAAGGAGATGACAG 160  
DB 234 GTTCTTCTCACACAGATTATACATCTATAAGTGGCCAGCAAAAGGAGATGACAG 293  
QY 161 GCGTGGTGCATCAAGTAGAAGATGACGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 220  
DB 294 GCGTGGTGCATCAAGTAGAAGATGACGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 353  
QY 221 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTTGCATGTAAGGATAGGGAAGTGA 280  
DB 354 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTTGCATGTAAGGATAGGGAAGTGA 413  
QY 281 TTCCAAGGTCACAGCAAGAGACACCGGTTTACCTGGGACCCAGCGCATGCGGT 340  
DB 414 TTCCAAGGTCACAGCAAGAGACACCGGTTTACCTGGGACCCAGCGCATGCGGT 473  
QY 341 TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGCGGTTCTGGATGTTGGAGAGAGGCC 400  
DB 474 TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGCGGTTCTGGATGTTGGAGAGAGGCC 533  
QY 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGCGCCAAAGGAAGTG 460  
DB 534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGCGCCAAAGGAAGTG 593  
QY 461 CCTATGGCTGGATTACTCAACTATCTGCTGGGCAAAATTCAGTCAGTCAAAACAGGTGGT 520  
DB 594 CCTATGGCTGGATTACTCAACTATCTGCTGGGCAAAATTCAGTCAGTCAAAACAGGTGGT 653  
QY 521 TCAGCATAGTCCCATATGAAACCAATAATCAGAAACCTTTGGAGCTTTGGACCTTTGGGG 580  
DB 654 TCAGCATAGTCCCATATGAAACCAATAATCAGAAACCTTTGGAGCTTTGGACCTTTGGGG 713  
QY 581 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCAGTATCCAGCAATAATG 640  
DB 714 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCAGTATCCAGCAATAATG 773  
QY 641 CTCTGCAATTTGGCTCTATGCGCAGAGACTACAAATGCTACACATAGCTTCTTGCT 700  
DB 774 CTCTGCAATTTGGCTCTATGCGCAGAGACTACAAATGCTACACATAGCTTCTTGCT 833  
QY 701 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAGGACATTCAGGTTGCAAGTAATG 760  
DB 834 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAGGACATTCAGGTTGCAAGTAATG 893  
QY 761 AAATTTCTCAGGACCCCATGCTTTTCATCTCTGGATATAAGAAGGTAGTGAACTGAAGTACC 820  
DB 894 AAATTTCTCAGGACCCCATGCTTTTCATCTCTGGATATAAGAAGGTAGTGAACTGAAGTACC 953  
QY 821 TTTACAAAGCCCTGCAAGCAAGAGATTGAGATGACTCTTCCATTCAGCAGGTTTGAAA 880  
DB 954 TTTACAAAGCCCTGCAAGCAAGAGATTGAGATGACTCTTCCATTCAGCAGGTTTGAAA 1013

QY 881 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAGCATCCTGGAGCTCTTCAACACCA 940  
DB 1014 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAGCATCCTGGAGCTCTTCAACACCA 1073  
QY 941 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTTCGCCACCACTCCAGGGGG 1000  
DB 1074 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTTCGCCACCACTCCAGGGGG 1133  
QY 1001 ATTTTGGGGCAATTTTTCAGCTTTTACTTTTGTGTGTAAGTGTAAACTTTGACATCAGAGA 1060  
DB 1134 ATTTTGGGGCAATTTTTCAGCTTTTACTTTTGTGTGTAAGTGTAAACTTTGACATCAGAGA 1193  
QY 1061 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGGAGG 1120  
DB 1194 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGGAGG 1253  
QY 1121 AGATAAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTTCTG 1180  
DB 1254 AGATAAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTTCTG 1313  
QY 1181 GTACCTACATTTCTCCCTCTTCCCTCTTCCAAAGGCTATCATTTACAGCTGATTTCTCTGGGAGC 1240  
DB 1314 GTACCTACATTTCTCCCTCTTCCCTCTTCCAAAGGCTATCATTTACAGCTGATTTCTCTGGGAGC 1373  
QY 1241 ACATCCATTTTCTGGCAAGATCCAGGGCAGCGCGCTGGAGCTTTGGGCTACATGC 1300  
DB 1374 ACATCCATTTTCTGGCAAGATCCAGGGCAGCGCGCTGGAGCTTTGGGCTACATGC 1433  
QY 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA 1360  
DB 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA 1493  
QY 1361 CCTA 1364  
DB 1494 CCTA 1497

RESULT 15

ADK60414  
ID ADK60414 standard; DNA; 1818 BP.

XX ADK60414;

XX AC

DT 06-MAY-2004 (first entry)

XX XX Angiogenesis differentially expressed gene #61.

XX ds; vasotropic; antirheumatic; antiarthritic; hypotensive; antianginal;

XX antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy;

XX angiogenesis; endothelial cell; diagnosis; tumor vascularization;

XX retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis.

XX Homo sapiens.

XX FR2836687-A1.

XX 05-SEP-2003.

XX 11-APR-2002; 2002FR-00004546.

XX 04-MAR-2002; 2002FR-00002717.

XX (GENE-) GENE SIGNAL.

XX (ALMA/) AL MAHMOOD S.

XX Colin S, Schneider C, Al Mahmood S;

XX WPI: 2004-013912/02.

XX P-PSDB; ADK60421.

XX PT Compositions for diagnosing, prognosing and treating angiogenic disorders  
PT including tumor vascularization and heart disease, comprise nucleic acid



or polypeptide differentially expressed in angiogenesis.

Claim 2; SEQ ID NO 290; 424pp; French.

The invention relates to a novel pharmaceutical composition active on angiogenesis comprising an endothelial cell nucleic acid whose expression is induced by an angiogenic factor and inhibited by an angiostatic agent or its complement or fragment, a polypeptide sequence encoded by the nucleic acid or its fragment, a molecule capable of inhibiting expression of the nucleic acid or a molecule which binds to the polypeptide sequence. The invention is used to diagnose, prognose or treat an angiogenic disorder in a mammal, particularly a human. The disorder is particularly tumor vascularization, a retinopathy, rheumatoid arthritis, Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis, endometriosis associated with neovascularization, restenosis due to angioplasty, overproduction of tissue due to cicatrization, a peripheral vascular disease, hypertension, vascular inflammation, Raynaud disease, aneurism, arterial restenosis, thrombophlebitis, ischemia, angina, myocardial infarction, chronic heart disease, cardiac congestion or macular degeneration due to age or osteoporosis. This sequence corresponds to a differentially expressed DNA used in the composition of the invention.

Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;

Query Match 96.6%; Score 1319.2; DB 12; Length 1818;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

41 GTTCAACCCAGAACAAAGCATTCGCCAGAAAACCTTAAGTATGGGATGTGCTGGATGCGG 100  
 174 GGTGACCCAGAACAAAGCATTCGCCAGAAAACCTTAAGTATGGGATGTGCTGGATGCGG 233  
 101 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAAATGACACAG 160  
 234 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAAATGACACAG 293  
 161 GCCTGGTGCATCAAGTAGAGAGATGAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 220  
 294 GCCTGGTGCATCAAGTAGAGAGATGAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 353  
 221 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTCATGATGGAAGAGCTAGGGAAGTGA 280  
 354 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTCATGATGGAAGAGCTAGGGAAGTGA 413  
 281 TTCCAAAGGTCCTCAGCACCAGAGACACCCCGTTTACCTGGAGGCCACGGCAGGATCGGTT 340  
 414 TTCCAAAGGTCCTCAGCACCAGAGACACCCCGTTTACCTGGAGGCCACGGCAGGATCGGTT 473  
 341 TGCTCAGGATGGAAGTAGAGCTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCC 400  
 474 TGCTCAGGATGGAAGTAGAGCTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCC 533  
 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAAGTCCCAAGAGAGAGGTTG 460  
 534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAAGTCCCAAGAGAGAGGTTG 593  
 461 CCTATGGCTGGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAACAAGGTGTT 520  
 594 CCTATGGCTGGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAACAAGGTGTT 593  
 521 TCAGCATAGTCCCATATGAACCAATTAATCAGAAAACCTTTGGAGCTTTGGACCTTGGGG 580  
 654 TCAGCATAGTCCCATATGAACCAATTAATCAGAAAACCTTTGGAGCTTTGGACCTTGGGG 713  
 581 GAGCCTCTACACAAGTCACATTTTGTACCCCAAAACAGAGCTATCAGTCCCAAGATAATG 640  
 714 GAGCCTCTACACAAGTCACATTTTGTACCCCAAAACAGAGCTATCAGTCCCAAGATAATG 773  
 641 CTCTGCAATTTGCGCTCTATGGCAAGGACTATCAAAATGTTACACATAGCTTCTTGCTGCT 700  
 774 CTCTGCAATTTGCGCTCTATGGCAAGGACTATCAAAATGTTACACATAGCTTCTTGCTGCT 833

701 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGACATTCAGGTGTCAGATTAATG 760  
 834 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGACATTCAGGTGTCAGATTAATG 893  
 761 AAATTTCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAGGTAGTGAACGTAAATGACC 820  
 894 AAATTTCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAGGTAGTGAACGTAAATGACC 953  
 821 TTTTACAAGACCCCTGCAACCAAGAGATTTGAGTACATCTCTCCATTTCCAGCAGTTTGA 880  
 954 TTTTACAAGACCCCTGCAACCAAGAGATTTGAGTACATCTCTCCATTTCCAGCAGTTTGA 1013  
 881 TCCAGGGTATTGGAAATCTATCAACCAATGCCATCAAAAGCATCTCTGGAGCTTTTCAACACCA 940  
 1014 TCCAGGGTATTGGAAATCTATCAACCAATGCCATCAAAAGCATCTCTGGAGCTTTTCAACACCA 1073  
 941 GTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCACCACTTCCAGGGGG 1000  
 1074 GTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCACCACTTCCAGGGGG 1133  
 1001 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTAACTTTGACATCAGAGA 1060  
 1134 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTAACTTTGACATCAGAGA 1193  
 1061 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCTTTGGGAGG 1120  
 1194 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCTTTGGGAGG 1253  
 1121 AGATAAAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1180  
 1254 AGATAAAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1313  
 1181 GTACCTTACATTTCTCCCTTCTCTGCAAGGCTATCATTTTACAGCTGATTTCTCTGGAGC 1240  
 1314 GTACCTTACATTTCTCCCTTCTCTGCAAGGCTATCATTTTACAGCTGATTTCTCTGGAGC 1373  
 1241 ACATCCATTTTCAATTTGGCAAGATCCAGGGCAGCAGCCGGCTGGACTTTTGGGCTACATGC 1300  
 1374 ACATCCATTTTCAATTTGGCAAGATCCAGGGCAGCAGCCGGCTGGACTTTTGGGCTACATGC 1433  
 1301 TGAACTGACCAACATGATCCAGCTGAGCAACCAATTTGTTCACACCTCTCTCCCACTCCA 1360  
 1434 TGAACTGACCAACATGATCCAGCTGAGCAACCAATTTGTTCACACCTCTCTCCCACTCCA 1493  
 1361 CCTA 1364  
 1494 CCTA 1497

Search completed: September 21, 2005, 17:05:27

Job time : 791.776 secs



Result No.	Query			DB	ID	Description
	Score	Match	Length			
c	1	1063.6	77.9	1760	3	CR617781 full+length
	2	940.6	68.9	984	5	BX436692
	3	863	63.2	2410	3	AK029512 Mus muscu
	4	863	63.2	4198	3	AK030601 Mus muscu
	5	812.4	59.5	861	5	BX371889
	6	743.4	54.5	3563	3	AK028625 Mus muscu
	7	730.2	53.5	1014	1	AL553150 Mus muscu
	8	727	53.3	1066	5	BM906668 AGENCOURT
	9	720.6	52.8	897	1	AL552123
	10	702.2	51.4	1025	5	BX402316
C	11	697.6	51.1	1023	1	AL547732
	12	656.8	48.1	952	5	BX327984
	13	652.6	47.8	1061	5	BM925184 AGENCOURT
	14	645.2	47.3	808	2	BF664417
	15	624.2	45.7	673	6	CB553295 MMS00075
	16	622.4	45.6	799	5	BX35123
	17	588.4	43.1	754	4	BI771056
	18	584.8	42.8	608	2	AW965942
	19	584.2	42.8	820	4	BI822675
	20	573.8	42.0	862	5	BP171342
C	21	561.2	41.1	656	5	BU947405
	22	561	41.1	1112	1	AL576332
	23	556.2	40.7	805	5	BX381864
	24	520.2	38.1	884	5	BQ711179 AGENCOURT

```
QY 101 GTTCTTCTCACACAAGTTTATACATCTATAGTGGCCAGCAGAAAAGGAGAAATGACACAG 160
Db 248 GTTCTTCTCACACAAGTTTATACATCTATAGTGGCCAGCAGAAAAGGAGAAATGACACAG 307
QY 161 GCCTGGTGCAATCAAGTAGAAGAAATGAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC 220
Db 308 GCCTGGTGCAATCAAGTAGAAGAAATGAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC 367
QY 221 AGAAAGTAAATGAATAGGCAATTTA CCTGACTGATTGTCATGGAAGAGCTTAGGGAAGTGA 280
Db 368 AGAAAGTAAATGAATAGGCAATTTA CCTGACTGATTGTCATGGAAGAGCTTAGGGAAGTGA 427
QY 281 TTCCAGGTCCTCAGCACCAGACACACACCCGTTTACCTGGGAGCCAGCGCAGCGATCGGT 340
Db 428 TTCCAGGTCCTCAGCACCAGACACACCCGTTTACCTGGGAGCCAGCGCAGCGATCGGT 487
QY 341 TGCTCAGGATGGAAGATGAAGAGTTGGCAGACAGAGGTTCTGGAATGTTGGTGGAGAGAGCC 400
Db 488 TGCTCAGGATGGAAGATGAAGAGTTGGCAGACAGAGGTTCTGGAATGTTGGTGGAGAGAGCC 547
QY 401 TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCAATTA CTGCGCCAAAGAGGAAGGTG 460
Db 548 TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCAATTA CTGCGCCAAAGAGGAAGGTG 607
QY 461 CCTATGGCTGATTACTATCACTATCTGCTGGGCAATTCAGTCAGAAAACAAGGTGCT 520
Db 608 CCTATGGCTGATTACTATCACTATCTGCTGGGCAATTCAGTCAGAAAACAAGGTGCT 667
QY 521 TCAGCATAGTCCCATAGAAACCAATAATCAGAAAACCTTTGGAGCTTTGGACCTTGGGG 580
Db 668 TCAGCATAGTCCCATAGAAACCAATAATCAGAAAACCTTTGGAGCTTTGGACCTTGGGG 727
QY 581 GAGCCTCTACACAAGTCACTTTTGTATCCCAAAACAGAGATATCGAGTCCCAAGATAATG 640
Db 728 GAGCCTCTACACAAGTCACTTTTGTATCCCAAAACAGAGATATCGAGTCCCAAGATAATG 787
QY 641 CTCTGCAATTTGCGCTTATGGAAGGACTACAAATCTCTACACATAGCTTCTTGCT 700
Db 788 CTCTGCAATTTGCGCTTATGGAAGGACTACAAATCTCTACACATAGCTTCTTGCT 847
QY 701 ATGGGAAGGATCAGGCACTCTGCGAGAACTGCGCAAGGACATTCAGGTTGCAAGTAATG 760
Db 848 ATGGGAAGGATCAGGCACTCTGCGAGAACTGCGCAAGGACATTCAGGTTGCAAGTAATG 894
QY 761 AAATCTCAGGAGCCCATGCTTTCATCCTGGATATAAGAAAGTAGTGAACGTAAGTGACC 820
Db 895 ----- 894
QY 821 TTTCAGACCCCTGCACCAAGAGATTGAGATGACTCTTCATTCCAGCAGTTTGAA 880
Db 895 -----GCAATTTGAAA 905
QY 881 TCACAGGATATTGGAACCTACAAATGCCATCAAGCATCTCGGAGCTCTTCAACACCA 940
Db 906 TCACAGGATATTGGAACCTACAAATGCCATCAAGCATCTCGGAGCTCTTCAACACCA 965
QY 941 GTTACTGCCCTTACTCCAGTGCCTTCAATGGGATTTTCTTGGCCACCATCTCAGGGG 1000
Db 966 GTTACTGCCCTTACTCCAGTGCCTTCAATGGGATTTTCTTGGCCACCATCTCAGGGG 1025
QY 1001 ATTTTGGGGATTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTGCACATCAGAG 1060
Db 1026 ATTTTGGGGATTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTGCACATCAGAG 1085
QY 1061 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGGAG 1120
Db 1086 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGGAG 1145
QY 1121 AGATAAAAAATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTCTG 1180
Db 1146 AGATAAAAAATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTCTG 1205
```

```
QY 1181 GTACCTACATTTCTCCCTCTCTTCGCAAGGCTATCATTTTCACAGCTGATTTCTTGGAGC 1240
Db 1206 GTACCTACATTTCTCTCCCTCTCTTCGCAAGGCTATCATTTTCACAGCTGATTTCTTGGAGC 1265
QY 1241 ACATCCATTTTCAATTTGGCAAGATCCAGGGCAGCGACGCCGGCTGGACTTTTGGGCTACATGC 1300
Db 1266 ACATCCATTTTCAATTTGGCAAGATCCAGGGCAGCGACGCCGGCTGGACTTTTGGGCTACATGC 1325
QY 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACTCTCTCTCCCACTCCA 1360
Db 1326 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACTCTCTCTCCCACTCCA 1385
QY 1361 CCTA 1364
Db 1386 CCTA 1389

RESULT 2
BX436692
LOCUS
DEFINITION BX436692 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP003YK21
5-PRIME, mRNA sequence.
ACCESSION BX436692
VERSION BX436692.2 GI:47007879
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 984)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi:30779500.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5524.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0CAP003AF11QPl&c=5524.f.

FEATURES
source
1..984
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP003YK21"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with NotI and cloned into
the NotI and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 68.9%; Score 940.6; DB 5; Length 984;
Best Local Similarity 97.9%; Pred. No. 7,6e-267;
Matches 949; Conservative 12; Mismatches 7; Indels 1; Gaps 1;

QY 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGCGATTGTGCTGGATCGCG 100
Db 17 GGTGACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGCGATTGTGCTGGATCGCG 76
QY 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAAATGACACAG 160
Db 77 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAAATGACACAG 136
```

QY	161	GGTGGTGCATCAAGTAGAAGAAATCGAGGGTTAAAGGCTCTGGAATCTCAAAATTTGTC	222
Db	137	GGTGGTGCATCAAGTAGAAGAAATCGAGGGTTAAAGGCTCTGGAATCTCAAAATTTGTC	196
QY	221	AGAAAGTAATGAATAGGCAATTTACCTGACATGATTGCATGGAAGAGCTAGGGAAGTGA	280
Db	197	AGAAAGTAATGAATAGGCAATTTACCTGACATGATTGCATGGAAGAGCTAGGGAAGTGA	256
QY	281	TTTCCAAGGTCCTCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATCGCGT	340
Db	257	TTTCCAAGGTCCTCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATCGCGT	316
QY	341	TGCTCAGGATGAAAGTAGAAGTTGGCAGACAGAGGGTTCTGGATGTGGTGGAGAGAGCC	400
Db	317	TGCTCAGGATGAAAGTAGAAGTTGGCAGACAGAGGGTTCTGGATGTGGTGGAGAGAGCC	376
QY	401	TCAGCAACTACCCCTTTGACATTTCCAGGTCGCCAGGATCATTTACCTGGCCCAAGAGGAAGTG	460
Db	377	TCAGCAACTACCCCTTTGACATTTCCAGGTCGCCAGGATCATTTACCTGGCCCAAGAGGAAGTG	436
QY	461	CCTATGGCTGGATTACTATCACTATCTGCTGGGCCAAATTCAGTCAGAAAAACAAGGTCGT	520
Db	437	CCTATGGCTGGATTACTATCACTATCTGCTGGGCCAAATTCAGTCAGAAAAACAAGGTCGT	496
QY	521	TCAGCATAGTCCCATATGAACCAATAATCAAGAAAACTTTGGAGCTTTGGACCTTTGGGG	580
Db	497	TCAGCATAGTCCCATATGAACCAATAATCAAGAAAACTTTGGAGCTTTGGACCTTTGGGG	556
QY	581	GAGCCTCTACACAGTCACTTTGTACCCCAAAACAGACATCTCGAGTCCCAAGATATG	640
Db	557	GAGCCTCTACACAGTCACTTTGTACCCCAAAACAGACATCTCGAGTCCCAAGATATG	616
QY	641	CTCTGCAATTTGCGCTCTATGGCAAGGACTCAATATGTTCTACACATAGCTTTCTGTGCT	700
Db	617	CTCTGCAATTTGCGCTCTATGGCAAGGACTCAATATGTTCTACACATAGCTTTCTGTGCT	676
QY	701	ATGGGAAGGATCAGGCATCTTGGCGAGAACTGGCCCAAGCAATTCAGGTTCAAGTAAATG	760
Db	677	ATGGGAAGGATCAGGCATCTTGGCGAGAACTGGCCCAAGCAATTCAGGTTCAAGTAAATG	736
QY	761	AAATTTCTCAGGAGCCCATGCTTTTCATCTCGATATAGAAAGGTAGTGAACGTAGTGACC	820
Db	737	AAATTTCTCAGGAGCCCATGCTTTTCATCTCGATATAGAAAGGTAGTGAACGTAGTGACC	796
QY	821	TTTACAAGACCCCTGCAACCAAGAGATTGAGATGACTCTTTCCATTCACGACAGTTTGAAA	880
Db	797	TTTACAAGACCCCTGCAACCAAGAGATTGAGATGACTCTTTCCATTCACGACAGTTTGAAA	856
QY	881	TCCAGGGTATTGGAAACTATCAACAATGCCATCAAGCATCTCGAGCTTTCAACACCA	940
Db	857	TCCAGGGTATTGGAAACTATCAAMAATGCCATCAAGCATCTCGAGCTTTCAAMAACA	916
QY	941	GTTACTGCCCTTACTCCCAAGTGGCTTCAATGGATTTTCTTGGCACCACCTCCAGGGGG	1000
Db	917	GTTACTGCCCTTCAATTCCKARTGCTCTCAWTGGGATTTTCTTGCA-CACTMCAGGGGG	975
QY	1001	ATTTTGGGG 1009	
Db	976	ATTTTGGGG 984	
RESULT 3			
AK029512			
LOCUS	AK029512	2410 bp	mRNA
DEFINITION	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921511C05 product:ectonucleoside triphosphate diphosphohydrolase 1, full insert sequence.	linear	HTC 03-APR-2004
ACCESSION	AK029512		
VERSION	AK029512.1	GI:26325463	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 93279253  
 PUBMED 10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes  
 MEDLINE Genome Res. 10 (10), 1617-1630 (2000)  
 PUBMED 20499374

3 Carninci, P., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
 Konno, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanishi, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
 JOURNAL sequencing pipeline with 384 multicapillary sequencer  
 MEDLINE Genome Res. 10 (11), 1757-1771 (2000)  
 PUBMED 20530913

4 Carninci, P., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
 Konno, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanishi, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
 JOURNAL sequencing pipeline with 384 multicapillary sequencer  
 MEDLINE Genome Res. 10 (11), 1757-1771 (2000)  
 PUBMED 20530913

5 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

6 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation  
 JOURNAL of 60,770 full-length cDNAs  
 MEDLINE Nature 420, 563-573 (2002)  
 PUBMED 12410240

7 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
 Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,  
 Sugabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,  
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)

8 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

9 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

10 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

11 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

12 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

13 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

14 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

15 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

16 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

17 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

18 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

19 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

20 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

21 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

22 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

23 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

24 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

25 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

26 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

27 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

28 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

29 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

30 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

31 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

32 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

33 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

34 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 MEDLINE 11076861

/db_xref="FANTOM DB:4921511C05"		Db	821	CAATTCCGCTCTTCTATGGCGAGGACTATATCTGTGTACACACACAGCTTCTGTGCTATGGG	880
/db_xref="taxon:10090"		Qy	706	RAGGATCAGGCACTCTGCGAGAAACTGGCCAGGACATTCAGGTTGCAAGTAATGAAAT	765
/clone="4921511C05"		Db	881	AAGGATCAGGCTCTCTGGCAGAAACTGGCCAGGACATTCAGGTTTCAAGTGGTGGCGTC	940
/sex="male"		Qy	766	CTCAGGAGCCCATGCTTTTCATCTCGATATATAAGAGGTAGTGAACGTAAAGTACCTTTAC	825
/issue_type="testis"		Db	941	CTTAAGGAGCCCATGCTTTAAACCCAGGATACGAGAAGGTGTGAATGTAAGTGAAGTCTAT	1000
/clone_lib="RIKEN full-length enriched mouse cDNA library"		Qy	826	AAGACCCCTTCACCAAGAGATTGAGATGACTCTTCATATCCAGCAGGTTTGAATCCAG	885
/dev_stage="adult"		Db	1001	GGCATCTCCCTGCACCAAGAGATTTCGAAAAGAGCTACCAATTTGATCAGTTTCGAATCCAG	1060
26_1645		Qy	886	GGTATTGGAACATATCAACATGCCATCAACATCTCTGGAGCTCTTCAACACCAAGTTAC	945
/notes="unamed protein product; ectonucleoside triphosphate diphosphohydrolase 1 (MGD MGI:102805, GBNM 009848, evidence: BLASTN, 100%, match=2284) putative"		Db	1061	GGCATCTGGAGACTAGAACAGTGCACCCAGAGCATCTTGAAGCTTTCAACACAGCCAC	1120
/codon_start=1		Qy	946	TGCCCTTACTCCCACTGTCCTTCAATGGGATTTCTTTCGCCACCACTCCAGGGGGATTTT	1005
/protein_id="BAC26486.1"		Db	1121	TGCCCTTACTCCCACTGTCCTTCAATGGGATTTCTTTCGCCACCACTCCATGGGAGTTT	1180
/translation="MAAGRLARFTDLBELDEVITERKYRHKLRYSQSKVRFCSC NTLILGFTLLAVLIALVLTQNKPKYGLVDLGSHTSLNLYIKWPABKEN DTGVQOLESEOSADVEIAVSTLSKYPDFQGAKITQOEQEGAYGITINYLGRF AGWRLLRMSBOSADVEIAVSTLSKYPDFQGAKITQOEQEGAYGITINYLGRF TQESWLSLISDSQKQETFGALDLDGASTQITFVPONSTIESPNSLOPRLYGEYTV YTHFLCYKQDALWOKLAKDQVSSGGVLKDPENPGYEKVVNVSELXTGTCTKRF EKKLPDFQRIQGTGDTYEQCHQSILELFFNNSHCPYSQCAFNGFVLPPLHSGFAGFAY FVMDFFKVAKMSVTSQEKMTETIKNFCSSWEETKTSYPSVKEKYLSSYCFSGAYIL SLQGYNFTDSSWEQIHFMGKIDSNAGWTGLYMLNLNMIPEQPLSPPLPHSTYIG LMVLFSLLLVAVAITGLFIYSKPSYFWEAV"		Qy	1006	GGGGCATTTTCAAGCTTTTACTTTGTGATGAAGTTTAACTTGACATCAGAGAA- ---	1061
		Db	1181	GGGGCGGTTTCTGCTTCTACTTTGTGATGGATTTTTTAAAGAGGTAGCGAAAAACAGT	1240
		Qy	1062	--AGTCTCTCAGGAAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCGCTCGGAG	1119
		Db	1241	GTCTCTCTCAGGAGAAATGACCGAGATAACAAAAATTTTGTCAAATCTTGGGAA	1300
		Qy	1120	GAGATAAAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATPATCTGTTTTCT	1179
		Db	1301	GAGACAAAGACATCTATCTCTTCAAGTAAAGGAGAGTACCTGAGTGAGTACTGCTTCTCG	1360
		Qy	1180	GGTACTCATTTCTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTCCTCGGAG	1239
		Db	1361	GGCGCTCATCTCTCTCTC---CTGCAAGGCTATAACTTTCACAGACAGCTCTCTGGAA	1417
		Qy	1240	CACATCCATTTTCATTTGGCAAGATCCAGGACGACGCGGTGGACTTTGGGCTACATG	1299
		Db	1418	CAGATTCTTTTATGGGCAAGATCAAGACAGAACGCGGGTGGACTTTGGGCTACATG	1477
		Qy	1300	CTGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCC	1359
		Db	1478	CTGAACCTGACCAACATGATCCAGCTGAACAGCGGTTGTCCCGGCTCTCTCCCTCACTCC	1537
		Qy	1360	ACCTA 1364	
		Db	1538	ACCTA 1542	
RESULT 4					
AK030601		4198 bp mRNA linear HTC 03-APR-2004			
LOCUS		Mus musculus adult male pituitary gland cDNA, RIKEN full-length			
DEFINITION		enriched library, clone:5330437E10 product:ectonucleoside triphosphate diphosphohydrolase 1, full insert sequence.			
ACCESSION		AK030601			
VERSION		AK030601.1 GI:26326590			
KEYWORDS		HTC; CAP trapper.			
SOURCE		Mus musculus (house mouse)			
ORGANISM		Mus musculus			
REFERENCE		1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)			
AUTHORS		Carninci, P. and Hayashizaki, Y.			
JOURNAL		Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE		99279253			
PUBMED		10349636			
REFERENCE		2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
AUTHORS		Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			

CDS

ORIGIN

Query Match		63.2%; Score 863; DB 3; Length 2410;
Best Local Similarity		79.8%; Pred. No. 1.1e-243;
Matches 1058; Conservative 0; Mismatches 255; Indels 12; Gaps 3;		
Qy	46	ACCCAGAACAAAGCATTCGCAAGAAACGTTTAAAGTATGGGATTTGCTGGATCGGGTTCT 105
Db	224	ACCCAGAACAAACCTTTGCGAGAAATGTTAAGTATGGGATTTGTTGGATCGGGGTCA 283
Qy	106	TCTCACACAAGTTTATACATCTATAAGTGGCGAGCAGCAAGAAAGAGAAATGACACAGCGGTG 165
Db	284	TCTCACACCACTGTATCTACATCTACAGTGGCGCGCCGAGNAGAGAAATGACACAGGGTG 343
Qy	166	GTGCATCAAGTAGAAGATGACGGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTCAGAA 225
Db	344	GTGCAGCAGTTAGAGGAATGCCAAGTGAAGGTCTCTGGAATCTCAAAATATGTCAGAAA 403
Qy	226	GTAATGAATAGGCATTTACCTGACTGATGATGCAAGAGAGCTAGGGAAGTATTCCA 285
Db	404	ACAGATGAATCGGTGCTACCTGGCCGAATGATGGAATCTCCACCGAACTGATACCA 463
Qy	286	AGGTCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGCGCATGCGGTTGCTC 345
Db	464	ACATCCAAGCATCACAGACTCTGTCTACTCTGGAGCCACAGCGCATGCGTTGCTT 523
Qy	346	AGGATGGAAGTAGAAGTTGGCAGACAGGGTTCTGTGATGTGTGAGAGAGCCCTCAGC 405
Db	524	AGAATGGAAGCGAAACAAATCGGAGACAGGCTCTGTGCTGAGTGTCAACAGCCTTAAG 583
Qy	406	AACACCCCTTTCACTTCCAGGTTGCCAGATCATTTACTGGCCAAAGGAGGTGCTAT 465
Db	584	AGCTACCCCTTTGACTTCCAGGTTGCCAAGATCATCTGGAACAGAGGAAGGTGCTAT 643
Qy	466	GGCTGGATTACTTCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGTCAGC 525
Db	644	GGGTGGATTACTTAACTATCTCTGGGCGAGATTCATCTCAGGAACAGAGTTGGCTAAGC 703
Qy	526	ATAGTCCCATPATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCC 585
Db	704	CTCATCTCA---GACAGTCAGAAACAGGAAACCTTTGGCGCTTTGGATCTCGCGGAGCC 760
Qy	586	TCTACACAAGTCACTTTGTACCCCAACAGACTATCAGTCCCGCCAGATATGCTCTG 645
Db	761	TCCACACAGATCACTCTCGTGGCCCCCAACAGCAGCTATAGTCCCCAGAAAACTCTCTG 820
Qy	646	CAATTTCCGCTCTATGCAAGGACTACAATGTCTTACACATAGCTTTCTGTGCTATGGG 705

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
JOURNAL Prepare full-length cDNA libraries for rapid discovery of new genes  
MEDLINE Genome Res. 10 (10), 1617-1630 (2000)  
PUBMED 20499374  
REFERENCE 11042159  
AUTHORS 3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
REFERENCE 4  
AUTHORS

TITLE The RIKEN Genome Exploration Research Group Phase II Team and the  
JOURNAL FANTOM Consortium.  
MEDLINE Functional annotation of a full-length mouse cDNA collection  
PUBMED Nature 409, 685-690 (2001)  
REFERENCE 5  
AUTHORS

TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research  
JOURNAL Group Phase I & II Team.  
MEDLINE Analysis of the mouse transcriptome based on functional annotation  
PUBMED of 60,770 full-length cDNAs  
REFERENCE Nature 420, 563-573 (2002)  
AUTHORS 6 (bases 1 to 4198)

TITLE Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
JOURNAL Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
REFERENCE Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
AUTHORS Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
CDNA library was prepared and sequenced in Mouse Genome  
CDNA library  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
Location/Qualifiers

FEATURES  
source  
1. .4198  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM DB:5330437E10"  
/db\_xref="taxon:10090"  
/clone="5330437E10"  
/sex="male"  
/tissue type="pituitary gland"  
/clone lib="RIKEN full-length enriched mouse cDNA library"  
/dev stage="adult"  
93. .1625  
/note="unnamed protein product; ectonucleoside  
triphosphate diphosphohydrolase 1 (MGD|MGI:102805,  
CDS

GB|NM\_009848, evidence: BLASTN, 100%, match=2284)  
putative"  
/codon\_start=1  
/protein\_id="BAC27039.1"  
/db\_xref="GI:26326591"  
/translation="MEDIKDSKVKRSCSNLILGFTSILAVIALIAGVLTOKPLP  
ENVKTVLDAGSSHTNLYIYKPAEKENDTGVOOLSECCQVKGFGISKVAQKTDEIG  
AYLAEICMELSTELIPTSKHQTPVYLGATAGMRLRMESEQSADVLAASVLSKSYG  
PFOGAKIITQBEAGAGWITINLLGRFTQESWLSLISDSQKQETFGALDGGAST  
QITFVPONSTIESNSLQFLRYGEDYTVYTHSFLCYGKDQALWOKLARDIQVSSGV  
LKPCFNPGEYKVVNSLYCTPCTKRPEKLPDPORIQGTGQDYEQCHOSLLELPNN  
SHQPSQCAFNGVELPLHSGFASFPYFMDPPKKVAKNSVISOEKMTKKNPCS  
KSWETKTSYPSVREKYLSEYCFSGAYILSLQGGYNFTDSSWEQIHFMGKIKDSNAGW  
TLGMLNLTNMPAEPQPLSPPLPHSTYIIGLMLVLSLLLVAVAITGLFTYSKPSYFWE  
AV"  
polyA\_signal 4171. .4176  
/note="putative"  
polyA\_site 4198  
/note="putative"  
ORIGIN  
Query Match 63.2%; Score 863; DB 3; Length 4198;  
Best Local Similarity 79.8%; Pred. No. 1.3e-243;  
Matches 1058; Conservative 0; Mismatches 255; Indels 12; Gaps 3;  
QY 46 ACCCAGAACAAAGCATTGCCAGAAACGTTAAAGTATGGGATTGTCTCGATCGCGGTTCT 105  
DB 204 ACCCAGAACAAACCTTTGCCAGAAATGTTAAAGTATGGGATTGTCTCGATCGCGGTTCT 263  
QY 106 TCTCACACAAAGTTTATACATCTNTAAGTGGCCAGCAGAGAAAGGAGATGACACAGCGTG 165  
DB 264 TCTCACACAAACCTGTATCATCTACAAAGTGGCCGCGGAGGAGGAGATGACACAGCGTG 323  
QY 166 GTGCATCAAGTAGAAGATGACAGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTCAGAAA 225  
DB 324 GTGCAGCAGTTAGAGGATGCAAGTGAAGGTCTCTGGAATCTCAAAATATGCTCAGAAA 383  
QY 226 GTAAATGAAATAGGCAATTTACCTGACTGATTGTCATGGAAGAGCTAGGGAAGTGAATCCA 285  
DB 384 ACAGATGAAATCGGTGCGTACCTGCGCGAATGTCATGGAACCTGTCCACCGAATGATACCA 443  
QY 286 AGGTCCCGACCAAGAGACACCCGTTTACCTGGGAGCCAGCGAGGATGCGGTTGCTC 345  
DB 444 ACATCCAGCATCACAGACTCTGTCTACCTGGGAGCCACAGCAGGATGCGGTTGCTT 503  
QY 346 AGGATGAAAGTGAAGAGTTTCGACAGAGGTTCTGGAATGTGTGACAGAGAGGCTCAGC 405  
DB 504 AGAATGGAAGCGAAACATTCGGCAGACAGAGTCTTGCTGAGTGTCAACAGCCCTTAAG 563  
QY 406 AACTACCCCTTTGACTTTCAGGGTCCAGGATCATTTACTGGCCAGAGGAAGGTGCTTAT 465  
DB 564 AGCTACCCCTTTGACTTTCAGGGTCCAGGATCATCTACTGGACAGAGGAGGTCCTTAT 623  
QY 466 GGCTGGATTACTCAACTATCTGCTGGGCAAAATTCAGTTCAGAAAACAAGGTGTTTACG 525  
DB 624 GGGTGGATTACTATTAACATCTGCTGGGCAAGATTCATCAGGAACAGAGTTGGCTAAGC 683  
QY 526 ATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTTGGGGGAGCC 585  
DB 684 CTCATCTCA --- GACAGTCAAGAAACAGAAACCTTTGGCGCTTTGGATCTCGGGGAGCC 740  
QY 586 TCTACACAAAGTCACTTTTGTACCCCAAAACACAGACTATCGAGTCCCCAGATAATGCTCTG 645  
DB 741 TCCACACAGATCACTCTTGGTGGCCCAAAACACAGACTATAGAGTCCCCAGAAAACCTCTG 800  
QY 646 CAATTTGCTCTATGGAAGGACTACAATGTGTACACACATAGCTTCTTGTGCTATGGG 705  
DB 801 CAATTCGCTCTATGCGAGGACTATAGTGTGTACACACACAGCTTCTCTGTGCTATGGG 860  
QY 706 AAGGATCAGGACTCTGCGAGAACTGCGCAAGGACATTCAGGTGCAAGTAATGAATTT 765  
DB 861 AAGGATCAGGCTCTCTGCGAGAAACCTGCGCAAGGACATTCAGGTTCAGGTGGGCGCTC 920











Qy 641 CTCTGCAATTTGGCTCTATGGCAAGGACTACAATGCTTACACACATAGCTTCTTGCT 700  
 Db 771 CTCTGCAATTTGGCTCTATGGCAAGGACTACAATGCTTACACACATAGCTTCTTGCT 830  
 Qy 701 ATGGGAAGGATCAGGACACTCTGCGAAGAACTGCGCAAGGACATTCAGGTTGCAAGTAATG 760  
 Db 831 ATGGGAAGGATCAGGACACTCTGCGAAGAACTGCGCAAGGACATTCAGGTTGCAAGTAATG 890  
 Qy 761 AAATTTCTCAGGGACC 775  
 Db 891 AAATTTCTCAGGGACC 905

RESULT 8  
 BM906668 1066 bp mRNA linear EST 12-MAR-2002  
 LOCUS AGENCOURT 6621802 NIH\_MGC\_125 Homo sapiens cDNA clone IMAGE:5724619  
 DEFINITION 5', mRNA Sequence.

ACCESSION BM906668  
 VERSION BM906668.1 GI:19357047  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS NIH-MGC http://mgc.mci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: c9apbs-r@mail.nih.gov

## Tissue Procurement: Invitrogen

cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: LLAM12714 row: c column: 20

High quality sequence start: 2

High quality sequence stop: 664.

## FEATURES

location/Qualifiers  
 1..1066

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5724619"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_125"

/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;  
 Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool  
 of three ovaries, from females ranging in age from 38 to  
 49 yo. Library is oligo-dT primed and directionally cloned  
 (EcoRV site is destroyed upon cloning). Average insert  
 size 2.1 kb, insert size range 1-3.5 kb. Library is  
 normalized and enriched for full-length clones and was  
 constructed by C. Gruber (Invitrogen). Research Genetics  
 tracking code 036."

## ORIGIN

Query Match 53.3%; Score 727; DB 5; Length 1066;  
 Best Local Similarity 93.6%; Pred. No. 1.6e-203;  
 Matches 825; Conservative 0; Mismatches 45; Indels 11; Gaps 6;

Qy 41 GTTCAACCAGAACACATTCGCAGAAAACGTTAAGTATGGATTGCTGGATGCGG 100

Db 185 GGTGACCCAGAACACATTCGCAGAAAACGTTAAGTATGGATTGCTGGATGCGG 244

Qy 101 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAAAAGAGAAATGCACAG 160

Db 245 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAAAAGAGAAATGCACAG 304

Qy 161 GCGTGGTGCATCAAGTAGAAGATGCAAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 220  
 Db 305 GCGTGGTGCATCAAGTAGAAGATGCAAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 364  
 Qy 221 AGAAGTAATGAATAGGCAATTTACCTGACTGATTGTCATGGAAGAGCTAGGGAAGTGA 280  
 Db 365 AGAAGTAATGAATAGGCAATTTACCTGACTGATTGTCATGGAAGAGCTAGGGAAGTGA 424  
 Qy 281 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGT 340  
 Db 425 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGT 484  
 Qy 341 TGCTCAGGATGGAAGTGAAGTGGCAGACAGGGTTCGTGATGTGTGGAGAGAGCC 400  
 Db 485 TGCTCAGGATGGAAGTGAAGTGGCAGACAGGGTTCGTGATGTGTGGAGAGAGCC 544  
 Qy 401 TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGGCCAAAGGAGAGTG 460  
 Db 545 TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGGCCAAAGGAGAGTG 604  
 Qy 461 CCTATGGCTGGATTACTATCAACTATCTGTGGGCAAAATTCAGTCAGAAAAACAAGTGT 520  
 Db 605 CCTATGGCTGGATTACTATCAACTATCTGTGGGCAAAATTCAGTCAGAAAAACAAGTGT 564  
 Qy 521 TCAGCATAGTCCCATAATGAAAACCAATATCAGGAAACCTTTGGAGCTTTGACCTTGGGG 580  
 Db 665 TCAGCATAGTCCCATAATGAAAACCAATATCAGGAAACCTTTGGAGCTTTGACCTTGGGG 724  
 Qy 581 GAGCCTCTACACAAAGTCACTTTTGTACCCCAAAACCCAGACTATGAGTCCCAAGTAATG 640  
 Db 725 GAGCCTCTACACAAAGTCACTTTTGTACCCCAAAACCCAGACTATGAGTCCCAAGTAATG 784  
 Qy 641 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGCTACACACATAGCTTCTTGCTGT 700  
 Db 785 CTCTGCAATTTGCGCTCTATGGCAAGGACTACCATGCTACACCATAGCTTCTTGCTGT 844  
 Qy 701 AT-GGGGAAGATCAGGCACTCTGCGAGAAACTGG-CCAAGGACATTCAGGTTGCAAGTAA 758  
 Db 845 ATGGGAAGGATCAGGCACTCTGCGCAAAACCTGGCCCAAGGACCTTCAGGTTGCAAGTAA 904  
 Qy 759 TGAATTTCTCAGGACCCCATGC--TTTCATCTCGATATAGAGGTAGTGAACGTAA-- 814  
 Db 905 TGAATTTCTCAGGACCCCATGCCTTTCATCCCGGAAATAGAAAGGAGTGAACGTAAAG 964  
 Qy 815 -GTGACCTTTACAAAGACCCCTCGACCAAGAGATTTGAGATGACTCTTCCATT--CCAGC 871  
 Db 965 GGACCTTTACAAAGACCCCTCGACCAAAATTTGAGAGGACTCTTCTTCTTCCCA 1024  
 Qy 872 AGTTTGAAT--CCAGGATTTGAAAACATATCAACAATGCC 910  
 Db 1025 AGTTTGAATCCCGGGTAATTTGAAAACATATTCACAAAGGC 1065

## RESULT 9

AL552123

LOCUS

DEFINITION

AL552123 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

clone CSODI059Y11 5-PRIME, mRNA sequence.

AL552123

ACCESSION

AL552123.3 GI:45856912

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

REFERENCE

1 (bases 1 to 897)

AUTHORS

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

JOURNAL

On Feb 15, 2001 this sequence version replaced gi:31273939.

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5524.f

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?8=CS0D1059AB060P1&c=5524.f.

#### FEATURES

Location/Qualifiers  
1. .897  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1059Y111"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

#### ORIGIN

Query Match 52.8%; Score 720.6; DB 1; Length 897;  
Best Local Similarity 94.3%; Pred. No. 1.2e-201;  
Matches 765; Conservative 13; Mismatches 28; Indels 5; Gaps 3;

Qy 41 GTTCAACCCAGAACAAAGCATTCAGAGAAACGTTAAGTATGGATGTTGCTGGATGCGG 100  
Db 92 GGTGTGACCCAGAGAAAGCATTCAGAGAAACGTTAAGTATGGATGTTGCTGGATGCGG 151  
Qy 101 GTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGACAGAAAGGAGATGACACAG 160  
Db 152 GTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGACAGAAAGGAGATGACACAG 211  
Qy 161 GCCTGTGTGATCAAGTAGAAGATTCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 220  
Db 212 GCCTGTGTGATCAAGTAGAAGATTCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 271  
Qy 221 AGAAAGTAATGAATAGGATTTTACTGACTGATTCATGTAAGTGAAGAGCTAGGGAAGTGA 280  
Db 272 AGAAAGTAATGAATAGGATTTTACTGACTGATTCATGTAAGTGAAGAGCTAGGGAAGTGA 331  
Qy 281 TTCCAGGTCCAGCACCAGACACCCGTTTACCTGGGAGCCAGCGGATCCGCT 340  
Db 332 TTCCAGGTCCAGCACCAGACACCCGTTTACCTGGGAGCCAGCGGATCCGCT 391  
Qy 341 TGCTCAGGATGGAAGTGAAGATTTGGCAGACAGGGTTCTGGATGTGGTGAGAGGAGCC 400  
Db 392 TGCTCAGGATGGAAGTGAAGATTTGGCAGACAGGGTTCTGGATGTGGTGAGAGGAGCC 451  
Qy 401 TCAGCAATACCCCTTTGACTTCAGGGTCCAGGATCAATTAATGCGCAAGAGAGGTTG 460  
Db 452 TCAGCAATACCCCTTTGACTTCAGGGTCCAGGATCAATTAATGCGCAAGAGAGGTTG 511  
Qy 461 CCTATGGCTGATTAATCAATCTATCTGCTGGGCAAAATTCAGTCAGAGAAACAGGTGCT 520  
Db 512 CCTATGGCTGATTAATCAATCTATCTGCTGGGCAAAATTCAGTCAGAGAAACAGGTGCT 571  
Qy 521 TCAGCATAGTCCCATATGAACCAATTAATCAGAGAAACCTTTGGAGCTTTGGAGCTTGGGG 580  
Db 572 TCAGCATAGTCCCATATGAACCAATTAATCAGAGAAACCTTTGGAGCTTTGGAGCTTGGGG 631  
Qy 581 GAGCCTCTACACAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCGAGATAATG 640  
Db 632 GAGCCTCTACACAGTCACTTTTGTGTA-CCCAAAACAGACTATCGAGTCCCGAGATAATG 690  
Qy 641 CTCTGCAATTTCCCTCTATGGCAAGACTACATGTTCTACACATAGCTTCTTGCT 700  
Db 691 CTCTGCAATTTCCCTCTATGGCAAGACTACATGTTCTACACATAGCTTCTTGCT 750  
Qy 701 ATGGGAAGGATCAGGCACCTCTGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATG 760  
Db 761 ATGGGAAGGATCAGGCACCTCTGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATG 810

Db 751 ATGGGAAGGATCAGGCACCTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG 810  
Qy 761 AATTTCTCAGGACCCATGCTTTTCATCTCGGTATATAAGAGGTAGTGAACGTAAAGTACC 820  
Db 811 AAA-TCTWVGCCCAAYGCTTTTCATCTCTGGG---AAARARGTAGTGACGTAARTACC 866  
Qy 821 TTTCACAGACCCCTGTCACCAAGAGATTGA 851  
Db 867 TTWMAARMCCCGCMARARATTTARATGA 897

#### RESULT 10

LOCUS BX402316 1025 bp mRNA linear EST 28-APR-2004  
DEFINITION BX402316 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CS0D1017YB13 5-PRIME, mRNA sequence.

ACCESSION BX402316

VERSION BX402316.2 GI:46844926

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 1025)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30610946.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

5524.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?8=CS1A1005ZB07QP1&c=5524.f.

#### FEATURES

Location/Qualifiers

1. .1025

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0D1017YB13"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

#### ORIGIN

Query Match 51.4%; Score 702.2; DB 5; Length 1025;  
Best Local Similarity 99.6%; Pred. No. 3.6e-196;  
Matches 704; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 41 GTTCAACCCAGAACAAAGCATTCAGAGAAACGTTAAGTATGGATGTTGCTGGATGCGG 100

Db 188 GGTGTGACCCAGAGAAAGCATTCAGAGAAACGTTAAGTATGGATGTTGCTGGATGCGG 247

Qy 101 GTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGAGAAAGGAGATGACACAG 160

Db 248 GTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGAGAAAGGAGATGACACAG 307

Qy 161 GCCTGTGTGATCAAGTAGAAGATTCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 220

Db 308 GCCTGTGTGATCAAGTAGAAGATTCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 367

Qy 221 AGAAAGTAATGAATAGGACATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA 280

Db 368 AGAAAGTAATGAATAGGACATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA 427

281 TTCCAAGGTCCTCAGACACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATCGCGT 340  
Db |||||  
341 TGCTCAGGATGANAAGTGAAGAGTTGGCAGACAGGGTCTCGATGTTGGAGAGAGCC 400  
Db |||||  
489 TGCTCAGGATGANAAGTGAAGAGTTGGCAGACAGGGTCTCGATGTTGGAGAGAGCC 547  
Qy |||||  
401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAAGTCCCAAGAGGAGGTG 460  
Db |||||  
548 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAAGTCCCAAGAGGAGGTG 607  
Qy |||||  
461 CCTATGGCTGGATTAATCAATCAATCTGCTCGGCAAAATTCAGTTCAGAAAAACAAGGTG 520  
Db |||||  
608 CCTATGGCTGGATTAATCAATCAATCTGCTCGGCAAAATTCAGTTCAGAAAAACAAGGTG 667  
Qy |||||  
521 TCAGCATAGTCCCATATGAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG 580  
Db |||||  
668 TCAGCATAGTCCCATATGAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG 727  
Qy |||||  
581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGATCCCCAGATAATG 640  
Db |||||  
728 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGATCCCCAGATAATG 787  
Qy |||||  
641 CTCTGCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 700  
Db |||||  
788 CTCTGCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 847  
Qy |||||  
701 ATGGGAAGGATCAGGACTCTGGCAGAACTGGCCAAAGACATTCAG 747  
Db |||||  
848 ATGGGAAGGATCAGGACTCTGGCAGAACTGGCCAAAGACATTCAG 894

## RESULT 11

AL547722 1023 bp mRNA linear EST 25-MAR-2004  
LOCUS AL547722 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CS0D1017YB13 5-PRIME, mRNA sequence.

AL547722

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1023)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31269551.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE

Email: seqre@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

5524.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?c=CS0D1017CA07QPI&amp;c=5524.f.

Location/Qualifiers

1..1023

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0D1017YB13"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_libs="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

normalized.

Unpublished (2001)

Full-length cDNA libraries and normalization

Unpublished (2001)

digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
Query Match 51.1%; Score 697.6; DB 1; Length 1023;  
Best Local Similarity 98.6%; Pred. No. 8.4e-195;  
Matches 697; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
Qy 41 GTTCAACCCAGAACAAAGCATTGGCCAGAAAAAGTTTAAAGTATGGGATTTGCTGGATGGCG 100  
Db |||||  
198 GGTTCACCCAGAACAAAGCATTGGCCAGAAAAAGTTTAAAGTATGGGATTTGCTGGATGGCG 247  
Qy 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGAGAAATGACACAG 160  
Db |||||  
248 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGAGAAATGACACAG 307  
Qy 161 GCGTGGTCATCAAGTGAAGAAATGCGAGGTTTAAAGTCTTGGATCTCAAAATTTGTTTC 220  
Db |||||  
308 GCGTGGTCATCAAGTGAAGAAATGCGAGGTTTAAAGTCTTGGATCTCAAAATTTGTTTC 367  
Qy 221 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTCATGCAATGGAAGAGCTAGGGAAAGTGA 280  
Db |||||  
368 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTCATGCAATGGAAGAGCTAGGGAAAGTGA 427  
Qy 281 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGCGCATGCGGT 340  
Db |||||  
428 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGCGCATGCGGT 487  
Qy 341 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTCTCGATGTTGGAGAGGAGCC 400  
Db |||||  
488 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTCTCGATGTTGGAGAGGAGCC 547  
Qy 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAAGTCCCAAGAGGAGGTG 460  
Db |||||  
548 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAAGTCCCAAGAGGAGGTG 607  
Qy 461 CCTATGGCTGGATTAATCAATCAATCTGCTCGGCAAAATTCAGTTCAGAAAAACAAGGTG 520  
Db |||||  
608 CCTATGGCTGGATTAATCAATCAATCTGCTCGGCAAAATTCAGTTCAGAAAAACAAGGTG 667  
Qy 521 TCAGCATAGTCCCATATGAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG 580  
Db |||||  
668 TCAGCATAGTCCCATATGAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG 727  
Qy 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGATCCCCAGATAATG 640  
Db |||||  
728 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGATCCCCAGATAATG 787  
Qy 641 CTCTGCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 700  
Db |||||  
788 CTCTGCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 847  
Qy 701 ATGGGAAGGATCAGGACTCTGGCAGAACTGGCCAAAGACATTCAG 747  
Db |||||  
848 ATGGGAAGGATCAGGACTCTGGCAGAACTGGCCAAAGACATTCAG 894

## RESULT 12

BX327984

LOCUS

DEFINITION

BX327984 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

clone CS0D1017YD08 5-PRIME, mRNA sequence.

ACCESSION

VERSION

BX327984.1 GI:30332721

KEYWORDS

SOURCE

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 952)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

## FEATURES

source

Db	623	CTGACATTGGGCTACATGCTGAACCTGACCACATGATCCAGCTGAGCAACCATTTGT- 681
Qy	1341	CACACCTCTCTCCCACTCCAC 1361
Db	682	CACACCTGCTCTCCCACTCCAC 702
RESULT 13		
BM925184		
LOCUS		
DEFINITION	BM925184	1061 bp mRNA linear EST 12-MAR-2002
ACCESSION	AGENCOURT_6627603	NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5762493
VERSION	5', mRNA sequence.	
KEYWORDS	BM925184.1	GI:19375563
SOURCE	EST.	
ORGANISM	Homo sapiens (human)	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	1 (bases 1 to 1061)	
TITLE	NIH-MGC http://mgc.nci.nih.gov/.	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.	
	Email: csapbs-remail.nih.gov	
	Tissue Procurement: Life Technologies, Inc.	
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	
	DNA Sequencing by: Agencourt Bioscience Corporation	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov	
	Plate: L1AM12812 row: m column: 22	
	High quality sequence start: 4	
	High quality sequence stop: 669.	
FEATURES	Location/Qualifiers	
source	1..1061	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:5762493"	
	/lab_host="DH10B"	
	/clone_lib="NIH_MGC_122"	
	/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."	
ORIGIN		
	Query Match 47.8%; Score 652.6; DB 5; Length 1061;	
	Best Local Similarity 92.8%; Pred. No. 1.9e-181;	
	Matches 773; Conservative 0; Mismatches 49; Indels 11; Gaps 8;	
Qy	310	GTTTACCTTGGGAGCCACCGCAGGCATGCGGTTGCTCAGGATGGAAGTGAAGTTGGCA 369
Db	172	GTTTACCTTGGGAGCCACCGCAGGCATGCGGTTGCTCAGGATGGAAGTGAAGTTGGCA 231
Qy	370	GACAGGGTCTGGATGTGGTGAGAGGACCTCAGCACTACCCCTTTGACTTCCAGGT 429
Db	232	GACAGGGTCTGGATGTGGTGAGAGGACCTCAGCACTACCCCTTTGACTTCCAGGT 291
Qy	430	GCCAGGATCATTTACTGGCCAGAGAGGTGCTTATGGCTGATTACTATCAACTATCTG 489
Db	292	GCCAGGATCATTTACTGGCCAGAGAGGTGCTTATGGCTGATTACTATCAACTATCTG 351
Qy	490	CTGGGCAATTCAGTCAAGAAAACAAGGTGGTTTCAGCATAGTCCCATATGAAACCAATAAT 549

Db 352 CTGGGCAATTTCAGTCAGAAAAACAGGTGCTCAGCATAGTCCCATATGAAACCAATAAT 411  
Qy 550 CAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACCTTTGTACCC 609  
Db 412 CAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACCTTTGTACCC 471  
Qy 610 CAAAACAGACTATCAGATCCCAAGATATGCTCTGCAATTTGCGCTCTATGGCAAGGAC 669  
Db 472 CAAAACAGACTATCAGATCCCAAGATATGCTCTGCAATTTGCGCTCTATGGCAAGGAC 531  
Qy 670 TACAATGCTTACACACATAGCTTTGCTGTATGGAAGGATCAGGACCTCTGGCAGAA 729  
Db 532 TACAATGCTTACACACATAGCTTTGCTGTATGGAAGGATCAGGACCTCTGGCAGAA 591  
Qy 730 CTGGCCAAAGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGGACCCATGCTTTCAATCCT 789  
Db 592 CTGGCCAAAGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGGACCCATGCTTTCAATCCT 651  
Qy 790 GGNATATAAGAGTAGTGAACGTAAAGTACCTTTTACAAGACCCCTGCAACCAAGATTTT 849  
Db 652 GGNATATAAGAGTAGTGAACGTAAAGTACCTTTTACAAGACCCCTGCAACCAAGATTTT 711  
Qy 850 GAGATGACTCTTCATTCAGCAGATTTGAAATCCAGGATATTGGAACCTATCAACAATGC 909  
Db 712 GAGATGACTCTTCATTCAGCAGATTTGAAATCCAGGATATTGGAACCTATCAACAATGC 771  
Qy 910 CATCAAGCATCTCGAGCTCTTCAACACAGTTACTGCGCTTTACTCC - AGTGTGCTT 968  
Db 772 CATCAAGCATCTCGAGCTCTTCAACACAGTTACTGCGCTTTACTCCCAAGTGTGCTT 831  
Qy 969 CAATGGG--ATTTTCTTGGCACCACCTCCAGGGG--ATTTTGGGGGATTTTCAAGC-TTTT 1023  
Db 832 CAATGGGGATTTTCTTGGCCACCACCTCCAGGGGGATTTTGGGGCATTTTTCAGCTTTT 891  
Qy 1024 TACTTTGTGATGAAGTTT--AACTTGACATCAGAG-AACTCTCAGGAAGG--T 1079  
Db 892 TACTTTGGGATGGATTTTAAACTTGACATCCGAGAAAGTCCCTCAGGAAAGGGTG 951  
Qy 1080 GACTGAGATGATG-AAAAAGTTCTGTGCTCAGCTTGGGAGGAGATAAAAACA 1131  
Db 952 ACCTGAATGATGAAAAAGTTCTGTGCTCAGCTTGGGAGGAGATGATAA 1004

RESULT 14  
BF664417  
LOCUS 602146163F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4309839 5',  
DEFINITION mRNA sequence.  
ACCESSION BF664417.1 GI:11938222  
VERSION BF664417  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 808)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-romail.nih.gov](mailto:cgapbs-romail.nih.gov)  
Tissue Procurement: Louis M.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCW1183 row: n column: 16  
High quality sequence stop: 758.  
Location/Qualifiers  
1..808  
/organism="Homo sapiens"

/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4309839"  
/tissue\_type="primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_48"  
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected by  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 47.3%; Score 645.2; DB 2; Length 808;  
Best Local Similarity 98.7%; Pred. No. 2.6e-179;  
Matches 693; Conservative 0; Mismatches 3; Indels 6; Gaps 4;

Qy 604 GTACCCCAAAACACAGACTATCAGTCCCAAGATATGCTCTGCAATTTGCGCTCTATGGC 663  
Db 2 GTACCCCAAAACACAGACTATCAGTCCCAAGATATGCTCTGCAATTTGCGCTCTATGGC 61  
Qy 664 AAGGACTACAATGCTTACACACATAGCTTTGCTGTATGGGAAGGATCAGGACCTCTGG 723  
Db 62 AAGGACTACAATGCTTACACACATAGCTTTGCTGTATGGGAAGGATCAGGACCTCTGG 121  
Qy 724 CAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGACCCATGCTTT 783  
Db 122 CAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGACCCATGCTTT 181  
Qy 784 CATCTGATATATAAGAGGTAGTAACTGTAAGTACCTTTTCAAGACCCCTGCAACCAAG 843  
Db 182 CATCTGATATATAAGAGGTAGTAACTGTAAGTACCTTTTCAAGACCCCTGCAACCAAG 241  
Qy 844 AGATTGAGATGACTCTTCCATTCAGCAGTTTGAATCCAGGGTATTGGAAACTATCAA 903  
Db 242 AGATTGAGATGACTCTTCCATTCAGCAGTTTGAATCCAGG--TATGGAACCTATCAA 299  
Qy 904 CAATGCCATCAAAGCATCCTCGAGCTCTTCAACACCAAGTACTGCGCTTACTCCAGTGT 963  
Db 300 CAATGCCATCAAAGCATCCTCGAGCTCTTCAACACCAAGTACTGCGCTTACTCCAGTGT 359  
Qy 964 GCCTTCAATGGGATTTCTTCCACCACTCCAGGGGATTTTGGGGCATTTTTCAGCTTTT 1023  
Db 360 GCCTTCAATGGGATTTCTTCCACCACTCCAGGGG--ATTGGGGCATTTTTCAGCTTTT 417  
Qy 1024 TACTTTGTGATGAAAGTTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACT 1083  
Db 418 TAC--TTGTGATGAAGTTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACT 476  
Qy 1084 GAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGGAGATGAAAAACATCTTACCTGGA 1143  
Db 477 GAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGGAGATGAAAAACATCTTACCTGGA 536  
Qy 1144 GTAAGGAGAGTACCTGAGTGAATACGCTTTTCTGTGTACCTACATCTCTCCCTCCTT 1203  
Db 537 GTAAGGAGAGTACCTGAGTGAATACGCTTTTCTGTGTACCTACATCTCTCCCTCCTT 596  
Qy 1204 CTGCAAGGCTATCATTTTCAACAGCTGATTTCTTGGGAGGACATCCATTTTTCATTTGGCAAGATC 1263  
Db 597 CTGCAAGGCTATCATTTTCAACAGCTGATTTCTTGGGAGGACATCCATTTTCA--TGGCAAGATC 655  
Qy 1264 CAGGGCAGCAGCGCGCTGGACCTTTGGGCTTACATGCTGAAC 1305  
Db 656 CAGGGCAGCAGCGCGCTGGACCTTTGGGCTTACATGCTGAAC 697

RESULT 15  
CB553295  
LOCUS CB553295 673 bp mRNA linear EST 01-JUN-2003

DEFINITION	MMSP0076_A03 MMSP Macaca mulatta cDNA, mRNA sequence.
ACCESSION	CB553295
VERSION	CB553295.1
KEYWORDS	ESf.
SOURCE	Macaca mulatta (rhesus monkey)
ORGANISM	Macaca mulatta
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
	Cercopithecinae; Macaca.
REFERENCE	1 (bases 1 to 673)
AUTHORS	Katze, M.G., Bungartner, R., Korth, M., Feldman, R., Amjadi, M. and Holzman, T.
TITLE	Expressed sequence tags from Rhesus macaque spleen
JOURNAL	Unpublished (2002)
COMMENT	Contact: Holzman T
	Katze Lab
	University of Washington
	Box 358070, Seattle, WA 98195-8070, USA
	Tel: 206 732 6156
	Fax: 206 732 6055
	Email: ted@locke.ha.washington.edu
	Similar to GenBank entry S73813 S73813 CD39=lymphoid cell
	activation antigen [human, B lymphoblastoid cell line, MP-1, mRNA,
	1818 nt]. 4/1995
	Plate: MMSP0076 row: A column: 03.
FEATURES	Location/Qualifiers
source	1..673
	/organism="Macaca mulatta"
	/mol_type="mRNA"
	/db_xref="taxon:9544"
	/sex="male"
	/cell_type="monocytes"
	/dev_stage="adult"
	/clone_lib="MMSP"
	/note="Organ: spleen"
ORIGIN	
Query Match	45.7%; Score 624.2; DB 6; Length 673;
Best Local Similarity	98.4%; Pred. No. 4.2e-173;
Matches 662; Conservative	0; Mismatches 8; Indels 3; Gaps 3;
QY	653 GCCTCTATGGCAAGGACTCAATGTCTACACATAGCTTTTGTG-CTATGGGAAGGAT 711
DB	1 GCCTCTATGGCAAGGACTCAATGTCTACACATAGCTTTGTGCTATGGGAAGGAT 60
QY	712 CAGGCACCTCTGGCAGAACTGGCCAGGACATTCAGTTGCCAAGTAATGAAATTCACAG 771
DB	61 CAGGCACCTCTGGCAGAACTGGCCAGGACATTCAGTTGCCAAGTAATGAAATTCACAG 120
QY	772 GACCCATGCTTTCATCTGGATATAGAAGGTAGTGAACGTAGTGACCTTTACAAGACC 831
DB	121 GACCCATGCTTTCATCCGGATATAGAAGGTAGTGAACGTAGTGACCTTTACAAGACC 180
QY	832 CCCTGCACCAAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAAATCCAGGGTATT 891
DB	181 CCCTGCACCAAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAAATCCAGGGTATT 240
QY	892 GGAAACTATCAACATGCCATCAAAAGCATCCTGGAGCTCTTCAACACACAGTTACTGCCCT 951
DB	241 GGAAACTATCAACATGCCATCAAAAGCGCTCTGGAGCTCTTCAACACACAGTTACTGCCCT 300
QY	952 TACTCCAGTGCTTCAATGGGATTTTCTGCCACCTCCAGGGGATTTTGGGGCA 1011
DB	301 TACTCCAGTGCTTCAATGGGATTTTCTGCCACCTCCAGGGGATTTTGGGGCA 360
QY	1012 TTTTCAGCTTTTACCTTTGTGATGAAGTTTAAACTTGACATCAGAGAAAGTCTCTCAG 1071
DB	361 TTTTCAGCTTTTACCTTTGTGATGAATTTTAAACTTGACATCAGAGAAAGTCTCTCAG 420
QY	1072 GAAAAGGTGACTGAGATGATAAAAGTTCTGTGCTCAGCCTTGGGAGGAGATAAAAACA 1131
DB	421 GAAAAGGTGACTGAGATGATAAAAGTTCTGTGCTCAGCCTTGGGAGGAGATAAAAACA 480
QY	1132 TCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTGGTACCTACATT 1191
DB	481 TCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTGGTACCTACATT 540
QY	1192 CTCTCCCTCTCTTCTGCAAGGCTATCA-TTTCAAGCTGATTCTCTGGAGCACATCCATTT 1250
DB	541 CTCTCCCTCTCTTCTGCAAGGCTATCATTTTCAAGCTGATTCTCTGGAGCACATCCATTT 600
QY	1251 CATTGGCAAGATCCAGGGCAGCGACCGGCT-GGACTTTTGGGCTACATGCTGAACCTGA 1309
DB	601 CATTGGCAAGATCCAGGGCAGCGACCGGCTGGGACTTTGGGCTACATGCTGAACCTGA 660
QY	1310 CCAACATGATCCC 1322
DB	661 CCAACATGATCCC 673
Search completed: September 21, 2005, 23:22:02	
Job time : 4882.93 secs	

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2005, 16:29:41 ; Search time 244.55 Seconds  
(without alignments)  
9133.162 Million cell updates/sec

Title: US-09-807-660C-5  
Perfect score: 1365  
Sequence: 1 gcacctattcaagttctac.....ctctctccactccacctaa 1365

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/prodata/1/ina/5A-COMB.seq:  
2: /cgn2\_6/prodata/1/ina/5B-COMB.seq:  
3: /cgn2\_6/prodata/1/ina/6A-COMB.seq:  
4: /cgn2\_6/prodata/1/ina/6B-COMB.seq:  
5: /cgn2\_6/prodata/1/ina/PCUS-COMB.seq:  
6: /cgn2\_6/prodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1319.2	96.6	1818	3	US-08-930-921-2
2	1319.2	96.6	1818	4	US-09-023-655-1475
3	1319.2	96.6	1818	4	US-09-781-796C-2
4	463.2	33.9	871	4	US-09-949-016-2106
5	291	21.3	2782	4	US-09-949-016-5457
6	291	21.3	2797	3	US-09-240-639-3
7	291	21.3	2797	4	US-09-908-510A-3
8	291	21.3	2797	4	US-09-905-744B-3
9	291	21.3	2797	4	US-10-107-660-3
10	291	21.3	2797	4	US-10-107-576-3
11	291	21.3	2797	4	US-09-905-732B-3
12	291	21.3	2797	4	US-09-923-304-3
13	291	21.3	2797	4	US-09-949-016-1178
14	291	21.3	2797	4	US-09-905-743B-3
15	270.2	19.8	46885	4	US-09-949-016-13848
16	245.8	18.0	601	4	US-09-949-016-71601
17	220.8	16.2	1500	4	US-09-949-016-5688
18	167.8	12.3	364	4	US-09-513-999C-196
19	167	12.2	601	4	US-09-949-016-71600
20	140.4	10.3	601	4	US-09-949-016-71607
21	139	10.2	742	2	US-08-966-316-2
22	96	7.0	601	4	US-09-949-016-71597
23	69.4	5.1	9422	4	US-09-949-016-117430
24	69	5.1	45539	4	US-09-949-016-11920
25	69	5.1	45540	4	US-09-949-016-117199
26	53.2	3.9	1643	3	US-09-129-112-1
27	52.6	3.9	7218	1	US-08-232-463-14

c

28	51.6	3.8	601	4	US-09-949-016-21380	Sequence 21380, A
29	51.6	3.8	601	4	US-09-949-016-190869	Sequence 190869, A
30	49.6	3.6	1458	3	US-09-129-112-8	Sequence 8, Appli
31	48	3.5	1489	3	US-09-129-112-13	Sequence 13, Appli
32	43.6	3.2	1434	3	US-09-129-112-18	Sequence 18, Appli
33	40.6	3.0	1287	3	US-09-608-285A-6	Sequence 6, Appli
34	40.6	3.0	1287	3	US-09-350-836B-6	Sequence 6, Appli
35	40.6	3.0	1287	3	US-09-370-265-6	Sequence 6, Appli
36	40.6	3.0	1287	4	US-09-557-800C-6	Sequence 6, Appli
37	40.6	3.0	1287	4	US-09-370-625A-6	Sequence 6, Appli
38	40.4	3.0	254964	4	US-09-949-016-12583	Sequence 12583, A
39	40.4	3.0	254964	4	US-09-949-016-17392	Sequence 17392, A
40	39.4	2.9	601	4	US-09-949-016-21395	Sequence 21395, A
41	39.4	2.9	601	4	US-09-949-016-190884	Sequence 190884, A
42	39.4	2.9	85963	4	US-09-949-016-13804	Sequence 13804, A
43	39.2	2.9	505	4	US-09-621-976-15639	Sequence 15639, A
44	39	2.9	300	3	US-09-608-285A-1	Sequence 1, Appli
45	39	2.9	300	3	US-09-350-836B-1	Sequence 1, Appli

#### ALIGNMENTS

#### RESULT 1

US-08-930-921-2  
; Sequence 2, Application US/08930921B  
; Patent No. 6287837  
; GENERAL INFORMATION:  
; APPLICANT: BEAUDOIN, Adrien R.  
; APPLICANT: SEVIGNY, Jean  
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION  
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT  
; TITLE OF INVENTION: TECHNOLOGY  
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN  
; CURRENT APPLICATION NUMBER: US/08/930,921B  
; CURRENT FILING DATE: 1998-01-02  
; EARLIER APPLICATION NUMBER: PCT/CA96/00223  
; EARLIER FILING DATE: 1996-04-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1818  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: unknown  
US-08-930-921-2

Query Match		96.6%	Score 1319.2;	DB 3;	Length 1818;
Best Local Similarity		99.8%	Pred. No. 0;		
Matches 1321;		Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	41	GTTCACCCAGCAAAAGCATTGCCAGAAAACGTTAAGTATGGATTTGCTGGATCGG	100		
Db	174	GGTTGACCCAGCAAAAGCATTGCCAGAAAACGTTAAGTATGGATTTGCTGGATCGG	233		
Qy	101	GTTCCTCTCACCAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGAGAAATGACACAG	160		
Db	234	GTTCCTCTCACCAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGAGAAATGACACAG	293		
Qy	161	GCGTGGTGCATCAAGTAGAAGAAATGCGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC	220		
Db	294	GCGTGGTGCATCAAGTAGAAGAAATGCGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC	353		
Qy	221	AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTCGATCGAAGAGCTAGGGAAGTGA	280		
Db	354	AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTCGATCGAAGAGCTAGGGAAGTGA	413		
Qy	281	TTCCAAAGGTCCAGCACCAGAGACACCCGTTTACCTGGGAGCCACGCGCATCGCGT	340		
Db	414	TTCCAAAGGTCCAGCACCAGAGACACCCGTTTACCTGGGAGCCACGCGCATCGCGT	473		
Qy	341	TGCTCAGGATGGAAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGTGGAGAGGCC	400		

Db 474 TGCTCAGGATGGAAGTGAAGAGTGGCAGACAGGGTTCGGATGTGGTGGAGAGGCC 533  
Qy 401 TCAGCAACTACCCCTTTGACTTCAGGGTCCAGGATCATTAATCTGCGCAAGAGAGGTG 460  
Db 534 TCAGCAACTACCCCTTTGACTTCAGGGTCCAGGATCATTAATCTGCGCAAGAGAGGTG 593  
Qy 461 CCTATGGCTGGATTAATCACTATCTGCTGGCAAAATTCAGTCAGAAAACAGGTGT 520  
Db 594 CCTATGGCTGGATTAATCACTATCTGCTGGCAAAATTCAGTCAGAAAACAGGTGT 653  
Qy 521 TCAGCATAGTCCCATATGAACCAATTAATCAGGAACCTTTGGAGCTTTGGACCTTTGGGG 580  
Db 654 TCAGCATAGTCCCATATGAACCAATTAATCAGGAACCTTTGGAGCTTTGGACCTTTGGGG 713  
Qy 581 GAGCCTCTACCAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 640  
Db 714 GAGCCTCTACCAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 773  
Qy 641 CTCTGCAATTTCCGCTCTATGCGAAGGACTACATGCTCTACACATAGCTTCTGTGCT 700  
Db 774 CTCTGCAATTTCCGCTCTATGCGAAGGACTACATGCTCTACACATAGCTTCTGTGCT 833  
Qy 701 ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAGGACATTCAGGTTCAGAAATAG 760  
Db 834 ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAGGACATTCAGGTTCAGAAATAG 893  
Qy 761 AAATTTCTCAGGGACCCATGTTTCACTCTGGATATAAGAAAGGTAGTGAAGTGAAC 820  
Db 894 AAATTTCTCAGGGACCCATGTTTCACTCTGGATATAAGAAAGGTAGTGAAGTGAAC 953  
Qy 821 TTTACAGACCCCTGCACCAAGAGATTCAGATGACTCTTCATTTCCAGCAGTTTGAA 880  
Db 954 TTTACAGACCCCTGCACCAAGAGATTCAGATGACTCTTCATTTCCAGCAGTTTGAA 1013  
Qy 881 TCAGGGTATTTGGAACCTATCAACAATGCCATCAAGCATCTCGGAGCTTCTCAACACCA 940  
Db 1014 TCCAGGGTATTTGGAACCTATCAACAATGCCATCAAGCATCTCGGAGCTTCTCAACACCA 1073  
Qy 941 GTTACTGCCCTTAATCCAGTGTGCTTCAATGGATTTTCTTGCCACCACTCCAGGGG 1000  
Db 1074 GTTACTGCCCTTAATCCAGTGTGCTTCAATGGATTTTCTTGCCACCACTCCAGGGG 1133  
Qy 1001 ATTTGGGGCATTTTCACTTTTACTTTCTGTGATGAATTTTAACTTGACATCAGAGA 1060  
Db 1134 ATTTGGGGCATTTTCACTTTTACTTTTGTGATGAATTTTAACTTGACATCAGAGA 1193  
Qy 1061 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAGTTTCTGTGCTCAGCCTTTGGAGG 1120  
Db 1194 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAGTTTCTGTGCTCAGCCTTTGGAGG 1253  
Qy 1121 AGATAAAAAATCTTACGCTGGAGTAAAGAGAGTAACTGAGTGAATATCTGCTTTCTG 1180  
Db 1254 AGATAAAAAATCTTACGCTGGAGTAAAGAGAGTAACTGAGTGAATATCTGCTTTCTG 1313  
Qy 1181 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGGAGC 1240  
Db 1314 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGGAGC 1373  
Qy 1241 ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGCGGCTGGACTTTGGGCTACATGC 1300  
Db 1374 ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGCGGCTGGACTTTGGGCTACATGC 1433  
Qy 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCA 1360  
Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCA 1493  
Qy 1361 CCTA 1364  
Db 1494 CCTA 1497

US-09-023-655-1475  
; Sequence 1475, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1475:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1818 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: 9765255  
US-09-023-655-1475

Query Match 96.6%; Score 1319.2; DB 4; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAAAGTTAAAGTATGGGATTTGCTGGATGCGG 100  
Db 174 GGTGTACCCAGAACAAAGCATTTGCCAGAAAAAGTTAAAGTATGGGATTTGCTGGATGCGG 233  
Qy 101 GTTCTTCTCACCAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAAATGACACAG 160  
Db 234 GTTCTTCTCACCAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAAATGACACAG 293  
Qy 161 GCGTGTGTGATCAAGTAGAAGAAATGAGGTTTAAAGGTCCTCGAATCTCAAAAATTTGTTTC 220  
Db 294 GCGTGTGTGATCAAGTAGAAGAAATGAGGTTTAAAGGTCCTCGAATCTCAAAAATTTGTTTC 353  
Qy 221 AGAAAGTAAATGAAATAGGCAATTTACCTGACATTTGATTCATGAAAGAGCTTAGGAAAGTGA 280  
Db 354 AGAAAGTAAATGAAATAGGCAATTTACCTGACATTTGATTCATGAAAGAGCTTAGGAAAGTGA 413  
Qy 281 TTCCAAGTCCAGACAGCAAGACACCCGTTTACTGGAGGCCAGCGGAGGATCGGCT 340  
Db 414 TTCCAAGTCCAGACAGCAAGACACCCGTTTACTGGAGGCCAGCGGAGGATCGGCT 473  
Qy 341 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACACAGGGTTCTCGATGTGTGGAGAGGACC 400



```
Db 474 TGTCTCAGGATGGAAGTGAAGTGTGGCAGACAGGGTCTTGATGTGGTGAAGAGAGCC 533
Qy 401 TCAGCAACTACCCCTTTGACTTCACAGGGTCCAGGATCATTTACTGGCCCAAGGAAGGTG 460
Db 534 TCAGCAACTACCCCTTTGACTTCACAGGGTCCAGGATCATTTACTGGCCCAAGGAAGGTG 593
Qy 461 CCTATGGCTGGATTACTATCACTATCTCTGTGGCAAAATTCAGTCAGAAAAACAAGTGT 520
Db 594 CCTATGGCTGGATTACTATCACTATCTCTGTGGCAAAATTCAGTCAGAAAAACAAGTGT 653
Qy 521 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 580
Db 654 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 713
Qy 581 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATG 640
Db 714 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATG 773
Qy 641 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 700
Db 774 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 833
Qy 701 ATGGGAAGGATCAGGCACCTCTGGCAGAACTGGCCNAGGACATTCAGGTGCAAGTAATG 760
Db 834 ATGGGAAGGATCAGGCACCTCTGGCAGAACTGGCCNAGGACATTCAGGTGCAAGTAATG 893
Qy 761 AAATTTCTCAGGACCCCATCTTCTCCTGGATATGAAGAGTGTGAACGTGAAGTGACC 820
Db 894 AAATTTCTCAGGACCCCATCTTCTCCTGGATATGAAGAGTGTGAACGTGAAGTGACC 953
Qy 821 TTTTCAAGACCCCTGCAACCAAGAGATTTGAGATGACTCTTCCATTCACAGCATTTGAAA 880
Db 954 TTTTCAAGACCCCTGCAACCAAGAGATTTGAGATGACTCTTCCATTCACAGCATTTGAAA 1013
Qy 881 TCCAGGATATGGAAACTATCAACATGCCATCAAGCATCTGAGCTCTTCAACACCA 940
Db 1014 TCCAGGATATGGAAACTATCAACATGCCATCAAGCATCTGAGCTCTTCAACACCA 1073
Qy 941 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGCCACCATCCAGGGGG 1000
Db 1074 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGCCACCATCCAGGGGG 1133
Qy 1001 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAACTTGACATCAGAGA 1060
Db 1134 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAACTTGACATCAGAGA 1193
Qy 1061 AGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCCTTGGGAGG 1120
Db 1194 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCCTTGGGAGG 1253
Qy 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACTGAGTGAATACTGCTTTTCTG 1180
Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACTGAGTGAATACTGCTTTTCTG 1313
Qy 1181 GTACCTACATCTCTCCCTCTCTTCTGCAAGGCTATCATTTACAGCTGATTCCTGGGAGC 1240
Db 1314 GTACCTACATCTCTCCCTCTCTTCTGCAAGGCTATCATTTACAGCTGATTCCTGGGAGC 1373
Qy 1241 ACATCCATTTCTTGGCAAGATCCAGGGCAGGACGCCGGCTGGACTTTGGGCTACATGC 1300
Db 1374 ACATCCATTTCTTGGCAAGATCCAGGGCAGGACGCCGGCTGGACTTTGGGCTACATGC 1433
Qy 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACTCTCTCCCACTCCA 1360
Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACTCTCTCCCACTCCA 1493
Qy 1361 CCTA 1364
Db 1494 CCTA 1497
```

RESULT 3

```
US-09-781-796C-2
; Sequence 2, Application US/09781796C
; Patent No. 6800284
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNY, Jean
; APPLICANT: BACH, Fritz H.
; APPLICANT: ROBSON, Simon
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; FILE REFERENCE: 920333.90019
; CURRENT APPLICATION NUMBER: US/09/781,796C
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 08/419,204
; PRIOR FILING DATE: 1995-04-10
; PRIOR APPLICATION NUMBER: CA96/00223
; PRIOR FILING DATE: 1996-04-10
; PRIOR APPLICATION NUMBER: 08/930,921
; PRIOR FILING DATE: 1998-02-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1818
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-781-796C-2
```

```
Query Match 96.6%; Score 1319.2; DB 4; Length 1818;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAAACGTTTAAGTATGGGATTTGCTGGATGCGG 100
Db 174 GTTGACCCAGACAAAGCATTTGCCAGAAAAACGTTTAAGTATGGGATTTGCTGGATGCGG 233
Qy 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGAGAAATGACACAG 160
Db 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGAGAAATGACACAG 293
Qy 161 GCGTGTGCATCAAGTAGAAGAAATGCAGGGTTAAAGTCTCTGGATCTCNAATTTTGTTC 220
Db 294 GCGTGTGCATCAAGTAGAAGAAATGCAGGGTTAAAGTCTCTGGATCTCNAATTTTGTTC 353
Qy 221 AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTTGCATGAAAGAGTAGGGAAGTGA 280
Db 354 AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTTGCATGAAAGAGTAGGGAAGTGA 413
Qy 281 TTCCAAGTCCCAAGCAGACACCCGTTTACCTGGGAGCCACGCGCATGCGGT 340
Db 414 TTCCAAGTCCCAAGCAGACACCCGTTTACCTGGGAGCCACGCGCATGCGGT 473
Qy 341 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAAGAGGCC 400
Db 474 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAAGAGGCC 533
Qy 401 TCAGCAACTACCCCTTTGACTTCACAGGGTCCAGGATCATTTACTGGCCCAAGGAAGGTG 460
Db 534 TCAGCAACTACCCCTTTGACTTCACAGGGTCCAGGATCATTTACTGGCCCAAGGAAGGTG 593
Qy 461 CCTATGGCTGGATTACTATCACTATCTCTGTGGCAAAATTCAGTCAGAAAAACAAGTGT 520
Db 594 CCTATGGCTGGATTACTATCACTATCTCTGTGGCAAAATTCAGTCAGAAAAACAAGTGT 653
Qy 521 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 580
Db 654 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 713
Qy 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATG 640
Db 714 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATG 773
Qy 641 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 700
```

```

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2106

Query Match      33.9%; Score 463.2; DB 4; Length 871;
Best Local Similarity 99.4%; Pred. No. 2.3e-144;
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 774 CTCTGCAATTTGGCCCTCTATGGCAAGGACTCAATGCTCTACACATAGCTTCTTGCT 833
QY 701 ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 760
DB 834 ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 893
QY 761 AAATTTCTCAGGGACCCAGTCTTTTCATCTCGATATAGAAGGTAGTGAAGTAAAGTACC 820
DB 894 AAATTTCTCAGGGACCCAGTCTTTTCATCTCGATATAGAAGGTAGTGAAGTAAAGTACC 953
QY 821 TTTTACAAGACCCCTGTCACCAAGAGATTTGAGATGACTCTTCATTTCCAGCAGTTTGAAA 880
DB 954 TTTTACAAGACCCCTGTCACCAAGAGATTTGAGATGACTCTTCATTTCCAGCAGTTTGAAA 1013
QY 881 TCCAGGGTATTGGAACTATCAACAATGCCATCAAGCATCTCGAGCTCTTCAACACCA 940
DB 1014 TCCAGGGTATTGGAACTATCAACAATGCCATCAAGCATCTCGAGCTCTTCAACACCA 1073
QY 941 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGGCCACCACTCCAGGGG 1000
DB 1074 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGGCCACCACTCCAGGGG 1133
QY 1001 ATTTTGGGGCAATTTTCAAGCTTTTACTTTGTGATGAAGTTTAACTTGACATCAGAGA 1060
DB 1134 ATTTTGGGGCAATTTTCAAGCTTTTACTTTGTGATGAAGTTTAACTTGACATCAGAGA 1193
QY 1061 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCCTTGGGAGG 1120
DB 1194 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCCTTGGGAGG 1253
QY 1121 AGATAAAACATCTTACGCTGGAGTAAAGAGAAAGTACCTGAGTGAATCTGCTTTCTG 1180
DB 1254 AGATAAAACATCTTACGCTGGAGTAAAGAGAAAGTACCTGAGTGAATCTGCTTTCTG 1313
QY 1181 GTACTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTGGGAGC 1240
DB 1314 GTACTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTGGGAGC 1373
QY 1241 ACATCCATTTTATTTGCAAGATCCAGGCGACGACGCGGCTGAGCTTTGGGCTACATGC 1300
DB 1374 ACATCCATTTTATTTGCAAGATCCAGGCGACGACGCGGCTGAGCTTTGGGCTACATGC 1433
QY 1301 TGAACCTGACCAATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCACTCCA 1360
DB 1434 TGAACCTGACCAATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCACTCCA 1493
QY 1361 CCTA 1364
DB 1494 CCTA 1497

RESULT 4
US-09-949-016-2106
; Sequence 2106, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2106
; LENGTH: 871

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5457

Query Match      21.3%; Score 291; DB 4; Length 2782;
Best Local Similarity 54.3%; Pred. No. 3.6e-86;
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

QY 48 CCAGAACAAAGCATTTGCCAGAAACCGTTAAGTATGGGATTTGCTCGATCGGGTTCTTC 107
DB 219 CAAGCAAGAGTCTCTCCCTCCAGGACTGAAGTATGTTGCTGATGCCGGTCTTTC 278
```

```

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2106

Query Match      33.9%; Score 463.2; DB 4; Length 871;
Best Local Similarity 99.4%; Pred. No. 2.3e-144;
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 41 GTTCAACCCAGCAACAAAGCATTTGCCAGAAAAAGTTAAGTATGGGATTTGCTGGATCGCG 100
DB 198 GGTTCAGCCAGAACAAAGCATTTGCCAGAAAAAGTTAAGTATGGGATTTGCTGGATCGCG 257
QY 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAAGGAGAAATGACACAG 160
DB 258 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAAGGAGAAATGACACAG 317
QY 161 GCGTGTGTCATCAAGTAGAAGAAATGCAGGGTTTAAAGGTCCTTGGAAATCTCAAAAATTTGTTTC 220
DB 318 GCGTGTGTCATCAAGTAGAAGAAATGCAGGGTTTAAAGGTCCTTGGAAATCTCAAAAATTTGTTTC 377
QY 221 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTCGATGAAAGAGCTAGGGAATGA 280
DB 378 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTCGATGAAAGAGCTAGGGAATGA 437
QY 281 TTCCAAAGTCCAGACCAAGAGACACCCGTTTACCTGGAGCCACCGCAGGCGATCGCGT 340
DB 438 TTCCAAAGTCCAGACCAAGAGACACCCGTTTACCTGGAGCCACCGCAGGCGATCGCGT 497
QY 341 TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGAGGTTCTTGGATGTGTGGAGAGGAGCC 400
DB 498 TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGAGGTTCTTGGATGTGTGGAGAGGAGCC 557
QY 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGAGTATCATTTAGTCCCAAGAGGAGGTTG 460
DB 558 TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGAGTATCATTTAGTCCCAAGAGGAGGTTG 617
QY 461 CCTATGGCTGGATTACTATCAACTCTCTGCGGCAAAATTCAGTCTAGA 508
DB 618 CCTATGGCTGGATTACTATCAACTCTCTGCGGCAAAATTCAGTCTAGA 665

RESULT 5
US-09-949-016-5457
; Sequence 5457, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5457
; LENGTH: 2782

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5457

Query Match      21.3%; Score 291; DB 4; Length 2782;
Best Local Similarity 54.3%; Pred. No. 3.6e-86;
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

QY 48 CCAGAACAAAGCATTTGCCAGAAACCGTTAAGTATGGGATTTGCTCGATCGGGTTCTTC 107
DB 219 CAAGCAAGAGTCTCTCCCTCCAGGACTGAAGTATGTTGCTGATGCCGGTCTTTC 278
```



Db	700	GGTGC-----ACCGCATGGAGTGGAAACCCAGGGTGCCTCGGACTTAAAGTGGTGCCTC	753
Qy	588	TACACAAGTCACCTTTTGTACCCCAAAACACAGACTATCGAGTCCCCAGATAATGCTCTGC	647
Db	754	CACCCAATATCTTTCGTGGCAGGAGAGATGGATCTGAACACACAGCAGCATCATGCA	813
Qy	648	ATTTCCGCTCTATGGCAAGGACTACAATGTCTCACACATAGCTTCTTGTGCTATGGAA	707
Db	814	GGTGTCCCTGTATGGCTACGTATACACGCTCTACACACACAGCTTCCAGTGTATGSCCG	873
Qy	708	GGATCAGGCACTCTGGCAGAGAACTGGGCCAAGGACAITTCAGGTTGCAAGTAAATGAAA--T	764
Db	874	GAATGAGGCTGAGAAGAAGTTTCTGGCAATGCTCCTGCAGAAATTTCTCTACCAAAAACCA	933
Qy	765	TCTCAGGGACCCATGCTTTCATCTCGATATATGAAGGTAGTGAACCTAAGTAGCACTTTA	824
Db	934	TCTCACCAATCCCTGTTACCTCGGGATTTATAGCATCAGCTTACCATGGGCCATGTATT	993
Qy	825	CAAGACCCCTCGAC-----CAAGAGATTGAGATGACTCTTCCTATCCAGCAGATTGA	878
Db	994	TGATAGCTGTGCACTGTGGACAGAGCCAGAAAAGTTATAACCCCAATGATGTCATCAC	1053
Qy	879	AATCCAGGGTATTGGAACATATCAACAATGCCATCAAAAGCATCTGTGGAGCTCTTCAACAC	938
Db	1054	TTTTGAAGGAACTGGGACCCATCTCTGTGTGAAGGAGAAGTGCTTCCCATATTGACTT	1113
Qy	939	CAGTTACTGCCCTTACTCCAG----TGTCCTTCAATGGGATTTCTTGGCCACCACCTCCA	995
Db	1114	CNAAGCTTGGCATGATCAAGAAACCTGTTCTTTGATGGGGTTTATCAGCCCAAGATTAA	1173
Qy	996	GGGGATTTTGGGGCATTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTGACATC	1055
Db	1174	AGGGCAATTTGTGGCTTTTGAGGATTTCTACTACACAGCCAGTCTTTAAATCT--TTC	1230
Qy	1056	AGAAAAGTCTCTCAGAAAAAGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTG	1115
Db	1231	AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTGGAAATTTCTGCTCACAAGATTG	1290
Qy	1116	GGAGGAGATAAAACATCTTACGTGGAGTAAAGGAGAAGTACTCTGAGTGAATACTGCTT	1175
Db	1291	GAGTCAGCTCCACTGTGCTGCCCAAATTTGATGAGGTATATGCCCGCTCTTACTGCTT	1350
Qy	1176	TTCTGGTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTACAGCTGATTCCTG	1235
Db	1351	CTCAGCCAACATCATATCAACTTTGTTGTGAACGGTTACAAATTCACAGAGGACATTG	1410
Qy	1236	GGAGCACAATCCATTTTGGCAAGATCCAGGGCAGCGAGCCCGGCTGGACTTTGGGCTA	1295
Db	1411	GCCCAATAACACTTTGAAAAGAAAGTGGGGAATAGCAGCATAGCTTGGTCTCTTGCGCTA	1470
Qy	1296	CATGCTGAACTGTACCAACATGATCCCAGCTGAGCAACCAATTG	1338
Db	1471	CATGCTCAGCTGTACCAACACAGATCCCGAGTCCAGGATGAAAGCCCTCTG	1513

## RESULT 7

```

US-09-908-510A-3
; Sequence 3, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120E
; CURRENT APPLICATION NUMBER: US/09/908,510A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3

```

QY 939 CAGTTACTGCGCTTACTCCAG---TGTGCTTCAATGGGATTTTCTTGCCACCACTCCA 995  
Db 1114 CAAAGCTTGCCATGATCAAGAAACCTGTTCTTTGATGGGTTTATCAGCCAAAGATTAA 1173  
QY 996 GGGGATTTTGGGGCATTTTTCAGCTTTTACTTTGTGTGAAGTTTAACTTGACATC 1055  
Db 1174 AGGGCCATTTGTGGCTTTTGCAGGATTTCTACTACAGCCAGTGTCTTAAATCT---TTC 1230  
QY 1056 AGAAGAGTCTCTCAGAAAAAGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTG 1115  
Db 1231 AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACTCGGAATTTCTGTCTCAGAAATTG 1290  
QY 1116 GGAGGAGATAAAACATCTTACCTGGAGTAAGGAGAGTACCTGAGTGAATACTGCTT 1175  
Db 1291 GAGTCAGCTCCCACTGCTGCTCCCAAAATTGATGAGGTATATGCCCGCTCTTACTGCTT 1350  
QY 1176 TTCTGTACTCATTTCTCTCCCTCTCTGCAAGGCTATCATTTCCACAGCTGATTCCTG 1235  
Db 1351 CTCAGCCAACTACATCTACCACCTTGTGTTGTAAGGTTACAAATTCACAGAGGACTTG 1410  
QY 1236 GGAGCACATCCATTTCAATTGGCAAGATCCAGGCGACGCGGCTGGACTTTGGGCTA 1295  
Db 1411 GCCCCAAATACACTTTGAAAAAGAGTGGGAATAGCAGCATAGCCTGTCTCTTGGCTA 1470  
QY 1296 CATGCTGAACCTGACCAACATGATCCAGCTGAGCAACATTG 1338  
Db 1471 CATGCTCAGCCTGACCAACAGATCCAGCTGAAAGCCCTCTG 1513

RESULT 8  
US-09-905-744B-3  
; Sequence 3, Application US/09905744B  
; Patent No. 6780410  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Friesch, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; TITLE OF INVENTION: ACIDS  
; FILE REFERENCE: 28110/36120A  
; CURRENT APPLICATION NUMBER: US/09/905,744B  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
; OTHER INFORMATION:  
US-09-905-744B-3

Query Match 21.3%; Score 291; DB 4; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 3.6e-86;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

QY 48 CCAGAACAAAGCATTTGCCAGAAACGTTAAGTATGGGATTTGCTGGATGCGGGTCTTC 107  
Db 220 CAAGCAAGAGGTCCTCCCTCCAGGACTGAAGTATGTTGCTGGATGCGGGTCTTC 279  
QY 108 TCACACAGTTTATACATCTATAAGTGGCCACAGAAAAGGAGAGATGACACAGGCGTGT 167  
Db 280 AAGAACCAAGCTTACGTGTATCAATGGCCACAGAAAAGAGAAATATACCGGAGTGT 339  
QY 168 GCATCAAGTAGAAGTAAGTACAGGGTTAAAGGCTCTGGAATCTCAAAATTTGTTCAAAAAGT 227  
Db 340 CAGTCAAAACCTTTCAAATGTAGTGTGAAAGGCTCTGGAATCTCCAGTATGGAATTAACCC 399  
QY 228 AAATGAAATAGGCATTTACCTGACTGATTTGCAATGGAAGAGCTAGGGAGTGAATTCGAAG 287

Db 400 CCAAGATGTCCCGAGAGCCTTTGAGGAGTGTATGCAAAAAAGTCAAGGGGAGGTTCCATC 459  
QY 288 GTCCAGCAGCAACAGAGACACCCGTTTACCTGGAGCCACGCGAGGATGCGGTGCTCAG 347  
Db 460 CCACCTCCAGCGATCCACCCCATTCACCTGGAGCCACGCGTGGATGGCTTGTCTGAG 519  
QY 348 GATGGAAGTGAAGATTTGGCAGACAGGGTTCTGAGTGTGGAGGAGGAGCCTCAGCAA 407  
Db 520 GTTGCAAAATGAACACAGCAGCTTAATGAAGTCTTGAAGTCCCTGAAAGCATCCAAAGCTACTTCAAGTC 579  
QY 408 CTACCCCTTTGACTTCCAGGGTGCAGGATCAATTAATCTGCGCAAGAGGAGGTCCTATGG 467  
Db 580 CAGGCCCTTTGACTTTAGGGGTGCTCAAAATCAATTTCTGGGCAAGAGAGGGGTATATGG 639  
QY 468 CTGGAATTACTATCAACTATCTCTGGGCAAAATTCAGTTCAGAAAAAACAAGTGGTTTCAGCAT 527  
Db 640 ATGGATTACAGCCAACTATTTAATGGGAAATTTCTCTGGAGAGAACCTCTGGCACATGTG 699  
QY 528 AGTCCCATATGAACCAATAATCAGGAAACCTTTTGAGGCTTTGGACCTTTGGGGAGGCTC 587  
Db 700 GGTGC-----ACCGCATGGAGTGGAAACCAACGCGTGGCTTGGACTTAGGTGGTGCCTC 753  
QY 588 TACACAAGTCACTTTTGTACCCCAACACAGACTATCGAGTCCCGAGATAATGCTCTGCA 647  
Db 754 CACCCAAATATCTTTCTGGGAGGAGAGATGGATCTGAACACGAGCGACATCATGCA 813  
QY 648 ATTTCCGCTCTATGGCAAGGACTACAAATGTCTACACACATAGCTCTTCTGTCTATGGGAA 707  
Db 814 GGTGCTCTGTATGGCTACGTATACACGCTCTACACACACAGCTTCCAGTGTATGGCG 873  
QY 708 GGATCAGGACTCTCTGGCAGAACTCGCCAAAGCAATTCAGGTTGCAAGTAATGAA---T 764  
Db 874 GAAAGGCTGAGAAAGATTTCTGGCAATGTCTCTGCAGAAATCTCTCTTACCAAAACCA 933  
QY 765 TCTCAGGACCATCTTTTCACTCTGATATAAGAGGTAGTGAAGTGAAGTGAAGTGA 824  
Db 934 TCTCACCATCTCTTACCTCGGGATATATAGCATCAGCTTTCACCATGGGCGCATGTAT 993  
QY 825 CAAGACCCCTGCAAC-----CAAGAGATTTGAGATGACTCTTCCATTCACAGCTTGA 878  
Db 994 TGATAGCTTGTGCACTGTGGACAGAGGCCAGAAAGTTATTAACCCCAATGATGTCATCAC 1053  
QY 879 AATCAGGGTATTTGAAACTATCAACAATGCCATCAAGAGCATCTCTGGAGCTCTTCAACAC 938  
Db 1054 TTTTGAAGGAACCTGGGACCCATCTCTGTGTAAGGAGAGGTGGCTTCCATATTTGACTT 1113  
QY 939 CAGTTACTGCGCTTACTCCAG---TGTGCTTCAATGGGATTTTCTTGCCACCACTCCA 995  
Db 1114 CAAAGCTTGCCATGATCAAGAAACCTGTCTTTTGTATGGGTTTATCAGCCAAAGATTAA 1173  
QY 996 GGGGATTTTGGGCGATTTTTCAGCTTTTACTTTTGTGATGAAGTTTAACTTGACATC 1055  
Db 1174 AGGGCCATTTGTGGCTTTTGAGGATTTCTACTACAGCCAGTGTCTTAAATCT---TTC 1230  
QY 1056 AGAGAAAGTCTCTCAGGAAAGGTAAGTGAAGATGATGAAAAAGTTCTGTGCTCAGCCTTG 1115  
Db 1231 AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTTGAATTTCTGCTCAGAGAAATTG 1290  
QY 1116 GGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTT 1175  
Db 1291 GAGTCAGCTCCCACTGCTGCTCCCAAAATTTGATGAGGTATATGCCCGCTCTTACTGCTT 1350  
QY 1176 TTCTGTGACTTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTTCAGAGCTGATTTCTG 1235  
Db 1351 CTCAGCCAACTACATCTACCACTTGTGTTGTAAGGTTTCAAAATTCACAGGAGACTTG 1410  
QY 1236 GGAGCACATCCATTTCAATTTGCAAGATCCAGGGCAGCGACCCGCGCTGGACTTTGGGCTA 1295  
Db 1411 GCCCCAAATACACTTTGAAAAAGAGTGGGGAATAGCAGCATAGCCTGTCTCTTGGCTA 1470  
QY 1296 CATGCTGACTGACCAACATGATCCAGCTGAGCAACATTG 1338  
Db 1471 CATGCTCAGCCTGACCAACAGATCCAGCTGAAAGCCCTCTG 1513

RESULT 9  
US-10-107-660-3  
; Sequence 3, Application US/10107660  
; Patent No. 6780977  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna-Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE  
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS  
; FILE REFERENCE: 9598-066  
; CURRENT APPLICATION NUMBER: US/10/107,660  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: US/09/240,639  
; PRIOR FILING DATE: 1998-01-29  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
US-10-107-660-3

Query Match 21.3%; Score 291; DB 4; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 3.6e-86;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

QY	48	CCAGAACAAAGCATTCGCCAGAAACCTTAAGTATGGATTGTGCTCGATGCGGTCTTC	107
DB	220	CAAGCAAGAGGTCCCTCCCTCCAGACTGAAGTATGTATTTGCTGGATGCCGGGTCTTC	279
QY	108	TCACACAAAGTTTATACATCTATAAGTGGCCAGACAGAAAGGAGAAATGACACAGGCGGTGT	167
DB	280	AAGAACCAACAGCTAGCTGTATCAATGGCCAGCAGAAAGAGAAATATACCGAGTGT	339
QY	168	GCATCAAGTAGAAGATGACAGGTTTAAAGTCTCGAAATCTCAAAATTTGTTCAAGAAAT	227
DB	340	CAGTCAAAACCTTCAAAATGATGTGAAGGCTCTGGAATCTCCAGCTATGGAATAACCC	399
QY	228	AAATGAATAGGATTTACCTGACTGATTCATGGAAGAGCTAGGGAAGTATTCAGAG	287
DB	400	CCAAGATGTCCCAGAGCCTTTGAGGAGTGTATGCAAAAAGTCAAGGGCAGGTTCCATC	459
QY	288	GTCCCAGCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATCGGTTGCTCAG	347
DB	460	CCACCTCCAGGATCCACCCCATTTACCTGGGAGCCACGGCTGGGATGGCTTGTCTAG	519
QY	348	GATGGAAGTGAAGAGTTGGCAGACAGGTTTCTGGATGTGGTGGAGAGAGCCTCAGAA	407
DB	520	GTGCAAAATGAAACAGCAGCTAATGAAGTCTTGAAGCATCAAAAGCTACTTCAAGTC	579
QY	408	CTACCCCTTGACTTCAGGGTCCAGGATCATTAATCTGGCCAGAGAGAGGTCCTATGG	467
DB	580	CCAGCCCTTTGACTTTAGGGGTGCTCAAAATCATTTCTGGGCAAGAGAGGGGTATATGG	639
QY	468	CTGGATTACTATCAACTATCTGCTGGCAAAATTCAGTCAGAAAAAAGGTGGTTTCAGCAT	527
DB	640	ATGGATTACAGCCAACTATTATTAATGGAAATTTCTGGAGAGAACTGTGGCAGATGTG	699
QY	528	AGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTC	587
DB	700	GGTGC-----ACCCGATGGAGTGAACACAGGGTGCCTGGACTTAGGTGGTGCCTC	753
QY	588	TACACAGTCACTTTGTACCCCAAAACCAAGACTATCGAGTCCCAGATAATGCTCTGCA	647
DB	754	CACCCAAATATCTTGTGGCAGAGAGAGATGGATCTGAAACACAGCGACATCATGCA	813
QY	648	ATTTCGCTCTATGGCAAGGACTACAAATGTCTACACACATAGCTTCTTTGTCTATGGAA	707

DB	814	GGTGTCCCTGTATGCTAGCTATACACGCTTACACACACACAGCTTCCAGTGTCTATGGCG	873
QY	708	GGATCAGGCATCTCGCAGAAACTGGCCAGAGACATTGAGGTGCAAGTAATGAAA---T	764
DB	874	GAATGAGGCTGAGAAAGTTTCTGGCAATGCTCTCGAAGAAATCTCTCTACCAAAACCA	933
QY	765	TCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAGGTAGTGAACGTAAAGTGACCTTTA	824
DB	934	TCACACCAATCCCTGTACCTCGGATATAGCATCAGCTTCCACATGGGCGCATGTATT	993
QY	825	CAAGACCCCTGCAC-----CAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTGA	878
DB	994	TGATAGCCTGTGCACTGTGGACCCAGAGGCCAGAAAGTTATAACCCCAATGATGTATCAC	1053
QY	879	AATCAGGGTATTGAAACTATCAACAATGCCATCAAGCATCCTCGAGCTCTTCAACAC	938
DB	1054	TTTGAAGGAACCTGGGACCCCATCTCTGTGAAGAGAGGTGGCTTCCATATTTGACTT	1113
QY	939	CAGTTACTGCCCTTACTCCAG---TGTCCTTCAATGGGATTTTCTTTGCCACCACTCCA	995
DB	1114	CAAGCTTGGCATGATCAAGAAACCTGTCTTTTGTGGGTTTATCAGCCAAAGATTAA	1173
QY	996	GGGGATTTGGGCAATTTTTCAGCTTTTACCTTTGTGATGAAGTTTAAACTTGACATC	1055
DB	1174	AGGGCAATTTGTGGCTTTTGCAGGATTTCTACTACACAGCCAGTGTCTTAAATCT---TTC	1230
QY	1056	AGAGAAATCTCTCAGGAAAGGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCTTG	1115
DB	1231	AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTTGGAAATTTCTGCTCAGAAATG	1290
QY	1116	GGAGGAGATAAAAACATCTTACGCTGGAGTAAAGAGAGTACCTGAGTGAATATCTGCTT	1175
DB	1291	GAGTCAGCTCCACCTGCTGCTCCCAAAATTTGATGAGGTATATGCCGCTCTTACTGCTT	1350
QY	1176	TTCTGGTACCTACATCTCTCCCTCTCTGCAAGGCTATCATTTTACAGCTGATTTCTTG	1235
DB	1351	CTCAGCAACTACATCTACCACTTGTGTTGAAACGTTTACAAATTCACAGAGGAGACTTG	1410
QY	1236	GGAGCACATCCATTTTCATTTGGCAAGATCCAGGGCAGGAGCGGCTGGACTTTGGGCTA	1295
DB	1411	GCCCCAAATACACTTTGAAAAAGAGTGGGAATAGCAGCATAGCCTGTGCTCTCTGGCTA	1470
QY	1296	CATGCTGAACCTGACCAACATGATCCAGCTGAGCAACCATTTG 1338	
DB	1471	CATGCTCAGCTGACCAACAGATCCAGCTGAAAGCCCTCTG 1513	

## RESULT 10

US-10-107-576-3  
; Sequence 3, Application US/10107576  
; Patent No. 6783959  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; TITLE OF INVENTION: ACIDS  
; FILE REFERENCE: 28110/36120H  
; CURRENT APPLICATION NUMBER: US/10/107,576  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
; OTHER INFORMATION:  
US-10-107-576-3

Query Match		21.3%;	Score 291;	DB 4;	Length 2797;
Best Local Similarity		54.3%;	Pred. No. 3.6e-86;		
Matches 707;		Conservative 0;	Mismatches 575;	Indels 21;	Gaps 5;
QY	48	CCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGATTGTGCTGGATGCGGTTCTTTC	107		
DB	220	CAAGCAAGAGTCTCCCTCCAGGACTGAAGTATGTTGTGTGATGCCGGTCTTTC	279		
QY	108	TCACACAAGTTTATACATCTATTAAGTGGCCAGAGAAAAGGAGAATGACACAGGCGTGT	167		
DB	280	AAGAACCAACAGTCTACGTGTATCAATGGCCAGCAGAAAAGAGAATAATACCGGAGTGT	339		
QY	168	GCATCAAGTAGAAGATGAGGTTAAAGTCTGGAATCTCAAAATTTGTTTCAGAAAT	227		
DB	340	CAGTCAAACTTCAAAATGAGTGTGAAGGCTCTGGAATCTCCAGCTATGGAATAACCC	399		
QY	228	AAATGAATAGGCATTATCTGACTGATTCATGGAAGAGCTAGGGAAGTATCCCAAG	287		
DB	400	CCAAGATGTCCCAGAGCCTTTGAGGAGTGTATGCANAAAGTCAAGGGCAGTTCCATC	459		
QY	288	GTCCCAGACCAAGACACCCGTTTACCTGGGAGCCACGGCAGCATGCGGTTGCTCAG	347		
DB	460	CCACCTCCACGGATCACCCCATTCACCTGGAGCCACGGCTGGGATGCGTGTGCTGAG	519		
QY	348	GATGGAAGTGAAGAGTTGGCAGACAGGTTCTGGATGTGGTGGAGAGGCTCAGCA	407		
DB	520	GTTCGAAAATGAACACAGCAGCTAATGAAGTCTTGAAGCATCCAAAGCTACTTCAAGTC	579		
QY	408	CTACCCCTTTGACTTCCAGGGTGCAGGATCAATCTGSCCAAGAGGAGTGCCATGG	467		
DB	580	CCAGCCCTTTGACTTTAGGGTGTCTCAATCAATTTCTGGCAAGAAGAGGGGTATATGG	639		
QY	468	CTGGATTACTATCAACTATCTCTGGGCAAAATTCAGTCCAGAAAACAAGTGTTTCAGCAT	527		
DB	640	ATGGATTACAGCAACTATTAATGGAAATTTCTCTGGAGAGAACCCTGTGSCACATGTG	699		
QY	528	AGTCCCATATGAACCAATATCAGGAACCTTTGGAGCTTTGGAGCTTTGGGGAGCCTC	587		
DB	700	GGTGC-----ACCCECATGGAGTGGAAACCAACCGGGTGCCTGGAGCTTAGTGTGGCTC	753		
QY	588	TACACAAGTCACTTTTGTATACCCAAACCCAGACTATCGAGTCCCCAGATAATGCTCGCA	647		
DB	754	CACCCAAATATCTCTGTGGCAGGAGAGAAAGATGATCTGAACACACGGGACATCATGCA	813		
QY	648	ATTTCCCTCTATGGCAAGGACTACAATGTCTTACACACATAGCTTCTTGTGCTATGGAA	707		
DB	814	GGTGTCCCTGTATGCTACGTATACAGCTCTACACACAGCTTCCAGTGTATGGCG	873		
QY	708	GGATCAGGCACTCTGGCAGAACTGGCCAGGACATTCAGGTTGCAAGTAATGAAA---T	764		
DB	874	GAAAGGGCTGAGAAAGATTTCTGGCAATGCTCCTGCAGAAATTCCTTACCAGAAACCA	933		
QY	765	TCTCAGGGACCCATCTTTATCTCTGGATATAGAAGGTAGTGAAGTAAAGTACCTTTA	824		
DB	934	TCTCACAATCTCTTACCCTCGGGATATAGCATCAGCTTCACCATGGGCCATGTAT	993		
QY	825	CAAGACCCCTGTCAC-----CAAGAGATTTGAGATGACTCTTCCATTCAGCAGTTGA	878		
DB	994	TGATAGCCTGTGCACTGTGGACACAGGCCAGAAAGTTATAACCCCAATGATCATCAC	1053		
QY	879	AATCAGGGTATGGAACATATCAACAATGCCATCAAGCATCTCGGAGCTTCTCAACAC	938		
DB	1054	TTTTGAAGAACTGGGGACCCATCTCTGTGTAAAGGAGGTGGCTTCCATATTTGACTT	1113		
QY	939	CAGTTACTGCCCTTACTCCAG---TGTGCCCTTCAATGGATTTTCTTGCCACCCTCCA	995		
DB	1114	CAAAGCTTGCCATGATCAAGAAACCTGTCTTTTGTATGGGTTTATACGCCAAAGATPAA	1173		
QY	996	GGGGGATTTGGGGCATTTTTCAGCTTTTATCTTTTGTGTGAAGTTTAAAACTTCGACATC	1055		
DB	1174	AGGGCCATTTGTGGCTTTTGGAGGATTTCTACTACACGCCAGTGTCTTAATCT---TTC	1230		
QY	1056	AGAGAAAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTG	1115		

DB	1231	AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTTGGAAATTTCTGCTCAGAAATG	1290		
QY	1116	GGAGGAGATAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTT	1175		
DB	1291	GAGTCAGCTCCACCTGCTGCTCCCAAAATTTGATGAGGTATATGCCGCTCTTACTGCTT	1350		
QY	1176	TTCTGGTACCTACATTTCTCCCTCTTCTGCAAGGCTATCATTTTTCACAGCTGATTCCTG	1235		
DB	1351	CTCAGCCAACTACATCTACCACCTTGTGTTGTAACGTTTACAAATTCACAGAGGAGACTT	1410		
QY	1236	GGAGCACATCCATTTTCATTTGGCAAGATCCAGGGCAGCAGCCGGCTGGACTTTGGGCTA	1295		
DB	1411	GCCCCAAAATACACTTTTGAAGGAAGTGGGGAATAGCAGCATAGCTTGGTCTCTTGGCTA	1470		
QY	1296	CATGCTGAACCTGACCAACATGATCCAGCTTGAGCAACCATTTG	1338		
DB	1471	CATGCTAGCCTGACCAACCAACAGATCCAGCTGGAAGCCCTCTG	1513		

RESULT 11

US-09-905-732B-3  
; Sequence 3, Application US/09905732B  
; Patent No. 6787328  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; FILE REFERENCE: 28110/36120B  
; CURRENT APPLICATION NUMBER: US/09/905,732B  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
; OTHER INFORMATION:  
US-09-905-732B-3

Query Match 21.3%; Score 291; DB 4; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 3.6e-86;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

QY	48	CCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTTGTGCTGGATGCGGTTCTTTC	107		
DB	220	CAAGCAAGAGTCTCCCTCCAGGACTGAAGTATGTTGTGTTGATGCCGGTCTTC	279		
QY	108	TCACACAAGTTTATACATCTTATTAAGTGGCCAGCAGAAAAGGAGAATGACACAGGCGTGT	167		
DB	280	AAGAACCAACAGTCTACGTGTATCAATGCCAGCAGAAAAGAGAATAATACCGGAGTGT	339		
QY	168	GCATCAAGTAGAAGAATGAGGTTAAAGTCTCGGAATCTCAAAATTTGTTTCAGAAAT	227		
DB	340	CAGTCAAACTTCAAAATGATGTGGAAGGCTCTGGAATCTCCAGCTATGGAATAACCC	399		
QY	228	AAATGAATAGGCATTTTACCTGACTGATTTGCATGGAAAGAGCTAGGGAAGTGAATTTCCAAG	287		
DB	400	CCAAGATGTCCCAGAGCCTTTGAGGAGTGTATGCANAAAGTCAAGGGCAGGTTCCATC	459		
QY	288	GTCCCAGACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGCATGCGGTTGCTCAG	347		
DB	460	CCACCTCCAGGATCCACCCCATTCACCTGGGAGCCACGGCTGGGATGCGCTGCTGAG	519		
QY	348	GATGGAAGTGAAGAGTTGGCAGACAGGTTCTGGATGTGGTGGAGAGGAGCCCTCAGCA	407		
DB	520	GTTCGAAAATGAACACAGCAGCTAATGAAGTCTTTGAAAGCATCCAAAGCTACTTCAAGTC	579		







```
QY      879  AATCCAGGATTTGGAAACTATCAACAATGCCATCAAGCATCTCTGAGCTCTTCAACAC  938
Db      1054  TTTTGAAGGAATCGGGACCCATCTCTGTGTGAAGGAAGGTGGCTTCCATATTTGACTT  1113
QY      939  CAGTTACTGCTTACTCTCCAG---TGTGCTTCAATGGATTTCTTCCACCACTCCA  995
Db      1114  CAAAGCTTGCCATGATCAAGAACCCTGTCTTTTGTATGGGTTTATCAGCCAAAGATTAA  1173
QY      996  GGGGATTTTGGGCATTTTACGCTTTTACTTTGTGTGAAGTTTAACTTGACATC  1055
Db      1174  AGGGCAATTTGGCTTTTTCAGGATTTCTACTACAGCCAGCTGCTTTAAATCT---TTC  1230
QY      1056  AGAGAAAGTCTCTCAGAAAAAGGTGACTGAGATGATGAATAAGTTCTGTGCTCAGCCTTG  1115
Db      1231  AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTTGAATTTCTGTCTCAGAAATTG  1290
QY      1116  GGAGGAGATAAACAATCTTACGCTGGAGTAAGGAGAAGTACCTGAGTGAATACTGCTT  1175
Db      1291  GAGTCAGCTCCCACTGCTCTCCCAAAATTTGATGAGGTATATGCCCGCTCTTACTGCTT  1350
QY      1176  TTCTGTACTACATTTCTCTCTCTCTCTGCAAGCTATCATTTTACAGCTGATTTCCTG  1235
Db      1351  CTCAGCAACTACTACTACACTTGTGTGTGAAGGTTACAAATTCACAGAGAGACTTG  1410
QY      1236  GGAGCACATCCATTTTCAITGGCAAGATCCAGGCGACGCGGCTGGACTTTGGGCTA  1295
Db      1411  GCCCAAAATACACTTTGAAAAAGAGTGGGGAATAGCAGCATAGCTGTGCTCTTTGGCTA  1470
QY      1296  CATGCTGAACCTGACCAACATATCCAGCTCAGCTGAGCAACCATTTG  1338
Db      1471  CATGCTCAGCTGACCAACCATATCCAGCTGAAAGCCCTCTG  1513
```

## RESULT 13

```
US-09-949-016-178
; Sequence 178, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 2797
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-178
```

```
Query Match      21.3%; Score 291; DB 4; Length 2797;
Best Local Similarity 54.3%; Pred. No. 3.6e-86;
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;
```

```
QY      48  CCAGAACAAAGCATTTCCAGAAAACGTTAAGTATCGGATTTGCTGGATCGGGTTCTTC  107
Db      220  CAAAGCAAGAGTCTCTCCCTCCAGGACTGAAGTATGGTATTTGCTGGATCGGGTCTTC  279
QY      108  TCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGATGACAGAGGCTGGT  167
Db      280  AAGAACCAAGCTTACGTGTATCAATGCGCAGCAGAAAAGAGATATATACCGGAGTGGT  339
QY      168  GCATCAAGTAGAAGAAATCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTCAGAAAGT  227
```

```
Db      340  CAGTCAAAACCTTTCAAATGTAGTGTGAAGGCTCTGGAATCTCCAGCTATGGAATAACCC  399
QY      228  AATGAAATAGGCAATTTTACCTGACTGATTGCATGAAAGAGCTAGGGAAGTATGTTCCAAG  287
Db      400  CCAAGATGTCCCAGAGCTTTTGAGGAGTGTATGCAAAAAGTCAAGGGCAGGTTCCATC  459
QY      288  GTCCAGACCAAGAGACACCCGTTTACTGAGAGCCACGGCAGGAGATGCGGTGCTCAG  347
Db      460  CCACCTCCACGGATCCACCCCATTTACCTGGAGGCCACGGCTGGATGCGCTTGTCTGAG  519
QY      348  GATGAAAGTGAAGATTTGGCAGACAGGGTCTCTGATGTGGTGGAGAGAGCCTCAGCAA  407
Db      520  GTTGCAAAATGAACAAGCAGCTAATGAAGTCTCTGAAAAGTCCAAAGCTACTTCAAGTC  579
QY      408  CTACCCCTTTGACTTTCCAGGGTGCAGGATCATTTACTGCCCAGAGGAAGGTGCTTATGG  467
Db      580  CCAGCCCTTTGACTTTAGGGGTGCTCAATCATTTCTGGCNAAGAAAGGGGTATATGG  639
QY      468  CTGGAATTACTATCAACTATCTGTGGGCAAAATTTAGTCAAGAAAACAAGGTGTTCAAGAT  527
Db      640  ATGGAATTACAGCAACTATTTAAATGGGAAATTTCTCTGGAGAAGAACCTGTGCGCATGTG  699
QY      528  AGTCCCATATGAACCAATATATCAGGAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTC  587
Db      700  GGTGCTGCTGATGGCTACGTATACACGCTCTACACACACAGCTTCCAGTGTATGGCG  753
QY      588  TACACAGTCACTTTTGTACCCCAAAACACAGACTATCGAGTCCCAGATAATGCTCTGCA  647
Db      754  CACCAAAATATCTTCTGTGGCAGGAGAGAAGATGGATCTGAACACACAGGACATCATGCA  813
QY      648  ATTTGCGCTCTATGGCAAGGACTCAATGTCTTACACATAGCTTTCTGTGCTATGGGAA  707
Db      814  GGTGCTGCTGATGGCTACGTATACACGCTCTACACACACAGCTTCCAGTGTATGGCG  873
QY      708  GGATCAGGCACTCTGGGAGAAACCTGGCCAAAGCAATTCAGGTTGCAAGTAAATGAA---T  764
Db      874  GAATGAGGCTGAGAAGAAAGTTTCTGGCAATGCTCTCTGCAGAAATTCCTCATCAAAAACA  933
QY      765  TCTCAGGACCCATGCTTTTCACTCTGGATATAAGAAAGGTAGTGAACGTAAAGTGAACCTTTA  824
Db      934  TCTCACCNAATCCCTGTTTACCCTCGGATTTATAGCATCAGCTTCACTATGGGCCATGTATT  993
QY      825  CAAGACCCCTTGCACT-----CAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTGA  878
Db      994  TGATAGCTGTGCTGCTGAGGACGAGGCCAGAAAGTTATAACCCCAATGATGTATCATCAC  1053
QY      879  AATCCAGGATTTGGAACACTATCAACATGCCATCAAGCATCTGGAGCTCTTCAACAC  938
Db      1054  TTTTGAAGGAACTGGGGACCCATCTCTGTGTGAAGGAGAAGGTGGCTTCCATATTTGACTT  1113
QY      939  CAGTTACTGCTTACTCTCCAG---TGTGCTTCAATGGGATTTTCTTGGCCACCACTCCA  995
Db      1114  CAAAGCTTGCCATGATCAAGAAAACCTGTTCTTTTGTATGGGTTTATCAGCCAAAGATTAA  1173
QY      996  GGGGATTTTGGGCAATTTTCAAGCTTTTACTTTTGTGATGAAGTTTAACTTCAAGATC  1055
Db      1174  AGGGCCATTTGTGGCTTTTTCAGGATTTCTACTACACAGCCAGTGTCTTTAAATCT---TTC  1230
QY      1056  AGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAATAAGTTCTGTGCTCAGCCTTG  1115
Db      1231  AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTTGGAAATTTCTGCTCAGCAATTTG  1290
QY      1116  GGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTT  1175
Db      1291  GAGTCAGCTCCCACTGCTGCTCCCAAAATTTGATGAGGTATATGCCCGCTCTTACTGCTT  1350
QY      1176  TTCTGGTACCTTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTCAAGCTGATTCCTG  1235
Db      1351  CTCAGCAACTACTACTACCACTTGTGTGTGAACGTTACAAATTCACAGAGGAGACTTG  1410
QY      1236  GGAGCACATCATTTTCAITGGCAAGATCCAGGCGACGCGGCTGGACTTTGGGCTA  1295
Db      1411  GCCCAAAATACACTTTGAAAAAGAGTGGGGAATAGCAGCATAGCTGTGCTCTTTGGCTA  1470
```



```
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(46885)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13848

Query Match      19.8%; Score 270.2; DB 4; Length 46885;
Best Local Similarity 98.9%; Pred. No. 2.8e-78;
Matches 272; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      741 CATTGAGGTGCAAGTAATGAATCTCAGGGACCCATGCTTTTCATCCTGGATATAAGAA 800
Db      26315 CATTGAGGTGCAAGTAATGAATCTCAGGGACCCATGCTTTTCATCCTGGATATAAGAA 26374

QY      801 GGTAGTGAACGTAAAGTGACCTTTTACAAGACCCCTGCACCAAGAGATTTGAGATGACTCT 860
Db      26375 GGTAGTGAACGTAAAGTGACCTTTTACAAGACCCCTGCACCAAGAGATTTGAGATGACTCT 26434

QY      861 TCCATTCCAGCAGTTTGAATCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCAT 920
Db      26435 TCCATTCCAGCAGTTTGAATCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCAT 26494

QY      921 CTGGAGCTCTTCAACACACAGTTACTGCCCTTACTCCCAAGTGTGCCTTCAATGGGATTTT 980
Db      26495 CTGGAGCTCTTCAACACACAGTTACTGCCCTTACTCCCAAGTGTGCCTTCAATGGGATTTT 26554

QY      981 CTTGCCACCACCTCCAGGGGGATTTTGGGGCATTTT 1015
Db      26555 CTTGCCACCACCTCCAGGGGGATTTTGGGGTAAGTT 26589
```

Search completed: September 21, 2005, 23:30:30  
Job time : 251.55 secs

**THIS PAGE BLANK (USPTO)**

**THIS PAGE BLANK (USPTO)**



; NAME/KEY: CDS		; LOCATION: (1)..(1362)	
US-09-835-147-5			
Query Match		100.0%; Score 1365; DB 9; Length 1365;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 1365; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	GCACCTACTTCAAGTGTCTACAAAGAAACACACAGCTAACTAGTTCAACCCAGCAACAAAGCA	60
Db	1	GCACCTACTTCAAGTGTCTACAAAGAAACACACAGCTAACTAGTTCAACCCAGCAACAAAGCA	60
Qy	61	TTGCCAGAAACCTTAAGTATGGATTGTCTGGATGCGGTTCTCTCACACAAGTTTA	120
Db	61	TTGCCAGAAACCTTAAGTATGGATTGTCTGGATGCGGTTCTCTCACACAAGTTTA	120
Qy	121	TACATCTATAAGTGGCCAGCAGAGAAAGGAGAATGACACAGCGCTGGTGCATCAAGTAGAA	180
Db	121	TACATCTATAAGTGGCCAGCAGAGAAAGGAGAATGACACAGCGCTGGTGCATCAAGTAGAA	180
Qy	181	GAATGACAGGGTTAAGGTCCTGGAATCTCAAAATTTTTCAGAAAAGTAATGAATAGGC	240
Db	181	GAATGACAGGGTTAAGGTCCTGGAATCTCAAAATTTTTCAGAAAAGTAATGAATAGGC	240
Qy	241	ATTTACTGACTGATTTGCATGGAAGAGCTAGGGAAGTGAATCCAAAGTCCACAGACCAA	300
Db	241	ATTTACTGACTGATTTGCATGGAAGAGCTAGGGAAGTGAATCCAAAGTCCACAGACCAA	300
Qy	301	GAGACACCCCTTTACCTGGGAGCCAGCGGATCGGTTGCTCAGGATGGAAGTGAA	360
Db	301	GAGACACCCCTTTACCTGGGAGCCAGCGGATCGGTTGCTCAGGATGGAAGTGAA	360
Qy	361	GAGTGGCAGACAGGGTTCTGGATGTGGTGGAGGAGCCCTCAGAACCTACCCCTTTGAC	420
Db	361	GAGTGGCAGACAGGGTTCTGGATGTGGTGGAGGAGCCCTCAGAACCTACCCCTTTGAC	420
Qy	421	TTCCAGGTGCCAGGATCAATTAAGTCCCAAGAGAGGAGTGCCTATCGCTGGATTACTATC	480
Db	421	TTCCAGGTGCCAGGATCAATTAAGTCCCAAGAGAGGAGTGCCTATCGCTGGATTACTATC	480
Qy	481	AACATATCTGCTGGGCAAAATTCAGTCAGAAAAACAAAGGTGGTTTCAGCATAGTCCCATATGAA	540
Db	481	AACATATCTGCTGGGCAAAATTCAGTCAGAAAAACAAAGGTGGTTTCAGCATAGTCCCATATGAA	540
Qy	541	ACCAATAATCAGAAACCTTTGAGCTTTGGAACCTTTGGGGAGCCCTCTACACAAAGTCACT	600
Db	541	ACCAATAATCAGAAACCTTTGAGCTTTGGAACCTTTGGGGAGCCCTCTACACAAAGTCACT	600
Qy	601	TTTGTACCCCAACACAGACTATCGAGTCCCAAGATAATGCTCTGCAATTTGGCCCTCTAT	660
Db	601	TTTGTACCCCAACACAGACTATCGAGTCCCAAGATAATGCTCTGCAATTTGGCCCTCTAT	660
Qy	661	GGCAAGGACTACAATGTCTACACACATAGCTTCTGTGCTATGGGAAGGATCAGGCACCTC	720
Db	661	GGCAAGGACTACAATGTCTACACACATAGCTTCTGTGCTATGGGAAGGATCAGGCACCTC	720
Qy	721	TGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGGACCCATGC	780
Db	721	TGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGGACCCATGC	780
Qy	781	TTTTCATCCTGGATATAGAGAGTGTGCAAGTAAAGTGACCTTTTACAGACCCCTCGACC	840
Db	781	TTTTCATCCTGGATATAGAGAGTGTGCAAGTAAAGTGACCTTTTACAGAGCCCTCGACC	840
Qy	841	AAGAGATTTTGAGATGACTCTTCCATCTCCAGCAGTTTGAATCCAGGGTATTGGAAACTAT	900
Db	841	AAGAGATTTTGAGATGACTCTTCCATCTCCAGCAGTTTGAATCCAGGGTATTGGAAACTAT	900
Qy	901	CAACAATGCCATCAAGAGCTCTGGAGCTCTTCAACACCAAGTTACTGCCCCCTTACTCCAG	960
Db	901	CAACAATGCCATCAAGAGCTCTGGAGCTCTTCAACACCAAGTTACTGCCCCCTTACTCCAG	960
Qy	961	TGTGCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGATTTTGGGGCATTTTTCAGCT	1020
; NAME/KEY: CDS		; LOCATION: (1)..(1362)	
US-09-835-147-5			
Query Match		100.0%; Score 1365; DB 9; Length 1365;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 1365; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	GCACCTACTTCAAGTGTCTACAAAGAAACACACAGCTAACTAGTTCAACCCAGCAACAAAGCA	60
Db	1	GCACCTACTTCAAGTGTCTACAAAGAAACACACAGCTAACTAGTTCAACCCAGCAACAAAGCA	60
Qy	61	TTGCCAGAAACCTTAAGTATGGATTGTCTGGATGCGGTTCTCTCACACAAGTTTA	120
Db	61	TTGCCAGAAACCTTAAGTATGGATTGTCTGGATGCGGTTCTCTCACACAAGTTTA	120
Qy	121	TACATCTATAAGTGGCCAGCAGAGAAAGGAGAATGACACAGCGCTGGTGCATCAAGTAGAA	180
Db	121	TACATCTATAAGTGGCCAGCAGAGAAAGGAGAATGACACAGCGCTGGTGCATCAAGTAGAA	180
Qy	181	GAATGACAGGGTTAAGGTCCTGGAATCTCAAAATTTTTCAGAAAAGTAATGAATAGGC	240
Db	181	GAATGACAGGGTTAAGGTCCTGGAATCTCAAAATTTTTCAGAAAAGTAATGAATAGGC	240
Qy	241	ATTTACTGACTGATTTGCATGGAAGAGCTAGGGAAGTGAATCCAAAGTCCACAGACCAA	300
Db	241	ATTTACTGACTGATTTGCATGGAAGAGCTAGGGAAGTGAATCCAAAGTCCACAGACCAA	300
Qy	301	GAGACACCCCTTTACCTGGGAGCCAGCGGATCGGTTGCTCAGGATGGAAGTGAA	360
Db	301	GAGACACCCCTTTACCTGGGAGCCAGCGGATCGGTTGCTCAGGATGGAAGTGAA	360
Qy	361	GAGTGGCAGACAGGGTTCTGGATGTGGTGGAGGAGCCCTCAGAACCTACCCCTTTGAC	420
Db	361	GAGTGGCAGACAGGGTTCTGGATGTGGTGGAGGAGCCCTCAGAACCTACCCCTTTGAC	420
Qy	421	TTCCAGGTGCCAGGATCAATTAAGTCCCAAGAGAGGAGTGCCTATCGCTGGATTACTATC	480
Db	421	TTCCAGGTGCCAGGATCAATTAAGTCCCAAGAGAGGAGTGCCTATCGCTGGATTACTATC	480
Qy	481	AACATATCTGCTGGGCAAAATTCAGTCAGAAAAACAAAGGTGGTTTCAGCATAGTCCCATATGAA	540
Db	481	AACATATCTGCTGGGCAAAATTCAGTCAGAAAAACAAAGGTGGTTTCAGCATAGTCCCATATGAA	540
Qy	541	ACCAATAATCAGAAACCTTTGAGCTTTGGAACCTTTGGGGAGCCCTCTACACAAAGTCACT	600
Db	541	ACCAATAATCAGAAACCTTTGAGCTTTGGAACCTTTGGGGAGCCCTCTACACAAAGTCACT	600
Qy	601	TTTGTACCCCAACACAGACTATCGAGTCCCAAGATAATGCTCTGCAATTTGGCCCTCTAT	660
Db	601	TTTGTACCCCAACACAGACTATCGAGTCCCAAGATAATGCTCTGCAATTTGGCCCTCTAT	660
Qy	661	GGCAAGGACTACAATGTCTACACACATAGCTTCTGTGCTATGGGAAGGATCAGGCACCTC	720
Db	661	GGCAAGGACTACAATGTCTACACACATAGCTTCTGTGCTATGGGAAGGATCAGGCACCTC	720
Qy	721	TGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGGACCCATGC	780
Db	721	TGGCAGAAATCGGCCAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGGACCCATGC	780
Qy	781	TTTTCATCCTGGATATAGAGAGTGTGCAAGTAAAGTGACCTTTTACAGACCCCTCGACC	840
Db	781	TTTTCATCCTGGATATAGAGAGTGTGCAAGTAAAGTGACCTTTTACAGAGCCCTCGACC	840
Qy	841	AAGAGATTTTGAGATGACTCTTCCATCTCCAGCAGTTTGAATCCAGGGTATTGGAAACTAT	900
Db	841	AAGAGATTTTGAGATGACTCTTCCATCTCCAGCAGTTTGAATCCAGGGTATTGGAAACTAT	900
Qy	901	CAACAATGCCATCAAGAGCTCTGGAGCTCTTCAACACCAAGTTACTGCCCCCTTACTCCAG	960
Db	901	CAACAATGCCATCAAGAGCTCTGGAGCTCTTCAACACCAAGTTACTGCCCCCTTACTCCAG	960
Qy	961	TGTGCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGATTTTGGGGCATTTTTCAGCT	1020

RESULT 2  
US-09-835-147-7  
; Sequence 7, Application US/09835147  
; Patent No. US20020002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Maliszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 1437  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion  
; OTHER INFORMATION: construct of human CD39  
; NAME/KEY: CDS  
; LOCATION: (1)..(1434)  
US-09-835-147-7

Query Match 100.0%; Score 1365; DB 9; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCACCTACTTCAAGTGTCTACAAAGAAACACACAGCTAACTAGTTCAACCCAGCAACAAAGCA 60  
Db 73 GCACCTACTTCAAGTGTCTACAAAGAAACACACAGCTAACTAGTTCAACCCAGCAACAAAGCA 132  
Qy 61 TTGCCAGAAACCTTAAGTATGGATTGTGCTGGATGCGGGTTCTTCTCACACAAGTTTA 120  
Db 133 TTGCCAGAAACCTTAAGTATGGATTGTGCTGGATGCGGGTTCTTCTCACACAAGTTTA 192

QY 121 TACATCTATAAGTGGCCAGCAGAGAAAAGGAGAAATGACACAGGCGTGGTGCATCAAGTAGAA 180  
DB 193 TACATCTATAAGTGGCCAGCAGAGAAAAGGAGAAATGACACAGGCGTGGTGCATCAAGTAGAA 252  
QY 181 GAATGACAGGTTAAAGGTCCTCGAATCTCAAAATTTGTTTCAGAAAGTAAATGAATAGGC 240  
DB 253 GAATGACAGGTTAAAGGTCCTCGAATCTCAAAATTTGTTTCAGAAAGTAAATGAATAGGC 312  
QY 241 ATTTACCTGACTGATTTGCATGAAAGAGCTAGGGAAGTGATTCGAAGTCCAGAGTCCAGCACCAA 300  
DB 313 ATTTACCTGACTGATTTGCATGAAAGAGCTAGGGAAGTGATTCGAAGTCCAGAGTCCAGCACCAA 372  
QY 301 GAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGTTGCTCAGGATGGAAGTGA 360  
DB 373 GAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGTTGCTCAGGATGGAAGTGA 432  
QY 361 GAGTTGGCAGACAGGTTCTGGATGTTGGAGAGAGGCGCTCAGCACTACCCCTTGC 420  
DB 433 GAGTTGGCAGACAGGTTCTGGATGTTGGAGAGAGGCGCTCAGCACTACCCCTTGC 492  
QY 421 TTCCAGGTCGCCAGGATCACTTACTTGCCCAAGGAAGTGCCCTATGCGCTGGATTACTATC 480  
DB 493 TTCCAGGTCGCCAGGATCACTTACTTGCCCAAGGAAGTGCCCTATGCGCTGGATTACTATC 552  
QY 481 AACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGTTTCAGCATAGTCCCATATGAA 540  
DB 553 AACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGTTTCAGCATAGTCCCATATGAA 612  
QY 541 ACCAATATCAGAAACCTTTGGAGCTTTGGAGCTTTGGAGCTTTGGAGAGCTTACACAACTACT 600  
DB 613 ACCAATATCAGAAACCTTTGGAGCTTTGGAGCTTTGGAGAGCTTACACAACTACT 672  
QY 601 TTGTACCCCAAAACAGACTATCAGTCCCGAGATAATGCTCTGCAATTTGCGCTCTAT 660  
DB 673 TTGTACCCCAAAACAGACTATCAGTCCCGAGATAATGCTCTGCAATTTGCGCTCTAT 732  
QY 661 GCGAAGGACTACAATGTGTACACATAGCTTCTTGTGCTATGGAAGGATCAGGACCTC 720  
DB 733 GCGAAGGACTACAATGTGTACACATAGCTTCTTGTGCTATGGAAGGATCAGGACCTC 792  
QY 721 TGGCAGAACTGCGCAAGACATTCAGGTGCAAGTAATGAATTTCTCAGGGACCCATGC 780  
DB 793 TGGCAGAACTGCGCAAGACATTCAGGTGCAAGTAATGAATTTCTCAGGGACCCATGC 852  
QY 781 TTTCATCTGGATATAAGAGGTAGTGAACGTAAAGTGACCTTTTCAAGACCCCTGCACC 840  
DB 853 TTTCATCTGGATATAAGAGGTAGTGAACGTAAAGTGACCTTTTCAAGACCCCTGCACC 912  
QY 841 AAGAGATTGAGATGACTCTTCCATTCAGCAGATTGGAATCCAGGGTATTGGAAACTAT 900  
DB 913 AAGAGATTGAGATGACTCTTCCATTCAGCAGATTGGAATCCAGGGTATTGGAAACTAT 972  
QY 901 CAACAATGCCATCAAGATCTCGAGCTCTTCAACACAGTTACTGCGCTTACTCCAG 960  
DB 973 CAACAATGCCATCAAGATCTCGAGCTCTTCAACACAGTTACTGCGCTTACTCCAG 1032  
QY 961 TGTGCTTTCAATGGGATTTCTTGCACACACTCCAGGGGGATTTTGGGGCATTTTTCAGCT 1020  
DB 1033 TGTGCTTTCAATGGGATTTCTTGCACACACTCCAGGGGGATTTTGGGGCATTTTTCAGCT 1092  
QY 1021 TTTTACTTTGTGATGAAGTTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAAAGGTG 1080  
DB 1093 TTTTACTTTGTGATGAAGTTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAAAGGTG 1152  
QY 1081 ACTGAGATGAAAAAGTTCTGCTCAGCCCTGGGAGGAGATAAAAACATCTTACGCT 1140  
DB 1153 ACTGAGATGAAAAAGTTCTGCTCAGCCCTGGGAGGAGATAAAAACATCTTACGCT 1212  
QY 1141 GGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTTCTGTTACCTACTACTCTCCCTC 1200  
DB 1213 GGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTTCTGTTACCTACTACTCTCCCTC 1272

QY 1201 CTTTGTCAAGGCTATCAITTTTCACTGATTCCTGGAGACATCAATTTCAATTGSCAAG 1260  
DB 1273 CTTTGTCAAGGCTATCAITTTTCACTGATTCCTGGAGACATCAATTTCAATTGSCAAG 1332  
QY 1261 ATCCAGGCGCAGCGCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1320  
DB 1333 ATCCAGGCGCAGCGCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1392  
QY 1321 CCAGCTGAGCAACCACTTGTCCACACCTCTCTCCCACTCCACCTAA 1365  
DB 1393 CCAGCTGAGCAACCACTTGTCCACACCTCTCTCCCACTCCACCTAA 1437

RESULT 3  
US-09-835-147-25  
; Sequence 25, Application US/09835147  
; Patent No. US2002002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Maliszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 1464  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1461)  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion  
; OTHER INFORMATION: construct of human CD39  
US-09-835-147-25

Query Match 97.3%; Score 1328; DB 9; Length 1464;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1334; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 11 CAAGTTCTACAAAGAAAACACAGCTAACTAGTTCAACCCAGAACAAAGCATTTGCCAGAAA 70  
DB 110 CTAGTTCAGGAGACTACAAAGATGACGATGACAAACCAGAACAAAGCATTTGCCAGAAA 169  
QY 71 ACGTTAAGTATGGGATTTGTCTGGATGCGGTTCTTCTCACACAAGTTTATACATCTATA 130  
DB 170 ACGTTAAGTATGGGATTTGTCTGGATGCGGTTCTTCTCACACAAGTTTATACATCTATA 229  
QY 131 AGTGGCAGCAGAAAAGGAGAAATGACACAGCGGTGGTGCATCAAGTAGAAGATGACGGG 190  
DB 230 AGTGGCAGCAGAAAAGGAGAAATGACACAGCGGTGGTGCATCAAGTAGAAGATGACGGG 289  
QY 191 TTAAGGTCTCGGAATCTCAAAATTTGTTTCAGAAAGTAAATGAAATAGGCATTTTACCTGA 250  
DB 290 TTAAGGTCTCGGAATCTCAAAATTTGTTTCAGAAAGTAAATGAAATAGGCATTTTACCTGA 349  
QY 251 CTGATTGCATGGAAGAGCTAGGGAAGTGAATTCGAAGTCCAGCACCAAGAGACACCCG 310  
DB 350 CTGATTGCATGGAAGAGCTAGGGAAGTGAATTCGAAGTCCAGCACCAAGAGACACCCG 409  
QY 311 TTTTACCTGGGAGCCAGCGCAGGCAATGCGGTTGCTCAGAGTGGAAAGTGAAGTTGGCAG 370

Db 410 TTTTACCTGGAGCACGGCAGGCATGCGGTGCTCAGAGTGAAGAGTTGGCAG 469  
QY 371 ACAGGGTTCTGGATGTGGTGGAGAGGCTCAGCAACTACCCCTTTGACTTCCAGGGTG 430  
Db 470 ACAGGGTTCTGGATGTGGTGGAGAGGCTCAGCAACTACCCCTTTGACTTCCAGGGTG 529  
QY 431 CCAGGATCATTTACTGGCCAAAGAGGAGTGCCTATGGCTGGATTACTATCAACTATCTGC 490  
Db 530 CCAGGATCATTTACTGGCCAAAGAGGAGTGCCTATGGCTGGATTACTATCAACTATCTGC 589  
QY 491 TGGGCAAAATTCAGTCAGAAACAAAGTGGTTCAGCATAGTCCCATATGAACCAATAATC 550  
Db 590 TGGGCAAAATTCAGTCAGAAACAAAGTGGTTCAGCATAGTCCCATATGAACCAATAATC 649  
QY 551 AGAAACCTTTGAGCTTTGGACCTTTGGGGAGCCTCTACAAAGTCACTTTTGTAACCC 610  
Db 650 AGAAACCTTTGAGCTTTGGACCTTTGGGGAGCCTCTACAAAGTCACTTTTGTAACCC 709  
QY 611 AAAACAGACTATCGAGTCCCCAGATAATGCTCTGCAATTTGCGCTCTATGGCAAGGACT 670  
Db 710 AAAACAGACTATCGAGTCCCCAGATAATGCTCTGCAATTTGCGCTCTATGGCAAGGACT 769  
QY 671 ACAATGTCTACACATAGCTTTCTGTGCTATGGGAAGGATCAGGCACCTCTGGCAGAAAC 730  
Db 770 ACAATGTCTACACATAGCTTTCTGTGCTATGGGAAGGATCAGGCACCTCTGGCAGAAAC 829  
QY 731 TGGCCCAAGGACATTCAGTTGCAAGTAAATGAATTTCTCAGGACCCATGCTTTTCCTTG 790  
Db 830 TGGCCCAAGGACATTCAGTTGCAAGTAAATGAATTTCTCAGGAGCCATGCTTTTCCTTG 889  
QY 791 GATATAAGAGGTAGTGAACGTAAAGTGACCTTTTACAAGACCCCTCGCAACAGAGATTG 850  
Db 890 GATATAAGAGGTAGTGAACGTAAAGTGACCTTTTACAAGACCCCTCGCAACAGAGATTG 949  
QY 851 AGATGACTCTTCATTCACAGCTTTGAAATCCAGGGTATTTGAAACTATCAACAATGCC 910  
Db 950 AGATGACTCTTCATTCACAGCTTTGAAATCCAGGGTATTTGAAACTATCAACAATGCC 1009  
QY 911 ATCAAGGACCTCTGGAGCTTTCAACACAGTTTACTGCGCTTACTCCAGTGTGCTTCA 970  
Db 1010 ATCAAGGACCTCTGGAGCTTTCAACACAGTTTACTGCGCTTACTCCAGTGTGCTTCA 1069  
QY 971 ATGGGATTTTCTTGCCACACTCCAGGGGATTTTGGGGCATTTTTCAGCTTTTACTTTG 1030  
Db 1070 ATGGGATTTTCTTGCCACACTCCAGGGGATTTTGGGGCATTTTTCAGCTTTTACTTTG 1129  
QY 1031 TGATGAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAAGGTGACTGAGATGA 1090  
Db 1130 TGATGAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAAGGTGACTGAGATGA 1189  
QY 1091 TGAAGAAAGTTCTGTCTCAGCCTTGGAGAGATTAACATCTTACGCTGGAGTAAAGG 1150  
Db 1190 TGAAGAAAGTTCTGTCTCAGCCTTGGAGAGATTAACATCTTACGCTGGAGTAAAGG 1249  
QY 1151 AGAAGTACCTGAGTGAATCTGCTTTCTGGTACCTACATTTCTCCCTCTCTCTGCAAG 1210  
Db 1250 AGAAGTACCTGAGTGAATCTGCTTTTCTGGTACCTACATTTCTCCCTCTCTCTGCAAG 1309  
QY 1211 GCTATCATTTTCAGAGCTGATTTCTGGAGACATATCCATTTTCATTGGCAAGATCCAGGCA 1270  
Db 1310 GCTATCATTTTCAGAGCTGATTTCTGGAGACATATCCATTTTCATTGGCAAGATCCAGGCA 1369  
QY 1271 GCACGCCGCTGAGCTTTGGGCTACATGCTGAACCTGACCAACATGATCCAGCTGAGC 1330  
Db 1370 GCACGCCGCTGAGCTTTGGGCTACATGCTGAACCTGACCAACATGATCCAGCTGAGC 1429  
QY 1331 AACCATTTGTCCACACCTCTCTCCACCTTCCACCTAA 1365  
Db 1430 AACCATTTGTCCACACCTCTCTCCACCTTCCACCTAA 1464

; Sequence 1, Application US/09835147  
; Patent No. US20020002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Maliszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1599  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (67)..(1596)  
US-09-835-147-1

Query Match 96.6%; Score 1319.2; DB 9; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 41 GTTCAACCCAGAACAAAGCAITGGCCAGAAAAAGTTAAAGTATGGGATGTGCTGGATCGCG 100  
Db 173 GGTTCACCCAGAACAAAGCAITGGCCAGAAAAAGTTAAAGTATGGGATGTGCTGGATCGCG 232  
QY 101 GTTCTTCTCACACAGTTTATACATCTAAGTGGCCAGACAGAAAAAGGAGAATGACACAG 160  
Db 233 GTTCTTCTCACACAGTTTATACATCTAAGTGGCCAGACAGAAAAAGGAGAATGACACAG 292  
QY 161 GCGTGTGTCATCAAGTAGAAGAAATGCAGGGTTAAAGGTCCTGGAAATCTCAAAATTTGTTT 220  
Db 293 GCGTGTGTCATCAAGTAGAAGAAATGCAGGGTTAAAGGTCCTGGAAATCTCAAAATTTGTTT 352  
QY 221 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTTGCATGGAAAGAGCTAGGGAAGTGA 280  
Db 353 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTTGCATGGAAAGAGCTAGGGAAGTGA 412  
QY 281 TTCCAGGTCCTCAGACCAAGAGACACCCGTTTACCTGGAGCCAGCGCAGGATCGCGT 340  
Db 413 TTCCAGGTCCTCAGACCAAGAGACACCCGTTTACCTGGAGCCAGCGCAGGATCGCGT 472  
QY 341 TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGTGGAGAGGAGCC 400  
Db 473 TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGTGGAGAGGAGCC 532  
QY 401 TCAGCAACTACCCCTTTGACTTTCAGGGGTGCAGGATCAATTAATCTGCCCAAGAGAGGTTG 460  
Db 533 TCAGCAACTACCCCTTTGACTTTCAGGGGTGCAGGATCAATTAATCTGCCCAAGAGAGGTTG 592  
QY 461 CCTATGGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAAGAAAAACAAGTGGT 520  
Db 593 CCTATGGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAAGAAAAACAAGTGGT 652  
QY 521 TCAGCATAGTCCCATATGAACCAATAATTCAGGAAACCTTTTGAGCTTTGGACCTTTGGGG 580  
Db 653 TCAGCATAGTCCCATATGAACCAATAATTCAGGAAACCTTTTGAGCTTTGGACCTTTGGGG 712  
QY 581 GAGCCTCTACACAGTCACTTTTGTACCCCAAAAACAGACTATCGAGTCCCGAGATAATG 640  
Db 713 GAGCCTCTACACAGTCACTTTTGTACCCCAAAAACAGACTATCGAGTCCCGAGATAATG 772



641 CTCTGCAATTTGGCTCTATGGCAAGGACTACAAATGCTACACACATAGCTTCTTGCT 700  
773 CTCTGCAATTTGGCTCTATGGCAAGGACTACAAATGCTACACACATAGCTTCTTGCT 832  
701 ATGGGAAGGATCAGGCACTCTGCGAAGGACTGCGCAAGGACTTCAAGTTGCAAGTAATG 760  
833 ATGGGAAGGATCAGGCACTCTGCGAAGGACTGCGCAAGGACTTCAAGTTGCAAGTAATG 892  
761 AAATTTCTCAGGACCCATCTTTTCATCTGGATATAAGGAGGTAGTGAACGTAAGTGACC 820  
893 AAATTTCTCAGGACCCATCTTTTCATCTGGATATAAGGAGGTAGTGAACGTAAGTGACC 952  
821 TTTTCAAGACCCCTGCAACAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 880  
953 TTTTCAAGACCCCTGCAACAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 1012  
881 TCCAGGTTATGGAACTATCAACATGCATCAAGCATCTGGAGCTCTTCAACACCA 940  
1013 TCCAGGTTATGGAACTATCAACATGCATCAAGCATCTGGAGCTCTTCAACACCA 1072  
941 GTTACTGCCCTTACTCCCACTGTCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG 1000  
1073 GTTACTGCCCTTACTCCCACTGTCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG 1132  
1001 ATTTTGGGCAATTTTCAGCTTTTACTTTTGTGATGAAGTTTAACTTGACATCAGAGA 1060  
1133 ATTTTGGGCAATTTTCAGCTTTTACTTTTGTGATGAAGTTTAACTTGACATCAGAGA 1192  
1061 AGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGTTCTGTGCTAGCCCTGGGAGG 1120  
1193 AGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGTTCTGTGCTAGCCCTGGGAGG 1252  
1121 AGATAAAACATCTTACGCTGAGTAAAGGAGAGTACCTGAGTGAATCTCTTTTCTG 1180  
1253 AGATAAAACATCTTACGCTGAGTAAAGGAGAGTACCTGAGTGAATCTCTTTTCTG 1312  
1181 GTACTACATTTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTTCCCTGGAGC 1240  
1313 GTACTACATTTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTTCCCTGGAGC 1372  
1241 ACATCCATTTCAATGGCAAGATCCAGGCGAGGAGCGCGCTGGAGCTTGGCTACATGC 1300  
1373 ACATCCATTTCAATGGCAAGATCCAGGCGAGGAGCGCGCTGGAGCTTGGCTACATGC 1432  
1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1360  
1433 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1492  
1361 CCTA 1364  
1493 CCTA 1496

RESULT 5

US-10-646-308-29  
; Sequence 29, Application US/10646308  
; Publication No. US20040136992A1  
; GENERAL INFORMATION:  
; APPLICANT: BURTON, Paul B. J.  
; APPLICANT: DEISHER, Theresa A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE  
; FILE REFERENCE: 3432-B  
; CURRENT APPLICATION NUMBER: US/10/646,308  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: --to be assigned--  
; PRIOR FILING DATE: 2003-08-12  
; PRIOR APPLICATION NUMBER: 60/406,418  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 29  
; LENGTH: 1599

; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (67)..(1596)  
US-10-646-308-29

Query Match 96.6%; Score 1319.2; DB 19; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTAAAGTATGGGATTTGCTTGGATGCCG 100  
Db 173 GGTTGACCCAGAACAAAGCATTTGCCAGAAAACGTTAAAGTATGGGATTTGCTTGGATGCCG 232  
QY 101 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAAGAAAGGAGAAATGACACAG 160  
Db 233 GTTCTTCTCACAAAGTTTATACATCTATAGTGGCCAGCAGAAAGGAGAAATGACACAG 292  
QY 161 GCGTGGTCCATCAAGTAGAAGAAATGACAGGTTTAAAGGTCCTGGAATCTCAAAAATTTGTTT 220  
Db 293 GCGTGGTGCATCAAGTAGAAGAAATGACAGGTTTAAAGGTCCTGGAATCTCAAAAATTTGTTT 352  
QY 221 AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTTGCATGCGAAAGAGCTAGGGAAGTGA 280  
Db 353 AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTTGCATGCGAAAGAGCTAGGGAAGTGA 412  
QY 281 TTCAAAGGTCCAGCACCAGCAGACACCCGTTTACCTGGAGCCACGCGCAGGCATGCGGT 340  
Db 413 TTCAAAGGTCCAGCACCAGCAGACACCCGTTTACCTGGAGCCACGCGCAGGCATGCGGT 472  
QY 341 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGTTTCTGATGTGGTGGAGAGAGCC 400  
Db 473 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGTTTCTGATGTGGTGGAGAGAGCC 532  
QY 401 TCAGCAACTACCCCTTTGACCTTCCAGGTCGAGGATCATTTACTGCGCCAGAGGAAGGTG 460  
Db 533 TCAGCAACTACCCCTTTGACCTTCCAGGTCGAGGATCATTTACTGCGCCAGAGGAAGGTG 592  
QY 461 CCTATGGCTGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 520  
Db 593 CCTATGGCTGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 652  
QY 521 TCAGCATAGTCCCATATGAAACCAATATTCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 580  
Db 653 TCAGCATAGTCCCATATGAAACCAATATTCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 712  
QY 591 GAGCCTCTACAAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCAGATAATG 640  
Db 713 GAGCCTCTACAAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCAGATAATG 772  
QY 641 CTCTGCAATTTTCGCTCTATGCGCAAGGACTACAATGCTACACACATAGCTTCTTGCTGT 700  
Db 773 CTCTGCAATTTTCGCTCTATGCGCAAGGACTACAATGCTACACACATAGCTTCTTGCTGT 832  
QY 701 ATGGGAAGGATCAGGCACTCTGCGCAGAAAATGCGCCAGAGCAATTCAGGTTGCAAGTAATG 760  
Db 833 ATGGGAAGGATCAGGCACTCTGCGCAGAAAATGCGCCAGAGCAATTCAGGTTGCAAGTAATG 892  
QY 761 AAATTTCTCAGGACCCATCTTTTCATCTCGATATAAGGAGGTAGTGAACGTAAGTGACC 820  
Db 893 AAATTTCTCAGGACCCATCTTTTCATCTCGATATAAGGAGGTAGTGAACGTAAGTGACC 952  
QY 821 TTTTCAAGACCCCTGCAACAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 880  
Db 953 TTTTCAAGACCCCTGCAACAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 1012  
QY 881 TCCAGGTTATGGAAACTATCAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACACCA 940  
Db 1013 TCCAGGTTATGGAAACTATCAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACACCA 1072  
QY 941 GTTACTGCCCTTACTCCCACTGTCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG 1000

Db 1073 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGG 1132  
Qy 1001 ATTTGGGGCATTTTCAAGCTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAGA 1060  
Db 1133 ATTTGGGGCATTTTCAAGCTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAGA 1192  
Qy 1061 AAGTCTCTCAGGAAAGGTCAGTGAAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGAGG 1120  
Db 1193 AAGTCTCTCAGGAAAGGTCAGTGAAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGAGG 1252  
Qy 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1180  
Db 1253 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1312  
Qy 1181 GTACCTACATTTCTCCCTCTTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGAGC 1240  
Db 1313 GTACCTACATTTCTCCCTCTTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGAGC 1372  
Qy 1241 ACATCCATTTTATTTGGCAAGATCCAGGCGAGCGAGCGGCTGGACTTTGGGCTACATGC 1300  
Db 1373 ACATCCATTTTATTTGGCAAGATCCAGGCGAGCGAGCGGCTGGACTTTGGGCTACATGC 1432  
Qy 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCCACACCTCTCTCCCACTCCA 1360  
Db 1433 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCCACACCTCTCTCCCACTCCA 1492  
Qy 1361 CCTA 1364  
Db 1493 CCTA 1496

RESULT 6  
US-10-641-643-1475  
; Sequence 1475, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; Susan G. Stuart  
; Jeffrey J. Sellhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/641,643  
; FILING DATE: 14-Aug-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1475:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1818 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: G76S255  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1475 :  
US-10-641-643-1475

Query Match 96.6%; Score 1319.2; DB 18; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 41 GTTCAACCCAGAACAAAGCATTTGCCAGAAAAAGTTAAAGTATGGGATTTGCTGGATCGG 100  
Db 174 GGTGACCCAGAACAAAGCATTTGCCAGAAAAAGTTAAAGTATGGGATTTGCTGGATCGG 233  
Qy 101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAAGGAGAATGACACAG 160  
Db 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAAGGAGAATGACACAG 293  
Qy 161 GCGTGTGCATCAAGTATGAAGAATGCAGGGTTAAAGGTCCTCGAATCTCAAAATTTGTTTC 220  
Db 294 GCGTGTGCATCAAGTATGAAGAATGCAGGGTTAAAGGTCCTCGAATCTCAAAATTTGTTTC 353  
Qy 221 AGAAAGTAAATGAAATAGGCATTTTACCTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGA 280  
Db 354 AGAAAGTAAATGAAATAGGCATTTTACCTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGA 413  
Qy 281 TTCCAAGGTCCAGACCAAGAGACACCCGTTTACCTGGAGGCCAGCGGATCGCGT 340  
Db 414 TTCCAAGGTCCAGACCAAGAGACACCCGTTTACCTGGAGGCCAGCGGATCGCGT 473  
Qy 341 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGAGGTTCTCGATGTGTGGAGAGGAGCC 400  
Db 474 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGAGGTTCTCGATGTGTGGAGAGGAGCC 533  
Qy 401 TCAGCAACTACCCCTTTTGACTTTCAGGGTGCAGGATCAATTAATGCGCCAAAGAGGAGTG 460  
Db 534 TCAGCAACTACCCCTTTTGACTTTCAGGGTGCAGGATCAATTAATGCGCCAAAGAGGAGTG 593  
Qy 461 CTATGGCTGGATTAATCAATCTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGTG 520  
Db 594 CCTATGGCTGGATTAATCAATCTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGTG 653  
Qy 521 TCAGCATAGTCCCATATGAACCAATATCAAGAACCTTTGAGCTTTGGACCTTTGGGG 580  
Db 654 TCAGCATAGTCCCATATGAACCAATATCAAGAACCTTTGAGCTTTGGACCTTTGGGG 713  
Qy 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAGATAATG 640  
Db 714 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAGATAATG 773  
Qy 641 CTCTGCAATTCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 700  
Db 774 CTCTGCAATTCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 833  
Qy 701 ATGGGAAGGATCAGGCACCTCTGCGAAGACTCGCAAGGACATTCAGGTTGCAAGTAATG 760  
Db 834 ATGGGAAGGATCAGGCACCTCTGCGAAGACTCGCAAGGACATTCAGGTTGCAAGTAATG 893  
Qy 761 AAATTCTCAGGACCCCATGCTTTTCATCTCTGGATATAAAGAGGTAGTGAACGTAAAGTACC 820  
Db 894 AAATTCTCAGGACCCCATGCTTTTCATCTCTGGATATAAAGAGGTAGTGAACGTAAAGTACC 953  
Qy 821 TTTCAGAAGACCCCTGCGACCAAGAGATTTGAGATGATCTTCCATCTCCAGCAGTTTGA 880  
Db 954 TTTCAGAAGACCCCTGCGACCAAGAGATTTGAGATGATCTTCCATCTCCAGCAGTTTGA 1013  
Qy 881 TCCAGGGTATTGGAAACTATCAACATGCGCATCAAGAGCTCTGGAGCTCTTCAACACCA 940  
Db 1014 TCCAGGGTATTGGAAACTATCAACATGCGCATCAAGAGCTCTGGAGCTCTTCAACACCA 1073  
Qy 941 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGG 1000

Db 1074 GTTACTGCCCTTACTCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG 1133  
Qy 1001 ATTTGGGGCAATTTTCAGCTTTTACTTTGTGATGAAGTTTAACTTTGACATCAGAGA 1060  
Db 1134 ATTTGGGGCAATTTTCAGCTTTTACTTTGTGATGAAGTTTAACTTTGACATCAGAGA 1193  
Qy 1061 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGTTCGTGCTCAGCTTGGGAGG 1120  
Db 1194 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGTTCGTGCTCAGCTTGGGAGG 1253  
Qy 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTCTG 1180  
Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTCTG 1313  
Qy 1181 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCAITTCACAGCTGATTCCTGGAGC 1240  
Db 1314 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCAITTCACAGCTGATTCCTGGAGC 1373  
Qy 1241 ACATCCATTTTCAITTTGGCAAGATCCAGGGCAGCGACGCCGGCTGGACTTTGGGCTACATGC 1300  
Db 1374 ACATCCATTTTCAITTTGGCAAGATCCAGGGCAGCGACGCCGGCTGGACTTTGGGCTACATGC 1433  
Qy 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGCCACACTCTCTCCCACTCCA 1360  
Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGCCACACTCTCTCCCACTCCA 1493  
Qy 1361 CCTA 1364  
Db 1494 CCTA 1497

RESULT 7

US-10-934-998-290  
; Sequence 290, Application US/10934998  
; Publication No. US20050153917A1  
; GENERAL INFORMATION:  
; APPLICANT: AL-MAHMOOD, SALMAN  
; APPLICANT: COLIN, SYLVIE  
; APPLICANT: SCHNEIDER, CHRISTOPHE  
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL  
; TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF  
; FILE REFERENCE: BMA-04-1206  
; CURRENT APPLICATION NUMBER: US/10/934,998  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: PCT/FR03/00695  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: FR02/02717  
; PRIOR FILING DATE: 2002-03-04  
; PRIOR APPLICATION NUMBER: FR02/04546  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 290  
; LENGTH: 1818  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Genbank/S73813  
; DATABASE ENTRY DATE: 1995-04-12  
US-10-934-998-290

Query Match 96.6%; Score 1319.2; DB 22; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 41 GTTCAACCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGTGCTGGATCGG 100  
Db 174 GGTTCACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGTGCTGGATCGG 233  
Qy 101 GTTCTTCTCACAGATTTTATACATCTATAGTGGCCAGCAGAAAGAGATGACACAG 160  
Db 234 GTTCTTCTCACAGATTTTATACATCTATAGTGGCCAGCAGAAAGAGATGACACAG 293

Qy 161 GCGTGGTGCATCAAGTAGAAGATGCAAGGTTTAAAGGTCCTTGGAAATCTCAAAATTTGTTTC 220  
Db 294 GCGTGGTGCATCAAGTAGAAGATGCAAGGTTTAAAGGTCCTTGGAAATCTCAAAATTTGTTTC 353  
Qy 221 AGAAGTAAATGAATAGGCATTTTACCTGACTGATTTGCATGGAAGAGCTAGGAGTCA 280  
Db 354 AGAAGTAAATGAATAGGCATTTTACCTGACTGATTTGCATGGAAGAGCTAGGAGTCA 413  
Qy 281 TTCCAAGGTCCAGCAGCAACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGCATCGCGT 340  
Db 414 TTCCAAGGTCCAGCAGCAACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGCATCGCGT 473  
Qy 341 TGCTCAGGATGGAAGTGAAGTGGGAGCAGACAGGGTTCCTGATGTGTGGAGAGAGCC 400  
Db 474 TGCTCAGGATGGAAGTGAAGTGGGAGCAGACAGGGTTCCTGATGTGTGGAGAGAGCC 533  
Qy 401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGATCATTTACTGGCCAAGAGGAGGTG 460  
Db 534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGATCATTTACTGGCCAAGAGGAGGTG 593  
Qy 461 CCTATGGCTGGATTAATACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGT 520  
Db 594 CCTATGGCTGGATTAATACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGT 653  
Qy 521 TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGAGCTTTGGGG 580  
Db 654 TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGAGCTTTGGGG 713  
Qy 581 GAGGCTCTACACAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAGATATG 640  
Db 714 GAGGCTCTACACAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAGATATG 773  
Qy 641 CTCTGCAATTTTGGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTGTCT 700  
Db 774 CTCTGCAATTTTGGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTGTCT 833  
Qy 701 ATGGGAAGATCAGGCACTCTGGCAGAAAATCTGGCCAAAGGATTCAGGTTCGAAATATG 760  
Db 834 ATGGGAAGATCAGGCACTCTGGCAGAAAATCTGGCCAAAGGATTCAGGTTCGAAATATG 893  
Qy 761 AAATTTCTCAGGAGCCCATGCTTTTCTCTGATATAGAAGGTAGTGAACGTAACTGACC 820  
Db 894 AAATTTCTCAGGAGCCCATGCTTTTCTCTGATATAGAAGGTAGTGAACGTAACTGACC 953  
Qy 821 TTTTCAAGACCCCTTGCAACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGATTTGAAA 880  
Db 954 TTTTCAAGACCCCTTGCAACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGATTTGAAA 1013  
Qy 881 TCCAGGGTATTTGGAAAACCTATCAACAATGCCATCAAAAGCATCTGGAGCTCTTCAACACA 940  
Db 1014 TCCAGGGTATTTGGAAAACCTATCAACAATGCCATCAAAAGCATCTGGAGCTCTTCAACACA 1073  
Qy 941 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCACCACCTCCAGGGGG 1000  
Db 1074 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCACCACCTCCAGGGGG 1133  
Qy 1001 ATTTTGGGGCAATTTTTCAGCTTTTACTTTGTGATGAAGTTTAACTTTGACATCAGAGA 1060  
Db 1134 ATTTTGGGGCAATTTTTCAGCTTTTACTTTGTGATGAAGTTTAACTTTGACATCAGAGA 1193  
Qy 1061 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGTTCGTGCTCAGCTTGGGAGG 1253  
Db 1194 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGTTCGTGCTCAGCTTGGGAGG 1313  
Qy 1121 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTG 1180  
Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTG 1313  
Qy 1181 GTACTCATTTCTCTCCCTCTGCAAGGCTATCATTTTCCAGCTGATTTCTTGGGAGC 1240  
Db 1314 GTACTCATTTCTCTCCCTCTGCAAGGCTATCATTTTCCAGCTGATTTCTTGGGAGC 1373  
Qy 1241 ACATCCATTTTCTTGGCAAGATCCAGGGCAGCGCGGCTGGAGCTTTTGGGCTACATGC 1300

Db 1374 ACATCCATTTCATGGCAAGATCCAGGCGACGACGCGGCTGGACTTTGGGCTACATGC 1433  
Qy 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGCCACACCTCTCTCCCATCCA 1360  
Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGCCACACCTCTCTCCCATCCA 1493  
Qy 1361 CCTA 1364  
Db 1494 CCTA 1497  
RESULT 8  
US-10-934-998-46  
; Sequence 46, Application US/10934998  
; Publication No. US20050153917A1  
; GENERAL INFORMATION:  
; APPLICANT: AL-MAHMOOD, SALMAN  
; APPLICANT: COLIN, SYLVIE  
; APPLICANT: SCHNEIDER, CHRISTOPHE  
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL  
; TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF  
; FILE REFERENCE: BMA-04-1206  
; CURRENT APPLICATION NUMBER: US/10/934, 998  
; PRIOR FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: PCT/FR03/00695  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: FR02/02717  
; PRIOR FILING DATE: 2002-03-04  
; PRIOR APPLICATION NUMBER: FR02/04546  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: Patencin version 3.2  
; SEQ ID NO 46  
; LENGTH: 2081  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: GS-N45  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GENBANK/AJ133133  
; DATABASE ENTRY DATE: 2000-01-19  
; RELEVANT RESIDUES: (1)..(2081)  
US-10-934-998-46

Query Match 96.6%; Score 1319.2; DB 22; Length 2081;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 41 GTTCAACCCAGAACCAAGCAATGCCAGAAAACGTTAAGTATGGATTTGCTGGATGCGG 100  
Db 311 GGTGACCCAGAACCAAGCAATGCCAGAAAACGTTAAGTATGGATTTGCTGGATGCGG 370  
Qy 101 GTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG 160  
Db 371 GTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG 430  
Qy 161 GCCTGTGTCATCAAGTAGAAGAAATGACAGGGTTAAAGGCTCTGGAATCTCAAAAATTTGTT 220  
Db 431 GCCTGTGTCATCAAGTAGAAGAAATGACAGGGTTAAAGGCTCTGGAATCTCAAAAATTTGTT 490  
Qy 221 AGAAGTAAATGAATAGGACATTTACTGACTGATTTGATGGAAGAGGCTAGGGAAGTGA 280  
Db 491 AGAAGTAAATGAATAGGACATTTACTGACTGATTTGATGGAAGAGGCTAGGGAAGTGA 550  
Qy 281 TTCAAGGTCCTCAGCACCAGACACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGT 340  
Db 551 TTCCNAGTCCAGCACCAGACACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGT 610  
Qy 341 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGCC 400  
Db 611 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGCC 670

RESULT 9  
US-10-240-965-242  
; Sequence 242, Application US/10240965  
; Publication No. US20030165924A1

Qy 401 TCAGCAATACCCCTTTTGACTTCCAGGGTGCAGAGTCAATTAAGTCTGAGGAGGAGG 460  
Db 671 TCAGCAATACCCCTTTTGACTTCCAGGGTGCAGAGTCAATTAAGTCTGAGGAGGAGG 730  
Qy 461 CCTATGGCTGGATTAATCAATCTCTGCTGGGCAAAATTCAGTCAAGAAAAAAGGTG 520  
Db 731 CCTATGGCTGGATTAATCAATCTCTGCTGGGCAAAATTCAGTCAAGAAAAAAGGTG 790  
Qy 521 TCAGCATAGTCCCATATGAAACCAATATCAGGAACCTTTGGAGCTTTGGACCTTGG 580  
Db 791 TCAGCATAGTCCCATATGAAACCAATATCAGGAACCTTTGGAGCTTTGGACCTTGG 850  
Qy 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAGATAATG 640  
Db 851 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAGATAATG 910  
Qy 641 CTCTCAATTTCCCTCTATATGGCAAGGACTCAATGTCTTACACATAGTCTTCTGTGCT 700  
Db 911 CTCTCAATTTCCCTCTATATGGCAAGGACTCAATGTCTTACACATAGTCTTCTGTGCT 970  
Qy 701 ATGGGAAGGATCAGGACCTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 760  
Db 971 ATGGGAAGGATCAGGACCTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 1030  
Qy 761 AAATTTCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAAGTACC 820  
Db 1031 AAATTTCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAAGTACC 1090  
Qy 821 TTTCACAAGACCCCTGCAACCAAGAGATTTGAGATGACTCTTCATTTCCAGCAGTTTGA 880  
Db 1091 TTTCACAAGACCCCTGCAACCAAGAGATTTGAGATGACTCTTCATTTCCAGCAGTTTGA 1150  
Qy 881 TCCAGGGTATTGGAACCTATCAACATGCCATCAAGGATCCTGGAGCTTTCAACACCA 940  
Db 1151 TCCAGGGTATTGGAACCTATCAACATGCCATCAAGGATCCTGGAGCTTTCAACACCA 1210  
Qy 941 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCACCACCTCCAGGGG 1000  
Db 1211 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCACCACCTCCAGGGG 1270  
Qy 1001 ATTTTGGGCAATTTTCAGCTTTTTCATTTTGTGATGAAGTTTAACTTTGACATCAGAGA 1060  
Db 1271 ATTTTGGGCAATTTTCAGCTTTTTCATTTTGTGATGAAGTTTAACTTTGACATCAGAGA 1330  
Qy 1061 AAGTCTCTCAGAAAAGGTGACTGAGATGATCAAAAAGTTCTGCTCAGCCTTGGGAGG 1120  
Db 1331 AAGTCTCTCAGAAAAGGTGACTGAGATGATCAAAAAGTTCTGCTCAGCCTTGGGAGG 1390  
Qy 1121 AGATAAAAACATCTTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTCTG 1180  
Db 1391 AGATAAAAACATCTTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTCTG 1450  
Qy 1181 GTACCTACATTTCTCCCTCTCTTTCGCAAGGCTATCATTTTCAAGTGAATCTTCTGGGAGC 1240  
Db 1451 GTACCTACATTTCTCCCTCTCTTTCGCAAGGCTATCATTTTCAAGTGAATCTTCTGGGAGC 1510  
Qy 1241 ACATCCATTTTCATTTGGCAGATCCAGGCGAGCGCGGCTGGACTTTGGGCTACATGC 1300  
Db 1511 ACATCCATTTTCATTTGGCAGATCCAGGCGAGCGCGGCTGGACTTTGGGCTACATGC 1570  
Qy 1301 TGAACCTGACCAACATGATCCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCACTCCA 1360  
Db 1571 TGAACCTGACCAACATGATCCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCACTCCA 1630  
Qy 1361 CCTA 1364  
Db 1631 CCTA 1634

GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: SHIFFMAN, Dov  
; APPLICANT: SOMOGYI, Roland  
; APPLICANT: LAWN, Richard M.  
; APPLICANT: SEILHAMER, Jeffrey J.  
; APPLICANT: PORTER, Gordon J.  
; APPLICANT: MIKITA, Thomas  
; APPLICANT: TAI, Julie  
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION  
; FILE REFERENCE: PA-0025 PCT  
; CURRENT APPLICATION NUMBER: US/10/240,965  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 2002-10-04  
; PRIOR FILING DATE: 2000-04-05  
; NUMBER OF SEQ ID NOS: 276  
; SOFTWARE: PERL Program  
; SEQ ID NO 242  
; LENGTH: 4411  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030165924A1 347965.2  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 3369  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-240-965-242

Query Match 96.6%; Score 1319.2; DB 16; Length 4411;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 41 GTTCAACCCAGAACCAAGCAATTGCCAGAAACGTTTAAGTATGCGATTGTGCTGGATGGG 100  
DB 184 GGTTCACCCAGAACCAAGCAATTGCCAGAAACGTTTAAGTATGCGATTGTGCTGGATGGG 243  
QY 101 GTTCTTCTCACAAAGTTTATACATCATATAAGTGGCCAGCAGAAAGAGGAATGACACAG 160  
DB 244 GTTCTTCTCACAAAGTTTATACATCATATAAGTGGCCAGCAGAAAGAGGAATGACACAG 303  
QY 161 GGTGGTGCATCAAGTAGAAGATGCGAGGTTAAAGGTCCTGGATCTCAAAATTTGTTTC 220  
DB 304 GGTGGTGCATCAAGTAGAAGATGCGAGGTTAAAGGTCCTGGATCTCAAAATTTGTTTC 363  
QY 221 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTGCAATGGAAGAGCTAGGGAAGTGA 280  
DB 364 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTGCAATGGAAGAGCTAGGGAAGTGA 423  
QY 281 TTCCAAGGTCCAGCACCAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATGCGGT 340  
DB 424 TTCCAAGGTCCAGCACCAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATGCGGT 483  
QY 341 TGCTCAGAGTGAAGAGTGAAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCC 400  
DB 484 TGCTCAGAGTGAAGAGTGAAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCC 543  
QY 401 TCAGCAACTACCCCTTGACTTCCAGGTCAGGATCAATTAAGTGGCCAGAGGAGGAGTG 460  
DB 544 TCAGCAACTACCCCTTGACTTCCAGGTCAGGATCAATTAAGTGGCCAGAGGAGGAGTG 603  
QY 461 CCTATGGCTGGATTACTCAACTATCTGCTGGCAAAATTCAGTCAGAAAAACAAGGTGGT 520  
DB 604 CCTATGGCTGGATTACTCAACTATCTGCTGGCAAAATTCAGTCAGAAAAACAAGGTGGT 663  
QY 521 TCAGCATAGTCCCATATGAACCAATAATCAGAAAACTTTGGAGCTTTGGACCTTTGGGG 580  
DB 664 TCAGCATAGTCCCATATGAACCAATAATCAGAAAACTTTGGAGCTTTGGACCTTTGGGG 723  
QY 581 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCAGTCCCAAGTAATG 640  
DB 724 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCAGTCCCAAGTAATG 783

QY 641 CTCTGCAATTTTCGCTCTATATGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCT 700  
DB 784 CTCTGCAATTTTCGCTCTATATGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCT 843  
QY 701 ATGGGAAGGATCAGGCACCTCTGGCAGAAACTGGCCAAAGGACATTCAGGTGCAAGTAATG 760  
DB 844 ATGGGAAGGATCAGGCACCTCTGGCAGAAACTGGCCAAAGGACATTCAGGTGCAAGTAATG 903  
QY 761 AAATTTCTCAGGGACCCATGCTTTTCATCTGGATATAAGAGGTAGTGAACGTAAGTGACC 820  
DB 904 AAATTTCTCAGGGACCCATGCTTTTCATCTGGATATAAGAGGTAGTGAACGTAAGTGACC 963  
QY 821 TTTTCAAGACCCCTTGCCACCAAGAGATTGAGATGACTCTTCCATTTCCAGCAGTTTGAAGA 880  
DB 964 TTTTCAAGACCCCTTGCCACCAAGAGATTGAGATGACTCTTCCATTTCCAGCAGTTTGAAGA 1023  
QY 881 TCCAGGTTATGGAAACTATCAACATGCCATCAAGCATCCTGGAGCTTCTCAACACCA 940  
DB 1024 TCCAGGTTATGGAAACTATCAACATGCCATCAAGCATCCTGGAGCTTCTCAACACCA 1083  
QY 941 GTTACTGCCCTTACTCCAGGTGCTTCAATGGGATTTCTTGCCACCACTCCAGGGGG 1000  
DB 1084 GTTACTGCCCTTACTCCAGGTGCTTCAATGGGATTTCTTGCCACCACTCCAGGGGG 1143  
QY 1001 ATTTTGGGGCAATTTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1060  
DB 1144 ATTTTGGGGCAATTTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1203  
QY 1061 AAGTCTCTCAGAAAAAGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGGAGG 1120  
DB 1204 AAGTCTCTCAGAAAAAGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGGAGG 1263  
QY 1121 AGATAAAAAACATCTTACGCTGGAGTAAAGAGAGAGTACTGAGTCAATCTGCTTTCTG 1180  
DB 1264 AGATAAAAAACATCTTACGCTGGAGTAAAGAGAGAGTACTGAGTCAATCTGCTTTCTG 1323  
QY 1181 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTTCAGCTGATTCCTGGGAGC 1240  
DB 1324 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTTCAGCTGATTCCTGGGAGC 1383  
QY 1241 ACATCCATTTTCTTGGGAGAGATCCAGGCGAGGAGCGGCTGGAGCTTTGGGCTACATGC 1300  
DB 1384 ACATCCATTTTCTTGGGAGAGATCCAGGCGAGGAGCGGCTGGAGCTTTGGGCTACATGC 1443  
QY 1301 TGAACCTGACCAACATGATCCAGCTGAGCAACATTTGTCACACCTCTCTCCCACTCCA 1360  
DB 1444 TGAACCTGACCAACATGATCCAGCTGAGCAACATTTGTCACACCTCTCTCCCACTCCA 1503  
QY 1361 CCTA 1364  
DB 1504 CCTA 1507  
RESULT 10  
US-10-934-998-147/c  
; Sequence 147, Application US/10934998  
; Publication No. US20050153917A1  
; GENERAL INFORMATION:  
; APPLICANT: AL-NAHMOOD, SALMAN  
; APPLICANT: COLIN, SYLVIE  
; APPLICANT: SCHNEIDER, CHRISTOPHE  
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL  
; FILE REFERENCE: BMA-04-1206  
; CURRENT APPLICATION NUMBER: US/10/934,998  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: PCT/FR03/00695  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: FR02/02717  
; PRIOR FILING DATE: 2002-03-04  
; PRIOR APPLICATION NUMBER: FR02/04546  
; PRIOR FILING DATE: 2002-04-11

```
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 147
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-934-998-147

Query Match      46.9%; Score 640.2; DB 22; Length 704;
Best Local Similarity 99.5%; Pred. No. 4.3e-193;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 720 CTGCGAGAAATCGCCCAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGAGCCCATG 779
Db 704 CTGCGAGAAATCGCCCAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGAGCCCATG 645

Qy 780 CTTTCATCTCGATATATAAGAGGTAGTGAACGTAAGTGACCTTTACAAGACCCCTCGCAC 839
Db 644 CTTTCATCTCGATATATAAGAGGTAGTGAACGTAAGTGACCTTTACAAGACCCCTCGCAC 585

Qy 840 CAAGAGATTGAGATGACTCTTCATTCAGCATCGAGGTTGAAATCCAGGGTATTGGAAACTA 899
Db 584 CAAGAGATTGAGATGACTCTTCATTCAGCATCGAGGTTGAAATCCAGGGTATTGGAAACTA 525

Qy 900 TCAACAATGCCATCAAGCATCTGGAGCTCTTCAACACAGTACTTGCCCTTACTCCCA 959
Db 524 TCAACAATGCCATCAAGCATCTGGAGCTCTTCAACACAGTACTTGCCCTTACTCCCA 465

Qy 960 GTGTGCCCTTCAATGGGATTTTCTTGCCACCACCTCCAGGGGGATTTTGGGGCAATTTTCAGC 1019
Db 464 GTGTGCCCTTCAATGGGATTTTCTTGCCACCACCTCCAGGGGGATTTTGGGGCAATTTTCAGC 405

Qy 1020 TTTTACTTTGTGATGAAGTTTAACTTGATGACATGAGAAAGTCTCTCAGGAAAAGGT 1079
Db 404 TTTTACTTTGTGATGAAGTTTAACTTGATGACATGAGAAAGTCTCTCAGGAAAAGGT 345

Qy 1080 GACTGAGATGATGAAAGTTCTGTCTCAGCCCTGGGAGGAGATATAAACAATCTTTACGC 1139
Db 344 GACTGAGATGATGAAAGTTCTGTCTCAGCCCTGGGAGGAGATATAAACAATCTTTACGC 285

Qy 1140 TGGAGTAAAGGAGGAGTACCTGAGTGAATCTGTTTCTGTTGCTACCTACATCTCTCCCT 1199
Db 284 TGGAGTAAAGGAGGAGTACCTGAGTGAATCTGTTTCTGTTGCTACCTACATCTCTCCCT 225

Qy 1200 CTTTCTGCAAGGCTATCTTTCAAGCTGATTTCTGAGGACATCGATTTGATGGCAA 1259
Db 224 CTTTCTGCAAGGCTATCTTTCAAGCTGATTTCTGAGGACATCGATTTGATGGCAA 165

Qy 1260 GATCCAGGCGAGCGAGCGCGCTGGACTTTGGGCTACATGCTGAACCTGAACCAACATGAT 1319
Db 164 GATCCAGGCGAGCGAGCGCGCTGGACTTTGGGCTACATGCTGAACCTGAACCAACATGAT 105

Qy 1320 CCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCACCTA 1364
Db 104 CCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCACCTA 60
```

```
RESULT 11
US-10-934-998-193/c
; Sequence 193, Application US/10934998
; Publication No. US20050153917A1
; GENERAL INFORMATION:
; APPLICANT: AL-WAHMOOD, SALMAN
; APPLICANT: COLIN, SYLVIE
; APPLICANT: SCHNEIDER, CHRISTOPHE
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
; FILE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
; FILE REFERENCE: BNA-04-1206
; CURRENT APPLICATION NUMBER: US/10/934, 998
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/FR03/00695
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: FR02/02717
```

```
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: FR02/04546
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 193
; LENGTH: 6164
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-934-998-193

Query Match      46.9%; Score 640.2; DB 22; Length 6164;
Best Local Similarity 99.5%; Pred. No. 1.6e-192;
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 720 CTGCGAGAAATCGCCCAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGAGCCCATG 779
Db 1811 CTGCGAGAAATCGCCCAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGAGCCCATG 1752

Qy 780 CTTTCATCTCGATATATAAGAGGTAGTGAACGTAAGTGACCTTTACAAGACCCCTCGCAC 839
Db 1751 CTTTCATCTCGATATATAAGAGGTAGTGAACGTAAGTGACCTTTACAAGACCCCTCGCAC 1692

Qy 840 CAAGAGATTGAGATGACTCTTCCATTCAGCAGATTTGAAATCCAGGGTATTGGAAACTA 899
Db 1691 CAAGAGATTGAGATGACTCTTCCATTCAGCAGATTTGAAATCCAGGGTATTGGAAACTA 1632

Qy 900 TCAACAATGCCATCAAGCATCTGGAGCTCTTCAACACAGTACTTGCCCTTACTCCCA 959
Db 1631 TCAACAATGCCATCAAGCATCTGGAGCTCTTCAACACAGTACTTGCCCTTACTCCCA 1572

Qy 960 GTGTGCCCTTCAATGGGATTTTCTTGCCACCACCTCCAGGGGGATTTTGGGGCAATTTTCAGC 1019
Db 1571 GTGTGCCCTTCAATGGGATTTTCTTGCCACCACCTCCAGGGGGATTTTGGGGCAATTTTCAGC 1512

Qy 1020 TTTTACTTTGTGATGAAGTTTAACTTGATGACATGAGAAAGTCTCTCAGGAAAAGGT 1079
Db 1511 TTTTACTTTGTGATGAAGTTTAACTTGATGACATGAGAAAGTCTCTCAGGAAAAGGT 1452

Qy 1080 GACTGAGATGATGAAAGTTCTGTGCTCAGCCCTGGGAGGAGATATAAACAATCTTTACGC 1139
Db 1451 GACTGAGATGATGAAAGTTCTGTGCTCAGCCCTGGGAGGAGATATAAACAATCTTTACGC 1392

Qy 1140 TGGAGTAAAGGAGGAGTACCTGAGTGAATCTGTTTCTGTTGCTACCTACATCTCTCCCT 1199
Db 1391 TGGAGTAAAGGAGGAGTACCTGAGTGAATCTGTTTCTGTTGCTACCTACATCTCTCCCT 1332

Qy 1200 CTTTCTGCAAGGCTATCTTTCAAGCTGATTTCTGAGGACATCCATTTTCAATGGCAA 1259
Db 1331 CTTTCTGCAAGGCTATCTTTCAAGCTGATTTCTGAGGACATCCATTTTCAATGGCAA 1272

Qy 1260 GATCCAGGCGAGCGAGCGCGCTGGACTTTGGGCTACATGCTGAACCTGAACCAACATGAT 1319
Db 1271 GATCCAGGCGAGCGAGCGCGCTGGACTTTGGGCTACATGCTGAACCTGAACCAACATGAT 1212

Qy 1320 CCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCACCTA 1364
Db 1211 CCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCACCTA 1167
```

```
RESULT 12
US-09-918-995-24656
; Sequence 24656, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918, 995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235, 076
; PRIOR FILING DATE: 1999-01-20
```

```
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24656
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-24656

Query Match      30.3%; Score 414; DB 10; Length 475;
Best Local Similarity 96.6%; Pred. No. 6.3e-121;
Matches 423; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 593 AAGTCACTTTGTACCCCAAAACAGACTATCCAGTCCCCAGATAATGCTCTGCAATTC 552
DB 38 AGGGCACTTATGTACCCCTTAACAGACTATCCAGTCCCCAGATAATGCTCTGCAATTC 97
QY 653 GCCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGCTATGGGAAGATC 712
DB 98 ACCTCTATGGCAGGACTACNATGTCTACACATAGCTTCTTGCTATGGGAAGATC 157
QY 713 AGGCACCTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCCAAGTAATGAAATTTCTCAGGG 772
DB 158 ATGCACTCTGGCATAAATCGGCAAGGACATTCAGGTTGCAAGTAATGAAACTCTTCAGGG 217
QY 773 ACCCATGCTTTCATCTCGATATAGAAGTAGTGAACGTAGTGAACCTTTTACAAGACCC 832
DB 218 ACCCATGCTTTCATCTCGATATAGAAGTAGTGAACGTAGTGAACCTTTTACAAGACCC 277
QY 833 CTGCAACCAAGAGATTGAGATGACTCTTCCATTCCAGCAGTTTGAATCCAGGGTATG 892
DB 278 CTGCAACCAAGAGATTGAGATGACTCTTCCATTCCAGCAGTTTGAATCCAGGGTATG 337
QY 893 GAACTATCAACAATGCCATCAAGCATCTCGAGCTCTTCAACACCACTTACTGCCCC 952
DB 338 GAACTATCATCAATGCCATCAAGCATCTCGAGCTCTTCAACACCACTTACTGCCCC 397
QY 953 ACTCCAGTGTGCTTCAATGGGATTTCTTGCCACCACTCCAGGGGGATTTTGGGGCAT 1012
DB 398 ACTCCAGTGTGCTTCAATGGGATTTCTTGCCACCACTCCAGGGGGATTTTGGGGCAT 457
QY 1013 TTTGAGCTTTTACTTTG 1030
DB 458 TTTGAGCTTTTACTTTG 475

RESULT 13
US-09-918-995-23052
; Sequence 23052, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23052
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(484)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-23052

Query Match      27.8%; Score 379; DB 10; Length 484;
Best Local Similarity 100.0%; Pred. No. 9.8e-110;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 986 CACCACTCCAGGGGGATTTTGGGCAATTTTTCAGCTTTTACCTTTGTGATGAAGTTTTTAA 1045
DB 50 CACCACTCCAGGGGGATTTTGGGCAATTTTTCAGCTTTTACCTTTGTGATGAAGTTTTTAA 109
QY 1046 ACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGATTTCTGTG 1105
DB 110 ACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAGATTTCTGTG 169
QY 1106 CTCAGCCTTGGGAGAGATATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACTCGAGTG 1165
DB 170 CTCAGCCTTGGGAGAGATATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACTCGAGTG 229
QY 1166 AATATGCTTTTCTGCTACCTACATTTCTCCCTCTCTCTGCAAGGCTATCATTTTCACAG 1225
DB 230 AATATGCTTTTCTGCTACCTACATTTCTCCCTCTCTCTGCAAGGCTATCATTTTCACAG 289
QY 1226 CTGATTCCTGGGAGCAGATCCATTTTCATTTGGCAAGATCCAGGCGAGCGCGGTGGA 1285
DB 290 CTGATTCCTGGGAGCAGATCCATTTTCATTTGGCAAGATCCAGGCGAGCGCGGTGGA 349
QY 1286 CTTTGGGCTTACATGCTGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACAC 1345
DB 350 CTTTGGGCTTACATGCTGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACAC 409
QY 1346 CTCTCTCCCACTCCACCTA 1364
DB 410 CTCTCTCCCACTCCACCTA 428

RESULT 14
US-10-002-631C-275/c
; Sequence 275, Application US/10002631C
; Publication No. US20030157486A1
; GENERAL INFORMATION:
; APPLICANT: Graff, Jonathon M.
; APPLICANT: Muenster, Matthew
; TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
; FILE REFERENCE: A34943 090495.0243
; CURRENT APPLICATION NUMBER: US/10/002,631C
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/300,309
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 275
; LENGTH: 703
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (656)...(698)
; OTHER INFORMATION: n = A, C, G, or T
US-10-002-631C-275

Query Match      24.6%; Score 335.8; DB 16; Length 703;
Best Local Similarity 80.2%; Pred. No. 7.8e-96;
Matches 394; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 46 ACCCAGAACAAAGCATTTCCAGAAACCGTTAAGTATGGGATTTGCTGATCGGGTTCT 105
DB 547 ACCCAGAACAAACCTTTCCAGAAATGTTAAGTATGGGATTTGCTGATCGGGTTCT 488
QY 106 TCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAGAAAGGAGAATGACACAGCGTG 165
DB 487 TCTCACACAACCTGTGTATCTACAAAGTGGCCGCGGAGAGAGAAATGACACAGCGTG 428
QY 166 GTGCATCAAGTAGAAGATGAGGGTTAAAGGTTCTCGAATCTCAAAATTTGTTTCAGAAA 225
DB 427 GTGCAGCAGTTAGAGGATGCAAGTGAAGAGTCTCTGGAATCTCAAAATATGCTCAGAAA 368
QY 226 GTAAATGAATAGGCAATTTACCTGACTGATTCATGCAATGCAAGAGCTAGGGAAGTGAATCCA 285
```



Db 367 ACAGATCAAAATCGGTGGTACTGGCCGCAATGATGCACTGCACTCCACCGAATGATACCA 308  
Qy 286 AGTCCAGCACCAGAGACACCCGTTTACTGGGAGCCACGCGCAGGATGCGGTTGCTC 345  
Db 307 ACATCAAGCATCACAGACTCCTGCTACTCTGGAGCCACAGCAGGCATGCGCTTGCTT 248  
Qy 346 AGATGGAAAGTGAAGATTGGCAGACAGGGTTCTGATGTTGTTGGAGGAGCCTCAGC 405  
Db 247 AGAATGGAAAGCAACAATCGGAGAGAGGTTCTGGCTGCACTGCAACAAGCCCTTAAG 188  
Qy 406 AACTACCCCTTTGACTTCCAGGGTGGCAGGATCAATTAAGTGGCCCAAGAGGAAGTGCCTAT 465  
Db 187 AGCTACCCCTTTGACTTCCAGGGTGGCAAGATCATCACTGGACAAGAGAGGTGCTTAT 128  
Qy 466 GGCTGGAATTAATCAACTATCTGCTGGGCAAAATTCAGTTCAGAAAAACAAGTGGTTCAGC 525  
Db 127 GGGTGGATTAATTAATCACTATCTGCTGGGCAGATTCACTCAGGAACAGAGTTGGCTAAGC 68  
Qy 526 ATAGTCCCAT 536  
Db 67 CTATCTCAGA 57

RESULT 15  
US-09-923-304-3  
; Sequence 3, Application US/09923304  
; Patent No. US20020081612A1  
; GENERAL INFORMATION:  
; APPLICANT: KATZ, RUTH  
; APPLICANT: JIANG, FENG  
; TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS  
; FILE REFERENCE: UTSC:658US  
; CURRENT APPLICATION NUMBER: US/09/923,304  
; CURRENT FILING DATE: 2001-08-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1672)  
US-09-923-304-3

Query Match 21.3%; Score 291; DB 9; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 3.7e-81;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

Qy 48 CCAGAACAAAGCATGGCCAGAAACGTTAAGTATGGGATTTGCTGGATGCGGGTTCTTC 107  
Db 220 CAAGCAAGAGTCTCTCCCTCCAGGACTGAAAGTATGTTATTTGCTGGATGCGGGTTCT 279  
Qy 108 TCACACAAGTTTATACATCTAATGTCGCCAGAGAAAGAGAAATGACACAGCGCTGGT 167  
Db 280 AAGAACCAAGTCTACGTGATCAATGGCCAGCAGAAAAAGAGAAATATACCGAGTGGT 339  
Qy 168 GCATCAAGTAGAAGAATGACAGGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTCAGAAAGT 227  
Db 340 CAGTCAAACTTCAAAATGTAGTGTGAAGGCTCTGGAATCTCCAGCTATGGAATAAACC 399  
Qy 228 AATGAATAGGATTTACTGACTGATTCATGTCATGGAAAGAGCTAGGGAAGTGAATTCAG 287  
Db 400 CCAAGATGTCCCCAGAGCCTTTGAGGAGTGTATGCAAAAAAGTCAAGGGGAGGTCTTCATC 459  
Qy 288 GTCCAGCACAGAGACACCCGTTTACCTGGGAGCCAGCGAGGATGCGGTTGCTCAG 347  
Db 460 CCACCTCCAGGATCCACCCCAATTCACCTGGGAGCCAGCGCTGGGATGCGCTTGCTGAG 519  
Qy 348 GATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTTGGAGAGGAGCCTCAGCAA 407  
Db 520 GTTGCAAAATGAAACAGCAGCTAATGAAGTCTTTGAAAGCATCCAAAGCTACTTCAAGTC 579

Qy 408 CTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGGCCCAAGAGGAAGGTGCTTATGG 467  
Db 580 CCAGCCCTTTGACTTTTAGGGGTGCTCAAAATCATTTCTGGGCAAGAAAGAGGGTATATGG 639  
Qy 468 CTGGATTACTCAACTATCTCTGGGCAAAATTCAGTTCAGAAAAACAAGTGGTTACAGCAT 527  
Db 640 ATGGATTACAGCCAACTATTTAATGGAAATTTCTGGAGAAAGAACCTCTGGCACATGTG 699  
Qy 528 AGTCCCATATGAAACCAATATACAGAAACCTTTGGAGCTTTGGAGCTTTGGGGGAGCCTC 587  
Db 700 GGTGC-----ACCCGCACTGGAGTGGAAACACCGGTGCTCCCTAGCTTAGGTGGTCCCTC 753  
Qy 588 TACACAAGTCACTTTGTACCCCAAAACCCAGACTATCGAGTCCCCAGATAATGCTCTGCA 647  
Db 754 CACCAAAATATCTTCTGGTGGCAGGAGAGAGATGATCTGAAACACACAGGACATCATGCA 813  
Qy 648 ATTTGCGCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTCTGTCTATGGAA 707  
Db 814 GGTGTCCTGTATGGCTACGTATACAGCTCTACACACACAGCTTCCAGTGTCTATGGCCG 873  
Qy 708 GGATCAGGCATCTGGCAGAAACTGGCCNAGACATTCAGGTTGCNAGTAATGAAA---T 764  
Db 874 GAATGAGGCTGAGAAAGTTTCTGGCAATGCTCTCGCAGAAATTCCTTACCAAAACCA 933  
Qy 765 TCTCAGGGACCATGCTTTTCATCTGGATATAAGAGGTAGTGAACGTAAAGTACCTTTA 824  
Db 934 TCTCACAATCCTGTTTACCCTGGGATTTATAGCATCAGCTTCAACATGGGCCATGTATT 993  
Qy 825 CAAGACCCCTGTCAC-----CAAGAGATTTGAGATGACTTCTTCCATTTCCAGCAGTTTGA 878  
Db 994 TGATAGCTGTGCACTGTGGACAGAGCCAGAAAGTTATATACCCCAATGTCATCAC 1053  
Qy 879 AATCCAGGATTTGAAACTATCACAATGCCATCAAGCATCCTGGAGCTCTTCAACAC 938  
Db 1054 TTTTGAAGGAAGTGGGGACCATCTCTGTGTAAAGAGAGAGTGGCTTCCATATTTGACTT 1113  
Qy 939 CAGTTACTGSCCTTACTCCAG--TGTCCTTCAATGGGATTTTCTTCCACCACTCCA 995  
Db 1114 CAAAGCTTCCCATGATCAAGAAACCTGTTCTTTGATGGGTTTATCAGCCAAAGATTAA 1173  
Qy 996 GGGGGAATTTGGGCAATTTTCAGCTTTTTCATTTTGTGATGAAAGTTTAAAACTTGACATC 1055  
Db 1174 AGGGCAATTTGTGGCTTTTTCAGGATTTCTACTACAGCCAGTGTCTTTAAATCT---TTC 1230  
Qy 1056 AGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATAAGAAAGTTCTGTGCTCAGCCTTG 1115  
Db 1231 AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTGGAATTTCTGCTCAGAAATTG 1290  
Qy 1116 GGAGGAGATAAAAAACATCTTACGCTGGAGTAAAGAGAGAGTACCTGAGTGAATACCTGCTT 1175  
Db 1291 GAGTCAGCTCCCACTGCTGCTCTCCCAATTTGATGAGGTATATGCCCGCTCTTACTGCTT 1350  
Qy 1176 TTTGCTGACTACATTTCTCCCTCTCTCTGCAAGGCTATCATTTTCAGAGCTGATTCCTG 1235  
Db 1351 CTCAGCCAACTACATCTACCCTGTTGTTGTGAACGGTTACAAATTCACAGAGAGAGCTTG 1410  
Qy 1236 GGAGCAGATCCATTTTCATTTGGCAAGATCCAGGGCAGCAGCGGCTGAGCTTTGGGCTA 1295  
Db 1411 GCCCCAAATACACTTTTGAAGAAAGAGTGGGGAATAGCAGCATAGCCTGCTCTCTGGGCTA 1470  
Qy 1296 CATGCTGAACCTGAGCAACATGATCCAGCTCAGCAACCATTTG 1338  
Db 1471 CATGCTCAGCTGAGCAACCATGATCCAGCTGAAAGCCCTCTG 1513

Search completed: September 22, 2005, 04:37:21  
Job time : 993.919 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2005, 16:22:35 ; Search time 6446.5 Seconds  
(without alignments)  
10801.234 Million cell updates/sec

Title: US-09-807-660C-7  
Perfect score: 1437  
Sequence: 1 atggccctgtgatcgacag.....ctctctccactccacctaa 1437

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues 9416466

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	1437	100.0	BD228700 Inhibitor
2	1400	97.4	BD228710 Inhibitor
3	1365	95.0	BD228699 Inhibitor
4	1319.2	91.8	BD228698 Inhibitor
5	1319.2	91.8	HSU87967 Human ATP d
6	1319.2	91.8	AR168353 Sequence
7	1319.2	91.8	AR380930 Sequence
8	1319.2	91.8	AX828644 Sequence
9	1319.2	91.8	S73813 CD39=lympho
10	1319.2	91.8	AX828400 Sequence
11	1319.2	91.8	AJ133133 Homo sapi
12	1319.2	91.8	CQ870272 Sequence
13	1319.2	91.8	CQ870276 Sequence
14	1319.2	91.8	CQ870270 Sequence
15	1319.2	91.8	AX281833 Sequence
16	1305.2	90.8	AX281833 Sequence
17	1039	72.3	CQ769356 Sequence
18	1019.8	71.0	BC047664 Homo sapi
19	888.4	61.8	AJ133746 Sus scrofa

20	863	60.1	2312	10	AF037366	Mus muscu
21	863	60.1	2386	10	BC011278	Mus muscu
22	858.2	59.7	1686	10	RNU81295	Rattus nori
23	835	58.1	2296	6	CQ870265	Sequence
24	827.8	57.6	1958	4	AF005940	Bos tauru
25	703.2	48.9	1488	6	CQ870268	Sequence
26	703.2	48.9	1815	9	HSAL33134	Homo sapi
27	640.2	44.6	704	6	AX828501	Sequence
28	640.2	44.6	6164	6	AX828547	Sequence
29	541.6	37.7	2928	5	BC073267	Xenopus l
30	524.4	36.5	3211	5	BC076662	Xenopus t
31	463.2	32.2	764	6	CQ721824	Sequence
32	438.8	30.5	4049	5	AJ720369	Gallus ga
33	383.6	26.7	2450	5	BC078240	Danio rer
34	291	20.3	2783	6	CQ715235	Sequence
35	291	20.3	2797	6	AR194793	Sequence
36	291	20.3	2797	6	AR562109	Sequence
37	291	20.3	2797	6	AR567207	Sequence
38	291	20.3	2797	6	AR567913	Sequence
39	291	20.3	2797	6	AX497067	Sequence
40	291	20.3	2797	9	AF039917	Homo sapi
41	291	20.3	2809	9	AF034840	Homo sapi
42	287.6	20.0	1494	6	CQ794578	Sequence
43	287.6	20.0	1786	10	AY364442	Mus muscu
44	286	19.9	2338	10	BC031143	Mus muscu
45	275	19.1	1482	5	AF426405	Gallus ga

ALIGNMENTS

RESULT 1  
BD228700 1437 bp DNA linear PAT 17-JUL-2003

LOCUS Inhibitors of platelet activation and recruitment.

DEFINITION

ACCESSION BD228700.1 GI:33038470

VERSION JP 2002527096-A/3.

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 1437)

AUTHORS Maliszewski, C.R., Ili, R.B.G., Price, V.L. and Gimpe, S.D.

TITLE Inhibitors of platelet activation and recruitment

JOURNAL Patent: JP 2002527096-A 3 27-AUG-2002;

IMMUNEX CORP

COMMENT OS Artificial Sequence

PN JP 2002527096-A/3

PD 27-AUG-2002

PF 13-OCT-1999 JP 2000577185

PR 16-OCT-1998 US 60/104585,06-NOV-1998 US 60/107466 PR

13-AUG-1999 US 60/149010

PI CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE, PI

STEVEN D GIMPEL

PC C12N15/09, A61K38/00, A61P9/00, C07K14/705, C12N1/15, C12N1/19, PC

C12N5/10,

PC C12P21/02, C12N9/14, C12N15/00, A61K37/02, C12N5/00 CC

Description of Artificial Sequence: Fusion construct of human CC

CD39

FH Key Location/Qualifiers

FT CDS

source

1. 1437

/organism="synthetic construct"

/mol\_type="genomic DNA"

/db\_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 1437; DB 6; Length 1437;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCCCTGTGGATCGACAGGATGCAACTCCTGTCTTGCATTGCACTTAAGTCTTGCATT 60

|||||  
1 ATGGCCCTGTGGATCGACAGGATGCAACTCCTGCTCTGTGCACTAAGTCTTGCACTT 60  
61 GTCAAAACAGTGCACCTACTCTCAAGTTCTTACAAAGAAAACACAGACTAACTAGTTCAACC 120  
61 GTCAAAACAGTGCACCTACTCTCAAGTTCTTACAAAGAAAACACAGACTAACTAGTTCAACC 120  
121 CAGAACAAAGCATTTGCCAGAAAACGTTNAGTATGGGATTTGTGCTGATGGGGTCTTCTT 180  
121 CAGAACAAAGCATTTGCCAGAAAACGTTTAAAGTATGGGATTTGTGCTGATGGGGTCTTCTT 180  
181 CACACAAGTTTATACATCTATAGTGGCCAGAGAAAAGAGAAATCACACAGCGCTGGTG 240  
181 CACACAAGTTTATACATCTATAGTGGCCAGAGAAAAGAGAAATCACACAGCGCTGGTG 240  
241 CATCAAGTAGAAGAAATGCGAGGTTAAAGGTCCTGGAAATCTCAAAAATTTGTTCAAGAAAGTA 300  
241 CATCAAGTAGAAGAAATGCGAGGTTAAAGGTCCTGGAAATCTCAAAAATTTGTTCAAGAAAGTA 300  
301 AATGAATAGGCATTTTACCTGACTGATTTGCATGGAAGAGCTAGGAAAGTATTCACAAG 360  
301 AATGAATAGGCATTTTACCTGACTGATTTGCATGGAAGAGCTAGGAAAGTATTCACAAG 360  
361 TCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGCGAGCATGGGTTGCTCAGG 420  
361 TCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGCGAGCATGGGTTGCTCAGG 420  
421 ATGGAAGTAGAAGATGGGAGACAGGGTTCTGGATGTGGTGAGAGGAGCGCTCAGCAAC 480  
421 ATGGAAGTAGAAGATGGGAGACAGGGTTCTGGATGTGGTGAGAGGAGCGCTCAGCAAC 480  
481 TAGCCCTTTGACTTCCAGGGTGCAGGATCAATCTAGCTGGCCAGAGAGGTGCTATGCG 540  
481 TAGCCCTTTGACTTCCAGGGTGCAGGATCAATCTAGCTGGCCAGAGAGGTGCTATGCG 540  
541 TGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGTTTCAAGATA 600  
541 TGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGTTTCAAGATA 600  
601 GTCCCATATGAAACCAATAATACAGAAACCTTTTGGAGCTTTTGACCTTTGGGGAGCGCTCT 660  
601 GTCCCATATGAAACCAATAATACAGAAACCTTTTGGAGCTTTTGACCTTTGGGGAGCGCTCT 660  
661 ACACAGTCACTTTTGTACCCCAAAACACAGACTATCGAGTCCCGCAGATATGCTCTGCAA 720  
661 ACACAGTCACTTTTGTACCCCAAAACACAGACTATCGAGTCCCGCAGATATGCTCTGCAA 720  
721 TTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTTGTGCTATGGGAAG 780  
721 TTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTTGTGCTATGGGAAG 780  
781 GATCAGGCACTCTGGCAGAAACTGGCCAGGACATTCAGGTTTCAAGTAAATGAAATTTCTC 840  
781 GATCAGGCACTCTGGCAGAAACTGGCCAGGACATTCAGGTTTCAAGTAAATGAAATTTCTC 840  
841 AGGAGCCCATGCTTTCACTCTGATATAGAAAGGTAGTGAACCTTGAAGTAACTTCAAG 900  
841 AGGAGCCCATGCTTTCACTCTGATATAGAAAGGTAGTGAACCTTGAAGTAACTTCAAG 900  
901 ACCCCCTGCAACCAAGATTTGAGATGACTTTTCCATTTCCAGCAGTTTGAATCCAGGGT 960  
901 ACCCCCTGCAACCAAGATTTGAGATGACTTTTCCATTTCCAGCAGTTTGAATCCAGGGT 960  
961 ATTGGAACCTATCAACAATGCCATCAAGCATCTCTGAGGCTTTCAACACCAAGTTACTGC 1020  
961 ATTGGAACCTATCAACAATGCCATCAAGCATCTCTGAGGCTTTCAACACCAAGTTACTGC 1020  
1021 CCTTACTCCAGTGTGCTTCAATGGATTTTCTGCCACCACTCCAGGGGGATTTTGG 1080  
1021 CCTTACTCCAGTGTGCTTCAATGGATTTTCTGCCACCACTCCAGGGGGATTTTGG 1080  
1081 GCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTAAACTTGCATCAGAGAAAGTCTCT 1140  
|||||

Db 1081 GCATTTTTCAGCTTTTACTTTGTGATGAAGTATTTTAAACTTGACATCAGAGAAAGTCTCT 1140  
Qy 1141 CAGGAAAAGGTGACTGAGATGATGAAAAGTTCTGCTGCTCAGCCTTGGGAGGAGATAAAA 1200  
Db 1141 CAGGAAAAGGTGACTGAGATGATGAAAAGTTCTGCTGCTCAGCCTTGGGAGGAGATAAAA 1200  
Qy 1201 ACATCTTACCGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTTCTGGTACCTAC 1260  
Db 1201 ACATCTTACCGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTTCTGGTACCTAC 1260  
Qy 1261 ATTCTCTCCCTCTTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGGAGCACATCCAT 1320  
Db 1261 ATTCTCTCCCTCTTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGGAGCACATCCAT 1320  
Qy 1321 TTCATTGGCAGATCCAGGCGACGACCGCGCTGGACTTTGGGCTACATGCTGCCACCTG 1380  
Db 1321 TTCATTGGCAGATCCAGGCGACGACCGCGCTGGACTTTGGGCTACATGCTGCCACCTG 1380  
Qy 1381 ACCAACATGATCCCAAGCTGAGCAACCATTTGTCCACACCTCTCTCCACTCCACCTAA 1437  
Db 1381 ACCAACATGATCCCAAGCTGAGCAACCATTTGTCCACACCTCTCTCCACTCCACCTAA 1437  
RESULT 2  
BD228710 1464 bp DNA linear PAT 17-JUL-2003  
LOCUS Inhibitors of platelet activation and recruitment.  
DEFINITION BD228710  
ACCESSION BD228710.1 GI:33038480  
VERSION JP 2002527096-A/13.  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 1464).  
AUTHORS Maliszewski, C.R., Iii, R.B.G., Price, V.L. and Gimpe, S.D.  
TITILE Inhibitors of platelet activation and recruitment  
JOURNAL Patent: JP 2002527096-A 13 27-AUG-2002;  
IMMUNEX CORP  
COMMENT OS Artificial Sequence  
PN JP 2002527096-A/13  
PD 27-AUG-2002  
PF 13-OCT-1999 JP 2000577185 60/107466 PR  
PR 16-OCT-1998 US 60/104585, 06-NOV-1998 US 60/107466 PR  
13-AUG-1999 US 60/149010  
PI CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE, PI  
STEVEN D GIMPEL  
PC C12N15/09, A61K38/00, A61P9/00, C07K14/705, C12N1/15, C12N1/19, PC  
C12N5/10,  
PC C12P21/02//C12N9/14, C12N15/00, A61K37/02, C12N5/00 CC  
Description of Artificial Sequence: Fusion construct of human CC  
PH Key Location/Qualifiers  
PT CDS (1)..(1461).  
FEATURES  
source  
1..1464  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Query Match 97.4%; Score 1400; DB 6; Length 1464;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1437; Conservative 0; Mismatches 0; Indels 27; Gaps 1;  
Qy 1 ATGGCCCTGTGATCGACAGGATGCAACTCCTGCTCTGTGCACTAAGTCTTGCACTT 60  
Db 1 ATGGCCCTGTGATCGACAGGATGCAACTCCTGCTCTGTGCACTAAGTCTTGCACTT 60  
Qy 61 GTCAAAACAGTGCACCTACTCTCAAGTTCTTACAAAGAAAACACAGACTAACTAGTTCAACC 120  
Db 61 GTCAAAACAGTGCACCTACTCTCAAGTTCTTACAAAGAAAACACAGACTAACTAGTTCAACC 120  
Qy 121 CAGAACAAAGCATTTGCCAGAAAACGTTNAGTATGGGATTTGTGCTGATGGGGTCTTCTT 180  
Db 121 CAGAACAAAGCATTTGCCAGAAAACGTTTAAAGTATGGGATTTGTGCTGATGGGGTCTTCTT 180  
Qy 181 CACACAAGTTTATACATCTATAGTGGCCAGAGAAAAGAGAAATCACACAGCGCTGGTG 240  
Db 181 CACACAAGTTTATACATCTATAGTGGCCAGAGAAAAGAGAAATCACACAGCGCTGGTG 240  
Qy 241 CATCAAGTAGAAGAAATGCGAGGTTAAAGGTCCTGGAAATCTCAAAAATTTGTTCAAGAAAGTA 300  
Db 241 CATCAAGTAGAAGAAATGCGAGGTTAAAGGTCCTGGAAATCTCAAAAATTTGTTCAAGAAAGTA 300  
Qy 301 AATGAATAGGCATTTTACCTGACTGATTTGCATGGAAGAGCTAGGAAAGTATTCACAAG 360  
Db 301 AATGAATAGGCATTTTACCTGACTGATTTGCATGGAAGAGCTAGGAAAGTATTCACAAG 360  
Qy 361 TCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGCGAGCATGGGTTGCTCAGG 420  
Db 361 TCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGCGAGCATGGGTTGCTCAGG 420  
Qy 421 ATGGAAGTAGAAGATGGGAGACAGGGTTCTGGATGTGGTGAGAGGAGCGCTCAGCAAC 480  
Db 421 ATGGAAGTAGAAGATGGGAGACAGGGTTCTGGATGTGGTGAGAGGAGCGCTCAGCAAC 480  
Qy 481 TAGCCCTTTGACTTCCAGGGTGCAGGATCAATCTAGCTGGCCAGAGAGGTGCTATGCG 540  
Db 481 TAGCCCTTTGACTTCCAGGGTGCAGGATCAATCTAGCTGGCCAGAGAGGTGCTATGCG 540  
Qy 541 TGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGTTTCAAGATA 600  
Db 541 TGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGTTTCAAGATA 600  
Qy 601 GTCCCATATGAAACCAATAATACAGAAACCTTTTGGAGCTTTTGACCTTTGGGGAGCGCTCT 660  
Db 601 GTCCCATATGAAACCAATAATACAGAAACCTTTTGGAGCTTTTGACCTTTGGGGAGCGCTCT 660  
Qy 661 ACACAGTCACTTTTGTACCCCAAAACACAGACTATCGAGTCCCGCAGATATGCTCTGCAA 720  
Db 661 ACACAGTCACTTTTGTACCCCAAAACACAGACTATCGAGTCCCGCAGATATGCTCTGCAA 720  
Qy 721 TTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTTGTGCTATGGGAAG 780  
Db 721 TTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTTGTGCTATGGGAAG 780  
Qy 781 GATCAGGCACTCTGGCAGAAACTGGCCAGGACATTCAGGTTTCAAGTAAATGAAATTTCTC 840  
Db 781 GATCAGGCACTCTGGCAGAAACTGGCCAGGACATTCAGGTTTCAAGTAAATGAAATTTCTC 840  
Qy 841 AGGAGCCCATGCTTTCACTCTGATATAGAAAGGTAGTGAACCTTGAAGTAACTTCAAG 900  
Db 841 AGGAGCCCATGCTTTCACTCTGATATAGAAAGGTAGTGAACCTTGAAGTAACTTCAAG 900  
Qy 901 ACCCCCTGCAACCAAGATTTGAGATGACTTTTCCATTTCCAGCAGTTTGAATCCAGGGT 960  
Db 901 ACCCCCTGCAACCAAGATTTGAGATGACTTTTCCATTTCCAGCAGTTTGAATCCAGGGT 960  
Qy 961 ATTGGAACCTATCAACAATGCCATCAAGCATCTCTGAGGCTTTCAACACCAAGTTACTGC 1020  
Db 961 ATTGGAACCTATCAACAATGCCATCAAGCATCTCTGAGGCTTTCAACACCAAGTTACTGC 1020  
Qy 1021 CCTTACTCCAGTGTGCTTCAATGGATTTTCTGCCACCACTCCAGGGGGATTTTGG 1080  
Db 1021 CCTTACTCCAGTGTGCTTCAATGGATTTTCTGCCACCACTCCAGGGGGATTTTGG 1080  
Qy 1081 GCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTAAACTTGCATCAGAGAAAGTCTCT 1140  
Db 117 -----AAACCAGAACAAAGCATTTGCCAGAAACCGTTAAGTAT 153

Db 121 GACTACAAAGATGACGATGACAAACCCAGAACAAAGCATTTGCCAGAAACCGTTAAGTAT 180  
Qy 154 GGGATTGTGCTGATCGGGTCTCTCTCACACAAGTTTATACATCTATAAGTGGCCAGCA 213  
Db 181 GGGATTGTGCTGATCGGGTCTCTCTCACACAAGTTTATACATCTATAAGTGGCCAGCA 240  
Qy 214 GAAAGGAGAAATGACACAGCGGTGGTGCATCAAGTAGAAGAATGCAAGGTTAAAGTCTT 273  
Db 241 GAAAGGAGAAATGACACAGCGGTGGTGCATCAAGTAGAAGAATGCAAGGTTAAAGTCTT 300  
Qy 274 GGAATCTCAAAATTTGTTTCAGAAAGTAAATGAATAGGCATTTACTGACTGATGTCATG 333  
Db 301 GGAATCTCAAAATTTGTTTCAGAAAGTAAATGAATAGGCATTTACTGACTGATGTCATG 360  
Qy 334 GAAAGAGCTAGGGAAGTGAATCCAGGTCCAGACCAAGAGACACCCGTTTACCTGGGA 393  
Db 361 GAAAGAGCTAGGGAAGTGAATCCAGGTCCAGACCAAGAGACACCCGTTTACCTGGGA 420  
Qy 394 GCCAGGCGAGCATGCGGTTGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGTTCTG 453  
Db 421 GCCAGGCGAGCATGCGGTTGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGTTCTG 480  
Qy 454 GATGTGGTGGAGAGNGCCTCAGCAACTACCCCTTTGACTTCCAGGTCGCCAGGATCAT 513  
Db 481 GATGTGGTGGAGAGNGCCTCAGCAACTACCCCTTTGACTTCCAGGTCGCCAGGATCAT 540  
Qy 514 ACTGGCAGAGAGAGGTCCTATGCTGATTTACTATCAACTATCTGCTGGGCAAAATTC 573  
Db 541 ACTGGCAGAGAGAGGTCCTATGCTGATTTACTATCAACTATCTGCTGGGCAAAATTC 600  
Qy 574 AGTCAGAAAACAAGTGGTTTCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTT 633  
Db 601 AGTCAGAAAACAAGTGGTTTCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTT 660  
Qy 634 GGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACT 693  
Db 661 GGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACT 720  
Qy 694 ATCGAGTCCCAAGATAATGCTCTGCAATTTGCGCTCTATGGCAAGGACTACAAATGCTAC 753  
Db 721 ATCGAGTCCCAAGATAATGCTCTGCAATTTGCGCTCTATGGCAAGGACTACAAATGCTAC 780  
Qy 754 ACACATAGTCTTCTGTCTATGGGAGGATCAGGCACCTTGGCAGAAACTTGGCCCAAGGAC 813  
Db 781 ACACATAGTCTTCTGTCTATGGGAGGATCAGGCACCTTGGCAGAAACTTGGCCCAAGGAC 840  
Qy 814 ATTCAGTTGCAAGTAAGTAATTTCTCAGGAGCCCATGCTTTCATCTCTGGATATAAGAG 873  
Db 841 ATTCAGTTGCAAGTAAGTAATTTCTCAGGAGCCCATGCTTTCATCTCTGGATATAAGAG 900  
Qy 874 TAGTGAACGTAAAGTGACCTTTTACAGACCCCTCGCACAGAGATTTGAGATGACTCTT 933  
Db 901 TAGTGAACGTAAAGTGACCTTTTACAGACCCCTCGCACAGAGATTTGAGATGACTCTT 960  
Qy 934 CCATTTCCAGCAGTTTGAATCCAGGGTATTTGAAACTATCACAATGCCATCAAGCATC 993  
Db 961 CCATTTCCAGCAGTTTGAATCCAGGGTATTTGAAACTATCACAATGCCATCAAGCATC 1020  
Qy 994 CTGGAGCTCTTCAACACCGATTACTGCCCCTTACTCCAGTGTCCTTCAATGGGATTTTC 1053  
Db 1021 CTGGAGCTCTTCAACACCGATTACTGCCCCTTACTCCAGTGTCCTTCAATGGGATTTTC 1080  
Qy 1054 TTGCACCACCTCCAGGGGATTTTGGGGCATTTTTCAGCTTTTTCATTTGTGATGAAGTTT 1113  
Db 1081 TTGCACCACCTCCAGGGGATTTTGGGGCATTTTTCAGCTTTTTCATTTGTGATGAAGTTT 1140  
Qy 1114 TTAACCTTGACATCAGAGAAAGTCTCTCAGGAAAAGTGGTCACTGAGATGATGAAAAGTTC 1173  
Db 1141 TTAACCTTGACATCAGAGAAAGTCTCTCAGGAAAAGTGGTCACTGAGATGATGAAAAGTTC 1200  
Qy 1174 TGTGCTCAGCCTTGGGAGAGATAAAACATCTTACGCTGGAGTAAAGGAGATGACCTG 1233

Db 1201 TGTGCTCAGCCTTGGAGGAGATAAAAACATCTTTACGTTGGAGTAAAGGAGAAATACCTG 1260  
Qy 1234 AGTGAATACTGCTTTTCTGGTACCTACATTTCTCTCCCTCTCTTCTGCAAGGCTATCATTTTC 1293  
Db 1261 AGTGAATACTGCTTTTCTGGTACCTACATTTCTCTCCCTCTCTTCTGCAAGGCTATCATTTTC 1320  
Qy 1294 ACAGCTGATTTCTTGGGAGCACATCATTTTCATTTGGCAAGATCCAGGCGACGACGCGGC 1353  
Db 1321 ACAGCTGATTTCTTGGGAGCACATCATTTTCATTTGGCAAGATCCAGGCGACGACGCGGC 1380  
Qy 1354 TGGACTTTGGGCTACATCTGNACTGACCAACATGATCCCAAGTGGAGCAACCATTTGTC 1413  
Db 1381 TGGACTTTGGGCTACATCTGNACTGACCAACATGATCCCAAGTGGAGCAACCATTTGTC 1440  
Qy 1414 ACACCTCTCTCCCACTCCACCTAA 1437  
Db 1441 ACACCTCTCTCCCACTCCACCTAA 1464

RESULT 3  
BD228699  
LOCUS BD228699 1365 bp DNA linear PAT 17-JUL-2003  
DEFINITION Inhibitors of platelet activation and recruitment.  
ACCESSION BD228699  
VERSION JP 2002527096-A/2.  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 1365)  
AUTHORS Maliszewski, C.R., Iii, R.B.G., Price, V.L. and Gimpe, S.D.  
TITLE Inhibitors of platelet activation and recruitment  
JOURNAL Patent: JP 2002527096-A 2 27-AUG-2002;  
IMMUNEX CORP  
COMMENT OS Artificial Sequence  
PN JP 2002527096-A/2  
PD 27-AUG-2002  
PF 13-OCT-1999 JP 2000577185 60/107466 PR  
PR 16-OCT-1998 US 60/104585, 06-NOV-1998 US  
13-AUG-1999 US 60/149010  
PI CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE, PI  
PC C12N15/09, A61K38/00, A61P9/00, C07K14/705, C12N1/15, C12N1/19, PC  
C12N5/10,  
PC C12P21/02//C12N9/14, C12N15/00, A61K37/02, C12N5/00 CC  
Description of Artificial Sequence: Fusion construct of human CC  
CD39

FH Key Location/Qualifiers  
FT CDS Location/Qualifiers  
1. 1365  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

FEATURES  
source  
ORIGIN  
Query Match 95.0%; Score 1365; DB 6; Length 1365;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 GCACCTACTTCAAGTCTTACAAAGAAAACACAGCTAACTAGTTTCAACCCAGAACAAAGCA 132  
Db 1 GCACCTACTTCAAGTCTTACAAAGAAAACACAGCTAACTAGTTTCAACCCAGAACAAAGCA 60  
Qy 133 TTGCAGAAAACGTTAAGTATGGATTTGCTGATGGGTTCTTCTCACACAAGTTTA 192  
Db 61 TTGCAGAAAACGTTAAGTATGGATTTGCTGATGGGTTCTTCTCACACAAGTTTA 120  
Qy 193 TACATCTATAAGTGGCCAGCAAGAAAGAGAAATGACACAGCGGTGGTGCATCAAGTAGAA 252  
Db 121 TACATCTATAAGTGGCCAGCAAGAAAGAGAAATGACACAGCGGTGGTGCATCAAGTAGAA 180  
Qy 253 GAATSCAGGGTTAAAGGTCCTGGAATCTCAAAATTTTGTTCAGAAAGTAAATGAATAGGC 312

Db 181 GAATGAGGGTTAAAGGCTCTCGAATCTCAAAATTTGTTTCAGAAAAGTAAATGAATAGGC 240  
Qy 313 ATTTACTGACTGATTCATGATGGAAGAGCTAGGAAAGTGATTTCCAAAGGTCCCGACACAA 372  
Db 241 ATTTACTGACTGATTCATGATGGAAGAGCTAGGAAAGTGATTTCCAAAGGTCCCGACACAA 300  
Qy 373 GAGACACCCGTTTACCTGGGAGCCAGCGAGGATCGGTTGCTCAGGATGGAAGTGAA 432  
Db 301 GAGACACCCGTTTACCTGGGAGCCAGCGAGGATCGGTTGCTCAGGATGGAAGTGAA 360  
Qy 433 GAGTTGGCAGACAGGGTTCTGGATGTGGTGGAAGGAGCCTCAGCAACTACCCCTTTTGAC 492  
Db 361 GAGTTGGCAGACAGGGTTCTGGATGTGGTGGAAGGAGCCTCAGCAACTACCCCTTTTGAC 420  
Qy 493 TTCAGGGTGCCAGGATCATTA CTGGCCAAAGAGAAAGGTGCCCTATGGCTGGATTAATATC 552  
Db 421 TTCAGGGTGCCAGGATCATTA CTGGCCAAAGAGAAAGGTGCCCTATGGCTGGATTAATATC 480  
Qy 553 AACTATCTGCTGGGCAAAATTCAGTTCAGAAACAAGGTGGTTTCAGCATAGTCCCATATGAA 612  
Db 481 AACTATCTGCTGGGCAAAATTCAGTTCAGAAACAAGGTGGTTTCAGCATAGTCCCATATGAA 540  
Qy 613 ACCAATAATCAGGAAACCTTTGGAGCTTTTGGACCTTTGGGGAGCCCTCTACACAAGTCACT 672  
Db 541 ACCAATAATCAGGAAACCTTTGGAGCTTTTGGACCTTTGGGGAGCCCTCTACACAAGTCACT 600  
Qy 673 TTTGTACCCCAAAACAGACTATCGATGTCGCCAGATAATGCTCTGCAATTTGCGCTCTAT 732  
Db 601 TTTGTACCCCAAAACAGACTATCGATGTCGCCAGATAATGCTCTGCAATTTGCGCTCTAT 660  
Qy 733 GSCAAGGACTACATGCTCTACACATAGTCTTCTGCTATGGGAAGGATCAGGCACATC 792  
Db 661 GSCAAGGACTACATGCTCTACACATAGTCTTCTGCTATGGGAAGGATCAGGCACATC 720  
Qy 793 TGGCAGAAATCGGCCAAGGACATTCAGGTTTGAAGTAATGAATTTCTCAGGGACCCCATGC 852  
Db 721 TGGCAGAAATCGGCCAAGGACATTCAGGTTTGAAGTAATGAATTTCTCAGGGACCCCATGC 780  
Qy 853 TTTATCTCTGGATATGAAGAGGTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 912  
Db 781 TTTATCTCTGGATATGAAGAGGTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 840  
Qy 913 AAGAGATTTGAGATGACTCTTCCATTCACAGCAGTTTGAATCCAGGATTTGGAACACTAT 972  
Db 841 AAGAGATTTGAGATGACTCTTCCATTCACAGCAGTTTGAATCCAGGATTTGGAACACTAT 900  
Qy 973 CAACAATGCCATCAAGGATCCTGGAGCTCTTCAACACCAAGTTTACTGCCCCCTACTCCAG 1032  
Db 901 CAACAATGCCATCAAGGATCCTGGAGCTCTTCAACACCAAGTTTACTGCCCCCTACTCCAG 960  
Qy 1033 TGTGCCCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGATTTTGGGGCATTTTTCAGCT 1092  
Db 961 TGTGCCCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGATTTTGGGGCATTTTTCAGCT 1020  
Qy 1093 TTTTACTTTGATGAGTTTAACTTGAATTCACATCAGAGAAAGTCTCTCAGGAAAGGTG 1152  
Db 1021 TTTTACTTTGATGAGTTTAACTTGAATTCACATCAGAGAAAGTCTCTCAGGAAAGGTG 1080  
Qy 1153 ACTGAGATGATGAAAAGTTTCTGTGCTCAGCCTTTGGGAGGAGATAAAAAACATCTTACGCT 1212  
Db 1081 ACTGAGATGATGAAAAGTTTCTGTGCTCAGCCTTTGGGAGGAGATAAAAAACATCTTACGCT 1140  
Qy 1213 GGAGTAAAGGAGTAACTCTGAGTGAATATCTGCTTTTCTGGTACCTACATTTCTCTCCCTC 1272  
Db 1141 GGAGTAAAGGAGTAACTCTGAGTGAATATCTGCTTTTCTGGTACCTACATTTCTCTCCCTC 1200  
Qy 1273 CTTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGGAGCACATTCATTTCAATTTGCGAAG 1332  
Db 1201 CTTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGGAGCACATTCATTTCAATTTGCGAAG 1260  
Qy 1333 ATCCAGGGCAGCAGCGCGCTGGACTTTGGGCTTACATGCTGAACCTGACCAACATGATC 1392

Db 1261 ATCCAGGGCAGCAGCGCGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1320  
Qy 1393 CCAGCTGAGCAGCACCATTGTCACACACTCTCTCCCACTCCACCTAA 1437  
Db 1321 CCAGCTGAGCAGCACCATTGTCACACACTCTCTCCCACTCCACCTAA 1365  
RESULT 4  
BD228698 1599 bp DNA linear PAT 17-JUL-2003  
LOCUS Inhibitors of platelet activation and recruitment.  
DEFINITION BD228698  
ACCESSION BD228698  
VERSION BD228698.1 GI:33038468  
KEYWORDS JP 2002527096-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1599)  
AUTHORS Maliszewski, C.R., Iii, R.B.G., Price, V.L. and Gimpe, S.D.  
TITLE Inhibitors of platelet activation and recruitment  
JOURNAL Patent: JP 2002527096-A 1 27-AUG-2002;  
IMMUNEX CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002527096-A/1  
PD 27-AUG-2002  
PF 13-OCT-1999 JP 2000577185  
PR 16-OCT-1998 US 60/104585, 06-NOV-1998 US 60/107466 PR  
13-AUG-1999 US 60/149010  
PI CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE, PI  
STEVEN D GIMPEL  
PC C12N15/09, A61K38/00, A61P9/00, C07K14/705, C12N1/15, C12N1/19, PC  
C12N5/10,  
PC C12P21/02//C12N9/14, C12N15/00, A61K37/02, C12N5/00 CC  
Inhibitors of platelet activation and recruitment PH Key  
Location/Qualifiers  
FT CDS (67)..(1596).  
FEATURES  
source  
1..1599  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 91.8%; Score 1319.2; DB 6; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 113 GTTCAACCCAGACAAAAGCATTGCCAGAAAACGTTAAAGTATGCGATTGTGCTGGATCGG 172  
Db 173 GGTTCACCCAGAACAAAGCATTTGCCAGAAAACGTTAAAGTATGCGATTGTGCTGGATCGG 232  
Qy 173 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGAGAAAAGGAGAATGACACAG 232  
Db 233 GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG 292  
Qy 233 GCGTGGTGCATCAAGTAGAAGAAATCAGGGTTAAAGGTCCTTGAATCTCAAAATTTGTTTC 292  
Db 293 GCGTGGTGCATCAAGTAGAAGAAATCAGGGTTAAAGGTCCTTGAATCTCAAAATTTGTTTC 352  
Qy 293 AGAAAAGTAAATGAAATAGGCATTTACCTGACATTTGATTCGATGAAAAGAGCTAGGGAAGTGA 352  
Db 353 AGAAAAGTAAATGAAATAGGCATTTACCTGACATTTGATTCGATGAAAAGAGCTAGGGAAGTGA 412  
Qy 353 TTCCAAAGGTCCAGCAACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGT 412  
Db 413 TTCCAAAGGTCCAGCAACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGT 472  
Qy 413 TGCTCAGGATGAAAGTGAAGGTTGGCAGACAGGGTTCTGATGTGTTGGAGAGAGGCC 472  
Db 473 TGCTCAGGATGAAAGTGAAGGTTGGCAGACAGGGTTCTGATGTGTTGGAGAGAGGCC 532  
Qy 473 TCAGCAACTACCCCTTTTGACTTTCCAGGGTGCCAGGATCATTTACTGCGCCAAAGGAGGTG 532

Db 533 TCAGCAACTACCCCTTTGACTTCACGGGTGCCAGGATCATTTACTGGCCAGAGGAGGTG 592  
Qy 533 CCTATGGCTGGATTACTATCAACTATCTCTGCTGGCAAAATTCAGTTCAGAAACAAAGTGTG 592  
Db 593 CCTATGGCTGGATTACTATCAACTATCTCTGCTGGCAAAATTCAGTTCAGAAACAAAGTGTG 552  
Qy 593 TCAGCATAGTCCCATATGAACCAATAATACAGAAACCTTTGGAGCTTTGGACCTTTGGGG 652  
Db 653 TCAGCATAGTCCCATATGAACCAATAATACAGAAACCTTTGGAGCTTTGGACCTTTGGGG 712  
Qy 653 GAGCCTCTACAGAGTCATTTGTACCCCAAAACAGAGACTATCGAGTCCCAAGATAATG 712  
Db 713 GAGCCTCTACAGAGTCATTTGTACCCCAAAACAGAGACTATCGAGTCCCAAGATAATG 772  
Qy 713 CTCTGCAATTTTCGCTCTATGCAAGGACTACAATGTCTACACACATAGCTTCTTGCTGT 772  
Db 773 CTCTGCAATTTTCGCTCTATGCAAGGACTACAATGTCTACACACATAGCTTCTTGCTGT 832  
Qy 773 ATGGGAAGGATCAGGCATCTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 832  
Db 833 ATGGGAAGGATCAGGCATCTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 892  
Qy 833 AAATTTCTCAGGACCCATGCTTTTCATCTCGGATATAAGAGTAGTGAACGTAAGTGACC 892  
Db 893 AAATTTCTCAGGACCCATGCTTTTCATCTCGGATATAAGAGTAGTGAACGTAAGTGACC 952  
Qy 893 TTTTCAAGACCCCTGCACCAAGAGATTGAGATGACTCTTCATTCAGACAGTTTGA 952  
Db 953 TTTTCAAGACCCCTGCACCAAGAGATTGAGATGACTCTTCATTCAGACAGTTTGA 1012  
Qy 953 TCCAGGTTATGGAACATATCAACATGCAATCAAGCATCTGGAGCTCTTCAACACCA 1012  
Db 1013 TCCAGGTTATGGAACATATCAACATGCAATCAAGCATCTGGAGCTCTTCAACACCA 1072  
Qy 1013 GTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTCTTGCCACCATCTCCAGGGG 1072  
Db 1073 GTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTCTTGCCACCATCTCCAGGGG 1132  
Qy 1073 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTAACTTGAACATCAGAGA 1132  
Db 1133 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTAACTTGAACATCAGAGA 1192  
Qy 1133 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCCTGGGAGG 1192  
Db 1193 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCCTGGGAGG 1252  
Qy 1193 AGATAAAACATCTTACGCTGAGTAAGGAGAGTACTGAGTGAATACTGCTTTTCTG 1252  
Db 1253 AGATAAAACATCTTACGCTGAGTAAGGAGAGTACTGAGTGAATACTGCTTTTCTG 1312  
Qy 1253 GTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTACACAGCTGATTTCTGGGAGC 1312  
Db 1313 GTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTACACAGCTGATTTCTGGGAGC 1372  
Qy 1313 ACATCCATTTTCAATGGCAAGATCCAGGGCAGCGCGGCTGGGCTTGGGCTACATGC 1372  
Db 1373 ACATCCATTTTCAATGGCAAGATCCAGGGCAGCGCGGCTGGGCTTGGGCTACATGC 1432  
Qy 1373 TGAACCTGACCAATGATCCAGCTGAGCAACCAATGTCACACCTCTCTCCCACTCA 1432  
Db 1433 TGAACCTGACCAATGATCCAGCTGAGCAACCAATGTCACACCTCTCTCCCACTCA 1492  
Qy 1433 CCTA 1436  
Db 1493 CCTA 1496

RESULT 5  
HSU87967  
LOCUS HSU87967 1704 bp mRNA linear PRI 18-FEB-1997  
DEFINITION Human ATP diphosphohydrolase mRNA, complete cds.  
ACCESSION U87967

VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

U87967.1 GI:1842119  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1704)  
Kaczmarek,E., Koziak,K., Sevigny,J., Siegel,J.B., Anrather,J.,  
Beaudoin,A.R., Bach,F.H. and Robson,S.C.  
Identification and characterization of CD39/vascular ATP  
diphosphohydrolase  
J. Biol. Chem. 271 (51), 33116-33122 (1996)  
97115858  
8955160  
2 (bases 1 to 1704)  
Robson,S.C., Kaczmarek,E., Siegel,J.B., Candinas,D., Koziak,K.,  
Millan,M., Hancock,W.W. and Bach,F.H.  
Loss of ATP diphosphohydrolase activity with endothelial cell  
activation  
J. Exp. Med. 185 (1), 153-163 (1997)  
97149443  
8996251  
3 (bases 1 to 1704)  
Kaczmarek,E., Koziak,K., Sevigny,J., Siegel,J.B., Anrather,J.,  
Beaudoin,A.R., Bach,F.H. and Robson,S.C.  
Direct Submission  
Submitted (30-JAN-1997) Medicine, Harvard University, 99 Brookline  
Avenue, BIDMC, RN, Boston, MA 02215, USA  
Location/Qualifiers  
1..1704  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/chromosome="10"  
/cell\_type="endothelial cells"  
/tissue\_type="umbilical vein"  
31..1563  
/note="CD39"  
/codon\_start=1  
/product="ATP diphosphohydrolase"  
/protein\_id="AAB47572.1"  
/db\_xref="GI:1842120"  
/translation="MEDTGSNVTFCSTKNILAILGPFSSIIAVIALAVGTQNKALP  
ENVKGVTLVDSGSHSLYIKWPAEKENDTVGVHVEECRVKGGISLKFQKVEIG  
IYLDCHMERAREVIPRSHOBTVPVLGATAGMLRLMESEBELADRLDLDVRSLSNYP  
FDPOGARITGQEGAGVMTINVLGKFSQKTFWFSIVPVETNNQTFGALDGGAS  
TQVTFVQNTIESPDNALQFRLYKGDYNYVTHSFLCYGKQDALWKLAKIQUASNE  
ILRDPCHPGTKKVVNVSDLYKTPCTKRFEMLTLPFQFEIGIQNYQQCHOSILLEFN  
TSYCPYSQAFNGIFLPLQDGFAPFVPMKPLNLTSEKVSQERKTEWKKFCAQ  
PWBEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHFTADSWEHIFTKIQGSDAGW  
TLGYMLNLNMIPEAQPLSTPLSHSTYVFLMVLPSLVLTVAIIIGLLIFHKPSYFWKD  
MV"

CDS

ORIGIN

Query Match 91.8%; Score 1319.2; DB 9; Length 1704;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 113 GTTCAACCCAGAACAAAGCATTCGCAGAAAACGTTAAGTATGGATGTGCTGGATGGG 172  
Db 137 GGTTCAGCCAGAACAAAGCATTCGCAGAAAACGTTAAGTATGGATGTGCTGGATGGG 196  
Qy 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGAGAAAAGAGAAATGACACAG 232  
Db 197 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGAGAAAAGAGAAATGACACAG 256  
Qy 233 GCGTGGTGCATCAAGTGAAGAATGACAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 292  
Db 257 GCGTGGTGCATCAAGTGAAGAATGACAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 316  
Qy 293 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATGATTCATGGAAGAGCTAGGGAAGTGA 352  
Db 317 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATGATTCATGGAAGAGCTAGGGAAGTGA 376

QY 353 TTCCAAGGTCCTCCAGACACCAGAGACACCCGTTTACCTGGAGGCCACGGCAGGCGATCGGT 412  
DB 377 TTCCAAGGTCCTCCAGACACCAGAGACACCCGTTTACCTGGAGGCCACGGCAGGCGATCGGT 436  
QY 413 TGCTCAGGATGGAAGTGAAGAGTCTGGCAGACAGGGTTCTCGATGTGGTGGAGAGAGCC 472  
DB 437 TGCTCAGGATGGAAGTGAAGAGTCTGGCAGACAGGGTTCTCGATGTGGTGGAGAGAGCC 496  
QY 473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGAGTCAATTAATCTGGCCAAAGAGAGGTG 532  
DB 497 TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGAGTCAATTAATCTGGCCAAAGAGAGGTG 556  
QY 533 CCTATGGCTGGATTAATCAACTATCTCTGGGCAAAATTCAGTCAGAAAAAAGAGTGT 592  
DB 557 CCTATGGCTGGATTAATCAACTATCTCTGGGCAAAATTCAGTCAGAAAAAAGAGTGT 616  
QY 593 TCAGCATAGTCCCATATGAACCAATAATCAGAAAACTTTGAGGCTTTGGACCTTGGGG 652  
DB 617 TCAGCATAGTCCCATATGAACCAATAATCAGAAAACTTTGAGGCTTTGGACCTTGGGG 676  
QY 653 GAGCCTCTACACAAGTCACTTTTGTATACCCCAAAACAGACTATCGAGTCCCCAGATAATG 712  
DB 677 GAGCCTCTACACAAGTCACTTTTGTATACCCCAAAACAGACTATCGAGTCCCCAGATAATG 736  
QY 713 CTCTGCAATTTCCGCTCTATGGCAAGGACTACAAATGCTTACACATAGCTTCTGTGCT 772  
DB 737 CTCTGCAATTTCCGCTCTATGGCAAGGACTACAAATGCTTACACATAGCTTCTGTGCT 796  
QY 773 ATGGGAAGGATCAGGCACCTCTGCAGAAAATCGGCCAAGGACATTCAGGTTTGCAGTAATG 832  
DB 797 ATGGGAAGGATCAGGCACCTCTGCAGAAAATCGGCCAAGGACATTCAGGTTTGCAGTAATG 856  
QY 833 AAATTTCTCAGGAGCCCATGCTTTCATCTCGGATATAAGAAAGGTAGTGAAGTGAAC 892  
DB 857 AAATTTCTCAGGAGCCCATGCTTTCATCTCGGATATAAGAAAGGTAGTGAAGTGAAC 916  
QY 893 TTTTACAGACCCCTCGCACCAGAGATTTGAGATGACTCTTCATTTCCAGCAGTTTGAAA 952  
DB 917 TTTTACAGACCCCTCGCACCAGAGATTTGAGATGACTCTTCATTTCCAGCAGTTTGAAA 976  
QY 953 TCAGGGTATTTGAAACTATCAACAATGCCATCAAAAGCATCTCTGGAGCTTTCAACACCA 1012  
DB 977 TCAGGGTATTTGAAACTATCAACAATGCCATCAAAAGCATCTCTGGAGCTTTCAACACCA 1036  
QY 1013 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGCCACACATCCAGGGGG 1072  
DB 1037 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGCCACACATCCAGGGGG 1096  
QY 1073 ATTTTGGGGCATTTTCAGCTTTTACTTTGTGTGATGAAGTTTTTAAACTTGAACATCAGAGA 1132  
DB 1097 ATTTTGGGGCATTTTCAGCTTTTACTTTGTGTGATGAAGTTTTTAAACTTGAACATCAGAGA 1156  
QY 1133 AAGTCTCTCAGGAAAAAGGTGACTGAGATGATGAAAAAGTTTCTGTGCTCAGCCTTGGGAGG 1192  
DB 1157 AAGTCTCTCAGGAAAAAGGTGACTGAGATGATGAAAAAGTTTCTGTGCTCAGCCTTGGGAGG 1216  
QY 1193 AGATAAAAAATCTTACGCTGGAGTAAAGAGAAAGTACCTGAGTGAATACTGCTTTTCTG 1252  
DB 1217 AGATAAAAAATCTTACGCTGGAGTAAAGAGAAAGTACCTGAGTGAATACTGCTTTTCTG 1276  
QY 1253 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAGCTGATTCCTCGGAGC 1312  
DB 1277 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAGCTGATTCCTCGGAGC 1336  
QY 1313 ACATCCATTTTCAITGGCAAGATCCAGGCGACGCGCGCTGGACTTTGGGCTACATGC 1372  
DB 1337 ACATCCATTTTCAITGGCAAGATCCAGGCGACGCGCGCTGGACTTTGGGCTACATGC 1396  
QY 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCACTCCA 1432  
DB 1397 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCACTCCA 1456

QY 1433 CCTA 1436  
DB 1457 CCTA 1460  
RESULT 6  
LOCUS AR168353 1818 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 2 from patent US 6287837.  
ACCESSION AR168353  
VERSION AR168353.1 GI:17904224  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 1818)  
AUTHORS Beaudoin,A.R. and Sevigny,J.  
TITLE Mammalian ATP-diphosphohydrolases and process of purification  
thereof  
JOURNAL Patent: US 6287837-A 2 11-SEP-2001;  
FEATURES Location/Qualifiers  
source 1..1818  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 91.8%; Score 1319.2; DB 6; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 113 GTTCAACCCAGAACAAAGCATTCGCCAGAAAACTTAAGTATGGGATTTGCTGGATGCGG 172  
DB 174 GGTGACCCAGAACAAAGCATTCGCCAGAAAACTTAAGTATGGGATTTGCTGGATGCGG 233  
QY 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCAGCAGAAAAAGAGAGATGACACAG 232  
DB 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGGAGAAATGACACAG 293  
QY 233 GGTGGTGCATCAAGTGTAGAAAGTGCAGGGTTAAAGGTCCTGAAATCTCAAAATTTGTTTC 292  
DB 294 GGTGGTGCATCAAGTGTAGAAAGTGCAGGGTTAAAGGTCCTGAAATCTCAAAATTTGTTTC 353  
QY 293 AGAAAGTAAATGAAATAGGCATTTTACCTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGA 352  
DB 354 AGAAAGTAAATGAAATAGGCATTTTACCTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGA 413  
QY 353 TTCCAAGTTCCTCAGCACCAGAGACACCCGTTTAACTGGGAGCCACGGCAGGATCGGT 412  
DB 414 TTCCAAGTTCCTCAGCACCAGAGACACCCGTTTAACTGGGAGCCACGGCAGGATCGGT 473  
QY 413 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGAGGTTCTGGATGTGGTGGAGAGAGCC 472  
DB 474 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGAGGTTCTGGATGTGGTGGAGAGAGCC 533  
QY 473 TCAGCAACTACCCCTTTTGAATTCCTGGGTCAGGATCAATTAATCTGGCCAAAGAGAGGTG 532  
DB 534 TCAGCAACTACCCCTTTTGAATTCCTGGGTCAGGATCAATTAATCTGGCCAAAGAGAGGTG 593  
QY 533 CCTATGGCTGGATTAATCAACTATCTCTGGGCAAAATTCAGTCAGAAAAAAGAGTGT 592  
DB 594 CCTATGGCTGGATTAATCAACTATCTCTGGGCAAAATTCAGTCAGAAAAAAGAGTGT 653  
QY 593 TCAGCATAGTCCCATATGAACCAATAATCAGAAAACTTTGGAGCTTTGGACCTTGGGG 652  
DB 654 TCAGCATAGTCCCATATGAACCAATAATCAGAAAACTTTGGAGCTTTGGACCTTGGGG 713  
QY 653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATG 712  
DB 714 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATG 773  
QY 713 CTCTGCAATTTCCGCTCTATGGCAAGGACTACAAATGCTTACACATAGCTTCTGTGCT 772  
DB 774 CTCTGCAATTTCCGCTCTATGGCAAGGACTACAAATGCTTACACATAGCTTCTGTGCT 833

QY	773	ATGGGAAGGATCAGGCATCTCTGGCAGAAA	CTGCCCAAGGACATTTGAGGTTGCAAGTAATG	832
Db	834	ATGGGAAGGATCAGGCATCTCTGGCAGAAA	CTGCCCAAGGACATTTGAGGTTGCAAGTAATG	893
QY	833	AAATTCTCAGGGACCCATCTTTCTCCTCGGATAT	TAAGAAGGTAGTGAACGTTAAGTGACC	892
Db	894	AAATTCTCAGGGACCCATCTTTCTCCTCGGATAT	TAAGAAGGTAGTGAACGTTAAGTGACC	953
QY	893	TTTACAAGACCCCTGSCACCAAGAGATTTGAGATG	ACTCTTCCATTTCCACGAGTTTGAAA	952
Db	954	TTTACAAGACCCCTGSCACCAAGAGATTTGAGATG	ACTCTTCCATTTCCACGAGTTTGAAA	1013
QY	953	TCAGGGTATTGGAAACTATCAACATGCAATG	CCATCAAGCATCTCTGGAGCTCTTCAACACCA	1012
Db	1014	TCAGGGTATTGGAAACTATCAACATGCAATG	CCATCAAGCATCTCTGGAGCTCTTCAACACCA	1073
QY	1013	GTACTCGCCCTTACTCCAGTGTGCTTCAATGG	GAATTTCTGCGCACCATCTCCAGGGGG	1072
Db	1074	GTACTCGCCCTTACTCCAGTGTGCTTCAATGG	GAATTTCTGCGCACCATCTCCAGGGGG	1133
QY	1073	ATTTTGGGGCATTTTCAGCTTTTACTTTGTGAT	GAAATTTTAACTTTGACATCAGAGA	1132
Db	1134	ATTTTGGGGCATTTTCAGCTTTTACTTTGTGAT	GAAATTTTAACTTTGACATCAGAGA	1193
QY	1133	AAGTCTCTCAGGAAAGGTGACTGAGATGAT	GAAAAAGTTCTGTGCTCAGCCCTTGGGAGG	1192
Db	1194	AAGTCTCTCAGGAAAGGTGACTGAGATGAT	GAAAAAGTTCTGTGCTCAGCCCTTGGGAGG	1253
QY	1193	AGATAAACAATCTTACGCTGAGTAAAGGAGA	GTACCTGAGTGAATCTGCTTTCTG	1252
Db	1254	AGATAAACAATCTTACGCTGAGTAAAGGAGA	GTACCTGAGTGAATCTGCTTTTCTG	1313
QY	1253	GTACCTACATCTCTCCCTCTCTGCAAGGCT	TATCATTTACAGCTGATTCCTGGGAGC	1312
Db	1314	GTACCTACATCTCTCCCTCTCTGCAAGGCT	TATCATTTACAGCTGATTCCTGGGAGC	1373
QY	1313	ACATCCATTTTCAATGGCAAGATCCAGGG	CAGCGCGGCTGGACTTTGGGCTACATGC	1372
Db	1374	ACATCCATTTTCAATGGCAAGATCCAGGG	CAGCGCGGCTGGACTTTGGGCTACATGC	1433
QY	1373	TGAACCTGACCAACATGATCCAGCTGAGCA	ACCAATTTGTCCACACTCTCTCCCACTCCA	1432
Db	1434	TGAACCTGACCAACATGATCCAGCTGAGCA	ACCAATTTGTCCACACTCTCTCCCACTCCA	1493
QY	1433	CCTA 1436		
Db	1494	CCTA 1497		

RESULT 7  
AR380930  
LOCUS AR380930 1818 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 1475 from patent US 6607879.  
ACCESSION AR380930  
VERSION AR380930.1 GI:40088564  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1818)  
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.  
TITLE Compositions for the detection of blood cell and immunological response gene expression  
JOURNAL Patent: US 6607879-A 1475 19-AUG-2003;  
FEATURES Location/Qualifiers  
1..1818  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 91.8%; Score 1319.2; DB 6; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;

		Matches 1121; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	113	GTTCACCCAGAACAAAGCATTTGCCAGAAAACGTT	TAAGTATGGGATTTGTCTGGATGCGG 172
Db	174	GGTTGACCCAGAACAAAGCATTTGCCAGAAAACGTT	TAAGTATGGGATTTGTCTGGATGCGG 233
QY	173	GTTCCTTCTCACACAAGTTTATACATCTATTAAGT	TGCGCCAGCAAGAAAGGAGAAATGACACAG 232
Db	234	GTTCCTTCTCACACAAGTTTATACATCTATTAAGT	TGCGCCAGCAAGAAAGGAGAAATGACACAG 293
QY	233	GGTGGTGCATCAACTAGAAAGTACGAGGTTTAA	AGGTCCTGGAATCTCAGAAATTTGTTTC 292
Db	294	GGTGGTGCATCAACTAGAAAGTACGAGGTTTAA	AGGTCCTGGAATCTCAGAAATTTGTTTC 353
QY	293	AGAAAGTAAATGAAATAGGCATTTTACCTGACT	GTGATTTGCATGGAAGAGCTAGGGAAGTGA 352
Db	354	AGAAAGTAAATGAAATAGGCATTTTACCTGACT	GTGATTTGCATGGAAGAGCTAGGGAAGTGA 413
QY	353	TTCCAAGGTGCCAGCACCAAGAGACACCCGTTT	TACCTGGAGCCACGGCAGGCGATCGCGT 412
Db	414	TTCCAAGGTGCCAGCACCAAGAGACACCCGTTT	TACCTGGAGCCACGGCAGGCGATCGCGT 473
QY	413	TGCTCAGGATGGAAAGTGAAGTTGGCAGACAG	GAGGTTCTGATGTGGGAGAGAGCC 472
Db	474	TGCTCAGGATGGAAAGTGAAGTTGGCAGACAG	GAGGTTCTGATGTGGGAGAGAGCC 533
QY	473	TCAGCAACTACCCCTTTGACTTTCCAGGGTGCC	CAGGATCATTACTGGCCCAAGAGGAGGTG 532
Db	534	TCAGCAACTACCCCTTTGACTTTCCAGGGTGCC	CAGGATCATTACTGGCCCAAGAGGAGGTG 593
QY	533	CCTATGGCTGGATTACTATCAACTATCTGCTGG	GCAAAATTCAGTCAGAAAAACAAGGTGT 592
Db	594	CCTATGGCTGGATTACTATCAACTATCTGCTGG	GCAAAATTCAGTCAGAAAAACAAGGTGT 653
QY	593	TCAGATAGTCCCATATGAAACCAATATCAGAA	ACCTTTGGAGCTTTGGACCTTTGGGG 652
Db	654	TCAGATAGTCCCATATGAAACCAATATCAGAA	ACCTTTGGAGCTTTGGACCTTTGGGG 713
QY	653	GAGCCTCTACACAAGTCACTTTTGTACCCCAA	AAACACAGACTATCAGTCCCCAGATAATG 712
Db	714	GAGCCTCTACACAAGTCACTTTTGTACCCCAA	AAACACAGACTATCAGTCCCCAGATAATG 773
QY	713	CTCTGCAATTTGGCTCTATGGCAAGGACTACA	ATGTCTACACATAGCTTTCTGTGT 772
Db	774	CTCTGCAATTTGGCTCTATGGCAAGGACTACA	ATGTCTACACATAGCTTTCTGTGT 833
QY	773	ATGGGAAGGATCAGGCATCTGGCAGAAAACCT	GGCCCAAGGACATTCAGSTTGCAGTAATG 832
Db	834	ATGGGAAGGATCAGGCATCTGGCAGAAAACCT	GGCCCAAGGACATTCAGSTTGCAGTAATG 893
QY	833	AAATTTCTCAGGGACCCATGCTTTTCATCTCG	TGATATAGAAGGTAGTGAACGTTAAGTGACC 892
Db	894	AAATTTCTCAGGGACCCATGCTTTTCATCTCG	TGATATAGAAGGTAGTGAACGTTAAGTGACC 953
QY	893	TTTACAAGACCCCTGSCACCAAGAGATTTGAG	ATGACTCTTCCATTTCCAGCAGATTTGAAA 952
Db	954	TTTACAAGACCCCTGSCACCAAGAGATTTGAG	ATGACTCTTCCATTTCCAGCAGATTTGAAA 1013
QY	953	TCAGGGTATTGGAAAACCTATCAACATGCCAT	CAAGCATCTCTGGAGCTCTTCAACACCA 1012
Db	1014	TCAGGGTATTGGAAAACCTATCAACATGCCAT	CAAGCATCTCTGGAGCTCTTCAACACCA 1073
QY	1013	GTACTCGCCCTTACTCCAGTGTGCTTCAATGG	ATTTCTCAATGGATTTTCTGCGCACCATCTCCAGGGGG 1072
Db	1074	GTACTCGCCCTTACTCCAGTGTGCTTCAATGG	ATTTCTCAATGGATTTTCTGCGCACCATCTCCAGGGGG 1133
QY	1073	ATTTTGGGGCATTTTCAGCTTTTACTTTGTGAT	GAAATTTTAACTTTGACATCAGAGA 1132
Db	1134	ATTTTGGGGCATTTTCAGCTTTTACTTTGTGAT	GAAATTTTAACTTTGACATCAGAGA 1193
QY	1133	AAGTCTCTCAGGAAAGGTGACTGAGATGAT	GAAAAAGTTCTGTGCTCAGCCCTTGGGAGG 1192
Db	1194	AAGTCTCTCAGGAAAGGTGACTGAGATGAT	GAAAAAGTTCTGTGCTCAGCCCTTGGGAGG 1253



```
QY 1193 AGTAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATCTGCTTTCTG 1252
Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATCTGCTTTCTG 1313
QY 1253 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTACAGCTGATTTCTCGGAGC 1312
Db 1314 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTACAGCTGATTTCTCGGAGC 1373
QY 1313 ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGACCGCGCTGGACTTTGGGCTACATGC 1372
Db 1374 ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGACCGCGCTGGACTTTGGGCTACATGC 1433
QY 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACATTTGTCCACACCTCTCTCCACTCCA 1432
Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACATTTGTCCACACCTCTCTCCACTCCA 1493
QY 1433 CCTA 1436
Db 1494 CCTA 1497

RESULT 8
AX828644
LOCUS
DEFINITION Sequence 290 from Patent WO03074073.
ACCESSION AX828644
VERSION AX828644.1 GI:39838595
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Al-Mahmood,S., Colin,S. and Schneider,C.
TITLE Genes involved in regulating angiogenesis, pharmaceutical
preparations containing same and applications thereof
JOURNAL Patent: WO 03074073-A 290 12-SEP-2003;
FEATURES
source Location/Qualifiers
1..1818
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 91.8%; Score 1319.2; DB 6; Length 1818;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GTTCAACCCGAAACAAAGCATTCGCAGAAACGTTAAGTATGGATTGTCTGGATCGCG 172
Db 174 GGTGACCCGAAACAAAGCATTCGCAGAAACGTTAAGTATGGATTGTCTGGATCGCG 233
QY 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG 232
Db 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG 293
QY 233 GCGTGGTGATCAAGTAGAAGAAATGCAAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 292
Db 294 GCGTGGTGATCAAGTAGAAGAAATGCAAGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 353
QY 293 AGAAAGTAAATGAATAGGCAATTTACTGATGATGATGGAAGAGCTAGGGAAGTGA 352
Db 354 AGAAAGTAAATGAATAGGCAATTTACTGATGATGATGGAAGAGCTAGGGAAGTGA 413
QY 353 TTCCAGGTCCTCCAGCAACAGACACCCCTTTTACCTTGGGAGCCAGCGGATCGGCT 412
Db 414 TTCCAGGTCCTCCAGCAACAGACACCCCTTTTACCTTGGGAGCCAGCGGATCGGCT 473
QY 413 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGCC 472
Db 474 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGCC 533
```

RESULT 9  
S73813  
LOCUS

S73813 1818 bp mRNA linear PRI 12-APR-1995



DEFINITION	CD39-lymphoid cell activation antigen [human, B lymphoblastoid cell line, MP-1, mRNA, 1818 nt].									
ACCESSION	S73813									
VERSION	S73813.1 GI:765255									
KEYWORDS										
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1818)									
AUTHORS	Maliszewski,C.R., Delepese,G.J., Schoenborn,M.A., Armitage,R.J., Fanslow,W.C., Nakajima,T., Baker,E., Sutherland,G.R., Poindexter,K., Birks,C. et,al.,									
TITLE	The CD39 lymphoid cell activation antigen. Molecular cloning and structural characterization									
JOURNAL	J. Immunol. 153 (8), 3574-3583 (1994)									
MEDLINE	95015846									
PUBMED	7930580									
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gi5668156681] from the original journal article.									
FEATURES	Location/Qualifiers									
source	1..1818									
	/organism="Homo sapiens"									
	/mol_type="mRNA"									
	/db_xref="taxon:9606"									
gene	1..1818									
	/gene="CD39"									
	/note="lymphoid cell activation antigen, CD39"									
CDS	68..1600									
	/gene="CD39"									
	/note="guanosine diphosphatase homolog; yeast guanosine diphosphatase homolog"									
	/codon_start=1									
	/product="lymphoid cell activation antigen"									
	/protein_id="AAB32152.1"									
	/db_xref="GI:765256"									
	/translation="MEDTCSNVKTFCKNILALGPFSSIIAVIALVGLTQNKALP ENYKGVLDAGSHTSLYTKWPAEKENDTVQHVQVECKRKGPSKFKVKNRIG IYLTDCMERAEVTPRSQHOETPVYLGKATAGMRLMSEBELADRLVDVVERLSLVG PDFOGARIITGOESGAYGWTINVLLGKFSQKTRWFSIVPTNNQETFGALDGGAS TQTVFVQNQTIESPNDALOFRLYKDKYNYVTHFSFLCYGKDQKLAKDIOVASNE ILKDPCHPHGKTKVNVSDLYKTPCKRFTMTLPFOFEIGQIGNYQQHQSLIELFN TSYCPYSCAFNGFILPPLQDGFAGSAYFVMKFLNLTSEKVSQKVTMMKKFCAQ PWBEIKTSYAGVKEKYLSEYCFSGTYILSLLOQYHTDASWEHIHFIKIQSGDAGM TLGYMLNLTNMIPAEQPLSTPLSHSTVTVFLMWLFSVLFTVAIIGLLIFHKPSYFVKD MV"									
ORIGIN										
Query Match	91.8%; Score 1319.2; DB 9; Length 1818;									
Best Local Similarity	99.8%; pred. No. 0;									
Matches 1321; Conservative	0; Mismatches 3; Indels 0; Gaps 0;									
Qy	113	GTTCACCCAGAACAAAGCATTCGCCAGAAACGTTAAGTATGGATTTGCTCGATCGCG	172							
Db	174	GGTTGACCCAGAACAAAGCATTCGCCAGAAACGTTAAGTATGGATTTGCTCGATCGCG	233							
Qy	173	GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAGGAGAAATGACACAG	232							
Db	234	GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAGGAGAAATGACACAG	293							
Qy	233	CGGTGGTGCATCAAGTAGAAGATTCAGGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTC	292							
Db	294	CGGTGGTGCATCAAGTAGAAGATTCAGGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTC	353							
Qy	293	AGAAAGTAAATGAATAGGCATTATCTGACTGATTCATGGAAGAGCTAGGGAAGTGA	352							
Db	354	AGAAAGTAAATGAATAGGCATTATCTGACTGATTCATGGAAGAGCTAGGGAAGTGA	413							
Qy	353	TTCCAGGTCCTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATCGGT	412							
Db	414	TTCCAGGTCCTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATCGGT	473							
Qy	413	TGCTCAGGATCGAAAGTAGAGATTGGCAGACAGGGTTCTGGATGTGGTGGAGGAGGCC	472							

## RESULT 10



source	1. .2081	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/tissue_type="placenta"	
gene	1. .2081	
CDS	184. .1737	
	/gene="PleA 1"	
	/EC_number="3.6.1.5"	
	/function="apyrase"	
	/codon_start=1	
	/product="ecto-ATP diphosphohydrolase I"	
	/protein_id="CAB41886.1"	
	/db_xref="GI:47411545"	
	/db_xref="GOA:P49961"	
	/db_xref="UniProt/Swiss-Prot:P49961"	
	/translation="MKSGKDLTSQKESNVKTFCSKNLILGFSIIITAVIALAVGL TQNKALPENYKIGVILDAGSSHTSLIYKMPAEKENDGVVHVQVSECRKVGPIKFPV QKNEIGIYLDTCMERAREVIPSQHQETPVYLGATAGMRLLRMESEBELADRLVDVE RSLSNYPDFQVQEGARIIQGEAGWIMITINYLKFSQKRWFSIYVETNNQETFGA LDLGASQTVFPQONQIESPDNALQFRLYKDYNVVTHSPLCYKQDQALWOKLAD IQVAGNEILRDCPHGPKVNVVSDLYKTPCTKRFEMTLPPQOPEIOGIGNYOQCHO SLELEPNYSYCSQAFNGIFLPLQDGFAPSAFYFMKFLNLTSSKVSQEKVTEM MKFCAQPEEIKTSIAGVKEKILSEYCFSGYIILSLQGHFTSWHEHIFHGKI QGSAGWTLGYMLNLNIPAEQPLSTPLSHSYVFLVFLVSLVLTVAIIIGLLIFHK PSYFVKDMV"	
ORIGIN		
Query Match 91.8%; Score 1319.2; DB 9; Length 2081;		
Best Local Similarity 99.8%; Pred. No. 0;		
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
Qy	113	GTTCACCCAGAACAAAGCAATTCAGAGAAACGTTAAAGTATGGGATTTGCTGGATGGG 172
Db	311	GGTTCACCCAGAACAAAGCAATTCAGAGAAACGTTAAAGTATGGGATTTGCTGGATGGG 370
Qy	173	GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAGAGAAATGACACAG 232
Db	371	GTTCTTCTCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAGAGAAATGACACAG 430
Qy	233	GGTGGTGGTCACAGTAGAAGATCCAGGGTTAAAGGTCCTGGATCTCAAAATTTGTTTC 292
Db	431	GGTGGTGGTCACAGTAGAAGATCCAGGGTTAAAGGTCCTGGATCTCAAAATTTGTTTC 490
Qy	293	AGAAAGTAAATGAAATAGGATTTACCTGACTGATTTGCATGGAAGAGAGCTAGGGAAGTGA 352
Db	491	AGAAAGTAAATGAAATAGGATTTACCTGACTGATTTGCATGGAAGAGAGCTAGGGAAGTGA 550
Qy	353	TTTCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGAGGCCACGGCAGGCATGCGGT 412
Db	551	TTTCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGAGGCCACGGCAGGCATGCGGT 610
Qy	413	TGCTCAGATGGAAGAGTGAAGAGTTGGCGACAGAGGTTCTGGATGTGGTGGAGAGGCC 472
Db	611	TGCTCAGATGGAAGAGTGAAGAGTTGGCGACAGAGGTTCTGGATGTGGTGGAGAGGCC 670
Qy	473	TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGGCCCAAGAGGAAGTG 532
Db	671	TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGGCCCAAGAGGAAGTG 730
Qy	533	CCTATGGCTGGATTACTCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 592
Db	731	CCTATGGCTGGATTACTCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 790
Qy	593	TCAGATAGTCCCATATGAACCAATAATACAGAAACCTTTGGAGCTTTGACCTTGGGG 652
Db	791	TCAGATAGTCCCATATGAACCAATAATACAGAAACCTTTGGAGCTTTGACCTTGGGG 850
Qy	653	GAGCCTCTACAAAGTCACTTTTGTACCCCAAAACACAGACTATCCAGTCCCAAGATAATG 712
Db	851	GAGCCTCTACAAAGTCACTTTTGTACCCCAAAACACAGACTATCCAGTCCCAAGATAATG 910

Qy	713	CTCTCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCT 772
Db	911	CTCTCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCT 970
Qy	773	ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCCAAGGACATTCAGGTTGCAAGTAATG 832
Db	971	ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCCAAGGACATTCAGGTTGCAAGTAATG 1030
Qy	833	AAATTTCTCAGGAGCCCATGCTTTTCATCTCTGGATATAAGAAGGTAGTGAACGTAAGTGACC 892
Db	1031	AAATTTCTCAGGAGCCCATGCTTTTCATCTCTGGATATAAGAAGGTAGTGAACGTAAGTGACC 1090
Qy	893	TTTACAAGACCCCTTGACCAAGAGATTTAGATGACTCTTCCATTCAGAGATTTTGAAGA 952
Db	1091	TTTACAAGACCCCTTGACCAAGAGATTTAGATGACTCTTCCATTCAGAGATTTTGAAGA 1150
Qy	953	TCCAGGGTATTGGAAACTATCAACAATGCCATCAAGGATCTCGAGGATCTTCAACACCA 1012
Db	1151	TCCAGGGTATTGGAAACTATCAACAATGCCATCAAGGATCTCGAGGATCTTCAACACCA 1210
Qy	1013	GTTACTGCCCTTACTCTCCAGTGTCCTTCAATGGGATTTTCTTGCCACACACTCCAGGGGG 1072
Db	1211	GTTACTGCCCTTACTCTCCAGTGTCCTTCAATGGGATTTTCTTGCCACACACTCCAGGGGG 1270
Qy	1073	ATTTTGGGGCATTTTACGCTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1132
Db	1271	ATTTTGGGGCATTTTACGCTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1330
Qy	1133	AAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAGAAAGTTCTGTGCTCAGCTTCGGAGG 1192
Db	1331	AAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAGAAAGTTCTGTGCTCAGCTTCGGAGG 1390
Qy	1193	AGATAAAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACCTGCTTTCTG 1252
Db	1391	AGATAAAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACCTGCTTTCTG 1450
Qy	1253	GTACTCATTTCTCTCCCTCTCTCTGCAAGGCTATCATTTACAGCTGATTCCTGGAGC 1312
Db	1451	GTACTCATTTCTCTCCCTCTCTCTGCAAGGCTATCATTTACAGCTGATTCCTGGAGC 1510
Qy	1313	ACATCCATTTTATGGGCAAGATCCAGGACGAGCGCGCTGGAGCTTTGGGCTACATGC 1372
Db	1511	ACATCCATTTTATGGGCAAGATCCAGGACGAGCGCGCTGGAGCTTTGGGCTACATGC 1570
Qy	1373	TGAACCTTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACACTCTCTCCCACTCCA 1432
Db	1571	TGAACCTTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACACTCTCTCCCACTCCA 1630
Qy	1433	CCTA 1436
Db	1631	CCTA 1634
RESULT 12		
CQ870272		
Sequence 693 from Patent WO2004/074320.		
DEFINITION		
CQ870272		
VERSION		
CQ870272.1 GI:51999878		
KEYWORDS		
SOURCE		
Homo sapiens (human)		
ORGANISM		
Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE		
AUTHORS		
Morris, D.W., Morris, D.W. and Malandro, M.S.		
TITLE		
Novel therapeutic targets in cancer		
JOURNAL		
Patent: WO 2004/074320-A 693 02-SEP-2004;		
Sagres Discovery, Inc. (US)		
FEATURES		
Location/Qualifiers		
1. .2986		
/organism="Homo sapiens"		
/mol_type="unassigned DNA"		

/db_xref="taxon:9606"									
ORIGIN									
Query Match 91.8%; Score 1319.2; DB 6; Length 2986;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
QY	113	GTTCACCCAGACAAAGCAATGCCAGAAACGTTAAGTATGGATTGTGCTGGATGCGG	172						
DB	182	GGTTGACCCAGAAACAAAGCAATGCCAGAAACGTTAAGTATGGATTGTGCTGGATGCGG	241						
QY	173	GTTCCTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG	232						
DB	242	GTTCCTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGNATGACACAG	301						
QY	233	GCCTGTGTCATCAAGTAGAAGAAATGACGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC	292						
DB	302	GCCTGTGTCATCAAGTAGAAGAAATGACGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC	361						
QY	293	AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTGGCAAGAGCTAGGGAAGTGA	352						
DB	362	AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTGGCAAGAGCTAGGGAAGTGA	421						
QY	353	TTCCAAAGGTCACAGCAACCAAGAGACACCCCGTTTACCTGGAGCCACGGCAGGCATCGGT	412						
DB	422	TTCCAAAGGTCACAGCAACCAAGAGACACCCCGTTTACCTGGAGCCACGGCAGGCATCGGT	481						
QY	413	TGCTCAGGATGGAAGTAGAAGTGTGGCAGACAGGGTTCTGGATGTGGTGAGAGAGCC	472						
DB	482	TGCTCAGGATGGAAGTAGAAGTGTGGCAGACAGGGTTCTGGATGTGGTGAGAGAGCC	541						
QY	473	TCAGCACTACCCCTTTGACTTCCAGGTCGCCAGGATCATTTACTGCCCAAGAGGAGTG	532						
DB	542	TCAGCACTACCCCTTTGACTTCCAGGTCGCCAGGATCATTTACTGCCCAAGAGGAGTG	601						
QY	533	CCTATGGCTGGATTACTCAACTATCTGTCTGGCCAAATTCAGTCAGAAAAACAAGTGGT	592						
DB	602	CCTATGGCTGGATTACTCAACTATCTGTCTGGCCAAATTCAGTCAGAAAAACAAGTGGT	661						
QY	593	TCAGCATAGTCCCATATGAACCAATAATCAGAAAAACCTTTGGAGCTTTGGACCTTGGGG	652						
DB	662	TCAGCATAGTCCCATATGAACCAATAATCAGAAAAACCTTTGGAGCTTTGGACCTTGGGG	721						
QY	653	GAGCCTCTACACAGTCACCTTTGTATCCCAACCAAGCACTATCGAGTCCCAAGATAAG	712						
DB	722	GAGCCTCTACACAGTCACCTTTGTATCCCAACCAAGCACTATCGAGTCCCAAGATAAG	781						
QY	713	CTCTGCAATTTCCGCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTCTTGCT	772						
DB	782	CTCTGCAATTTCCGCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTCTTGCT	841						
QY	773	ATGGGAAGGATCAGGCATCTGCGAGAAACTGCGCAAGGACATTCAGTTGCAAGTAATG	832						
DB	842	ATGGGAAGGATCAGGCATCTGCGAGAAACTGCGCAAGGACATTCAGTTGCAAGTAATG	901						
QY	833	AAATTTCTCAGGGACCCATGCTTTTCATCTCGATATAAGAGGTAGTGAACGTAAGTGACC	892						
DB	902	AAATTTCTCAGGGACCCATGCTTTTCATCTCGATATAAGAGGTAGTGAACGTAAGTGACC	961						
QY	893	TTTACAAAGACCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA	952						
DB	962	TTTACAAAGACCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA	1021						
QY	953	TCAGGGTATTTGAAACTATCAACAATGCCATCAAAAGCATCTCGAGGCTTCCAAACCA	1012						
DB	1022	TCAGGGTATTTGAAACTATCAACAATGCCATCAAAAGCATCTCGAGGCTTCCAAACCA	1081						
QY	1013	GTTCCTCCCTTACTCCAGTGTCCCTCAATGGGATTTCTTCCACCATCTCCAGGGG	1072						
DB	1082	GTTCCTCCCTTACTCCAGTGTCCCTCAATGGGATTTCTTCCACCATCTCCAGGGG	1141						
QY	1073	ATTTTGGGGCATTTTTCAGCTTTTATCTTGTGATGAAGTTTTTAAACTTTGACATCAGAG	1132						

Db	1142	ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA	1201
QY	1133	AGTCTCTCAGGAAAGGCTGACTGAGATGATGAAAGATTTCTGTCTCAGCCTTTGGGAGG	1192
Db	1202	AAGTCTCTCAGGAAAGGCTGACTGAGATGATGAAAGATTTCTGTCTCAGCCTTTGGGAGG	1261
QY	1193	AGATAAAAAACATCTTTACGCTGGAGTAAAGGAGAACTCCTGAGTGAATACTGCTTTTCTG	1252
Db	1262	AGATAAAAAACATCTTTACGCTGGAGTAAAGGAGAACTCCTGAGTGAATACTGCTTTTCTG	1321
QY	1253	GPACCTACATTTCTCCCTCTCTTCTGCAAGGCTATCTTTCACAGTGAATCTCTGGGAGC	1312
Db	1322	GPACCTACATTTCTCCCTCTCTTCTGCAAGGCTATCTTTCACAGTGAATCTCTGGGAGC	1381
QY	1313	ACATCCATTTCAATTCGGCAGATCCAGGGCAGCGCGCTGGACTTTGGGCTACATGC	1372
Db	1382	ACATCCATTTCAATTCGGCAGATCCAGGGCAGCGCGCTGGACTTTGGGCTACATGC	1441
QY	1373	TGAACCTGACCAACATGATCCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCCTCCA	1432
Db	1442	TGAACCTGACCAACATGATCCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCCTCCA	1501
QY	1433	CCTA 1436	
Db	1502	CCTA 1505	

RESULT 13

Q0870276

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

Q0870276

Sequence 697 from Patent WO2004074320.

Q0870276

Q0870276.1 GI:51999880

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Morris, D.W., Morris, D.W. and Malandro, M.S.

Novel therapeutic targets in cancer

Patent: WO 2004074320-A 697 02-SEP-2004;

Sagres Discovery, Inc. (US)

Location/Qualifiers

1..3236

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 91.8%; Score 1319.2; DB 6; Length 3236;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	113	GTTCACCCAGACAAAGCAATGCCAGAAACGTTAAGTATGGATTGTGCTGGATGCGG	172
DB	432	GGTTGACCCAGAAACAAAGCAATGCCAGAAACGTTAAGTATGGATTGTGCTGGATGCGG	491
QY	173	GTTCCTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG	232
DB	492	GTTCCTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAATGACACAG	551
QY	233	GCCTGTGTCATCAAGTAGAAGAAATGACGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC	292
DB	552	GCCTGTGTCATCAAGTAGAAGAAATGACGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC	611
QY	293	AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTGGCAAGAGCTAGGGAAGTGA	352
DB	612	AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTGGCAAGAGCTAGGGAAGTGA	671
QY	353	TTCCAAAGGTCACAGCAACCAAGAGACACCCCGTTTACCTGGAGCCACGGCAGGCATCGGT	412
DB	672	TTCCAAAGGTCACAGCAACCAAGAGACACCCCGTTTACCTGGAGCCACGGCAGGCATCGGT	731

```
Qy 413 TGCTCAGGATGGAAGTGAAGTTCGCAGACAGGGTTCCTGGATGTGTGGAGAGGCC 472
Db |||||
Qy 732 TGCTCAGGATGGAAGTGAAGTTCGCAGACAGGGTTCCTGGATGTGTGGAGAGGCC 791
Db |||||
Qy 473 TCAGGAACCTACCCCTTTGACTCCAGGGTCCAGGATCATTAATGCGCCAAAGAGGAGGTG 532
Db |||||
Qy 792 TCAGGAACCTACCCCTTTGACTCCAGGGTCCAGGATCATTAATGCGCCAAAGAGGAGGTG 851
Db |||||
Qy 533 CCTATGGCTGGATTACTATCAATATCTCTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 592
Db |||||
Qy 852 CCTATGGCTGGATTACTATCAATATCTCTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 911
Db |||||
Qy 593 TCAGCATATGCCATATGAACCAATAATCAGAAAACTTTTGGAGCTTTGGACCTTTGGGG 652
Db |||||
Qy 912 TCAGCATATGCCATATGAACCAATAATCAGAAAACTTTTGGAGCTTTGGACCTTTGGGG 971
Db |||||
Qy 653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 712
Db |||||
Qy 972 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 1031
Db |||||
Qy 713 CTCTGCAATTTCCCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTTGTGT 772
Db |||||
Qy 1032 CTCTGCAATTTCCCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTTGTGT 1091
Db |||||
Qy 773 ATGGAAGGATCAGGACCTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 832
Db |||||
Qy 1092 ATGGAAGGATCAGGACCTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 1151
Db |||||
Qy 833 AAATTTCTCAGGACCCATGCTTTTCATCTGGATATAAGAGTAGTAGAAGTGAAGTACC 892
Db |||||
Qy 1152 AAATTTCTCAGGACCCATGCTTTTCATCTGGATATAAGAGTAGTAGAAGTGAAGTACC 1211
Db |||||
Qy 893 TTTTCAAGACCCCTGCACCAAGAGATTTGAGATCACTCTTCATCTTCAGCAGATTTGAAA 952
Db |||||
Qy 1212 TTTTCAAGACCCCTGCACCAAGAGATTTGAGATCACTCTTCATCTTCAGCAGATTTGAAA 1271
Db |||||
Qy 953 TCCAGGGTATTTGGAACCTATCAACCAATGCCATCAAAAGCATCTCGAGCTTTCAACACCA 1012
Db |||||
Qy 1272 TCCAGGGTATTTGGAACCTATCAACCAATGCCATCAAAAGCATCTCGAGCTTTCAACACCA 1331
Db |||||
Qy 1013 GTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTCTTGCCACACACTCCAGGGGG 1072
Db |||||
Qy 1332 GTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTCTTGCCACACACTCCAGGGGG 1391
Db |||||
Qy 1073 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTAACTTTGACATCAGAGA 1132
Db |||||
Qy 1392 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTAACTTTGACATCAGAGA 1451
Db |||||
Qy 1133 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGGCTTTGGGAGG 1192
Db |||||
Qy 1452 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGGCTTTGGGAGG 1511
Db |||||
Qy 1193 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATPACTGCTTTTCTG 1252
Db |||||
Qy 1512 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATPACTGCTTTTCTG 1571
Db |||||
Qy 1253 GTACCTACATCTCTCCCTCTCTCTGCAAGGCTATCAATTCACAGCTGATTCCTGGGAGC 1312
Db |||||
Qy 1572 GTACCTACATCTCTCCCTCTCTCTGCAAGGCTATCAATTCACAGCTGATTCCTGGGAGC 1631
Db |||||
Qy 1313 ACATCCATTTTCAATTTGGCAAGATCCAGGGCAGCGAGCGGCTGGACTTTGGGCTACATGC 1372
Db |||||
Qy 1632 ACATCCATTTTCAATTTGGCAAGATCCAGGGCAGCGAGCGGCTGGACTTTGGGCTACATGC 1691
Db |||||
Qy 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATGTCACACCTCTCTCCCACTCCA 1432
Db |||||
Qy 1692 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATGTCACACCTCTCTCCCACTCCA 1751
Db |||||
Qy 1433 CCTA 1436
Db |||||
Qy 1752 CCTA 1755
```

```
RESULT 14
CQ870270
LOCUS CQ870270 3502 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 691 from Patent WO2004074320.
ACCESSION CQ870270
VERSION CQ870270.1 GI:51999877
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Morris,D.W., Morris,D.W. and Malandro,M.S.
TITLE Novel therapeutic targets in cancer
JOURNAL Patent: WO 2004074320-A 691 02-SEP-2004;
Sagres Discovery, Inc. (US)
FEATURES
source
1..3502
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 91.8%; Score 1319.2; DB 6; Length 3502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 113 GTTCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTTGCTGGATGCGG 172
Db |||||
Qy 698 GGTTCAGCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTTGCTGGATGCGG 757
Db |||||
Qy 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGCAGCAGAAAAGGAGAAATGACACAG 232
Db |||||
Qy 758 GTTCTTCTCACACAAGTTTATACATCTATAAGTGCAGCAGAAAAGGAGAAATGACACAG 817
Db |||||
Qy 233 GCGTGGTGCAATCAAGTAGAAGATTCAGGGTTAAAGTCTCTGGAATCTCAAAATTTGTTC 292
Db |||||
Qy 818 GCGTGGTGCAATCAAGTAGAAGATTCAGGGTTAAAGTCTCTGGAATCTCAAAATTTGTTC 877
Db |||||
Qy 293 AGAAGTAAATGAATAGGCATTTTACCTGACTGATTCGATGCGAAGAGCTAGGGAAGTGA 352
Db |||||
Qy 878 AGAAGTAAATGAATAGGCATTTTACCTGACTGATTCGATGCGAAGAGCTAGGGAAGTGA 937
Db |||||
Qy 353 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGCGCATGCGGT 412
Db |||||
Qy 938 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGCGCATGCGGT 997
Db |||||
Qy 413 TGCTCAGGATGGAAGTGAAGATTCGAGACAGGGTTCTGGATGTGTGGAGAGGAGCC 472
Db |||||
Qy 998 TGCTCAGGATGGAAGTGAAGATTCGAGACAGGGTTCTGGATGTGTGGAGAGGAGCC 1057
Db |||||
Qy 473 TCAGCAACTACCCCTTTGACTTCAGGGTGCAGGATCATTTACTGGCCCAAGAGGAGTG 532
Db |||||
Qy 1058 TCAGCAACTACCCCTTTGACTTCAGGGTGCAGGATCATTTACTGGCCCAAGAGGAGTG 1117
Db |||||
Qy 533 CCTATGCTGATTTACTATCAACTATCTCTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 592
Db |||||
Qy 1118 CCTATGCTGATTTACTATCAACTATCTCTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 1177
Db |||||
Qy 593 TCAGCATATGCCATATGAACCAATAATCAGGAAAACCTTTGGAGCTTTGGACCTTTGGGG 652
Db |||||
Qy 1178 TCAGCATATGCCATATGAACCAATAATCAGGAAAACCTTTGGAGCTTTGGACCTTTGGGG 1237
Db |||||
Qy 653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATTCAGTCCCAAGATAATG 712
Db |||||
Qy 1238 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATTCAGTCCCAAGATAATG 1297
Db |||||
Qy 713 CTCTGCAATTTCCCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTTGTGT 772
Db |||||
Qy 1298 CTCTGCAATTTCCCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTTGTGT 1357
Db |||||
Qy 773 ATGGGAAGGATCAGGCACTCTGGCAGAAAACCTGGCCAAAGGACATTCAGGTTGCAAGTAATG 832
```

Db	1358	ATGGGAAGATCAGGACCTCTGGCAGAACTGGCCAAAGACATTCAGGTTCGAAGTAATG	1417	
Qy	833	AAATTCCTCAGGGACCCATGCTTTATCTCTGGATATAAGAAAGGTAAGTGAACGTAAGTGACC	892	
Db	1418	AAATTCCTCAGGGACCCATGCTTTATCTCTGGATATAAGAAAGGTAAGTGAACGTAAGTGACC	1477	
Qy	893	TTTACAAGACCCCTCGACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA	952	
Db	1478	TTTACAAGACCCCTCGACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA	1537	
Qy	953	TCCAGGATATTTGAAACTATCAACAATGCCATCAAAAGCATCTCTGGAGCTCTTCAACACCA	1012	
Db	1538	TCCAGGATATTTGAAACTATCAACAATGCCATCAAAAGCATCTCTGGAGCTCTTCAACACCA	1597	
Qy	1013	GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGCCACCACCTCCAGGGGG	1072	
Db	1598	GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGCCACCACCTCCAGGGGG	1657	
Qy	1073	ATTTTGGGGCATTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA	1132	
Db	1658	ATTTTGGGGCATTTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA	1717	
Qy	1133	AGCTCTCTCAGGAAAGGTGACTGAGATGATGAAAGTTTCTGTGCTCAGCCCTTGGGAGG	1192	
Db	1718	AGCTCTCTCAGGAAAGGTGACTGAGATGATGAAAGTTTCTGTGCTCAGCCCTTGGGAGG	1777	
Qy	1193	AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG	1252	
Db	1778	AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG	1837	
Qy	1253	GTAACCTACATCTCTCCCTCTCTCTGCAAGGCTATCATTTTCAGCTGATTCCTGGGAGC	1312	
Db	1838	GTAACCTACATCTCTCCCTCTCTCTGCAAGGCTATCATTTTCAGCTGATTCCTGGGAGC	1897	
Qy	1313	ACATTCATTTTATTTGGCAGATCCAGGACGAGCGCGCTGGACTTTTGGGCTACATGC	1372	
Db	1898	ACATTCATTTTATTTGGCAGATCCAGGACGAGCGCGCTGGACTTTTGGGCTACATGC	1957	
Qy	1373	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA	1432	
Db	1958	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA	2017	
Qy	1433	CCTA 1436		
Db	2018	CCTA 2021		
RESULT 15				
AX281833				
LOCUS				
DEFINITION				
Sequence 242 from Patent WO0177389.				
ACCESSION				
AX281833.1				
VERSION				
AX281833.1				
KEYWORDS				
GI:16609084				
SOURCE				
Homo sapiens (human)				
ORGANISM				
Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE				
1				
Shiffman,D., Somogyi,R., Lawn,R., Seilhamer,J.J., Porter,G.J.,				
AUTHORS				
Mikita,T. and Tai,J.				
TITLE				
Genes expressed in foam cell differentiation				
Patent: WO 0177389-A 242 18-OCT-2001;				
Juncyte Genomics, Inc. (US)				
FEATURES				
Location/Qualifiers				
1..4411				
/organism="Homo sapiens"				
/mol_type="unassigned DNA"				
/db_xref="taxon:9606"				
/note="Incyte ID No: 347965.2"				
ORIGIN				

Query Match		91.8%;	Score 1319.2;	DB 6;	Length 4411;
Best Local Similarity		99.8%;	Pred. No. 0;		
Matches 1321;		Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
Qy	113	GTTCACCCAGAACAAAGCATTTGCCAGAAAAAGTAAAGTATGGGATTTGCTGGATGCGG	172		
Db	184	GTTTACCCAGAACAAAGCATTTGCCAGAAAAAGTAAAGTATGGGATTTGCTGGATGCGG	243		
Qy	173	GTTCTTCTCACACAAGTTTATACATCTATAGTGGCCAGCAGAAAAAGGAGATGACACAG	232		
Db	244	GTTCTTCTCACACAAGTTTATACATCTATAGTGGCCAGCAGAAAAAGGAGATGACACAG	303		
Qy	233	GGTGTGTCATCAAGTAGAAGAAATCAGGGTTTAAAGGTCTCTGAAATCTCAAAATTTGTTT	292		
Db	304	GGTGTGTCATCAAGTAGAAGAAATCAGGGTTTAAAGGTCTCTGAAATCTCAAAATTTGTTT	363		
Qy	293	AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTTGCATGGAAGAGAGCTAGGGAAGTGA	352		
Db	364	AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTTGCATGGAAGAGAGCTAGGGAAGTGA	423		
Qy	353	TTCCAAAGTCCAGCAGCAACAGAGACACCCGTTTACTGGAGCCACGGCAGGCATCGCGT	412		
Db	424	TTCCAAAGTCCAGCAGCAACAGAGACACCCGTTTACTGGAGCCACGGCAGGCATCGCGT	483		
Qy	413	TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGAGGTTCTGGATGTGTGGAGAGAGCC	472		
Db	484	TGCTCAGGATGAAAGTGAAGAGTTGGCAGACAGAGGTTCTGGATGTGTGGAGAGAGCC	543		
Qy	473	TCAGCAACTACCCCTTTTGACTTTCCAGGGTGCAGGATCATTTACTGGCCAAAGAGAGGTG	532		
Db	544	TCAGCAACTACCCCTTTTGACTTTCCAGGGTGCAGGATCATTTACTGGCCAAAGAGAGGTG	603		
Qy	533	CTATGGCTGGATTAATCATCTATCAACTATCTGCTGGCCAAATTCAGTCAGAAAAAAGGTG	592		
Db	604	CTATGGCTGGATTAATCATCTATCAACTATCTGCTGGCCAAATTCAGTCAGAAAAAAGGTG	663		
Qy	593	TCAGCATAGTCCATATGAAACCAATTAATCAGGAAACCTTTTGGAGCTTTGGACCTTTGGGG	652		
Db	664	TCAGCATAGTCCATATGAAACCAATTAATCAGGAAACCTTTTGGAGCTTTGGACCTTTGGGG	723		
Qy	653	GAGCCTCTACAAAGTCACTTTTGTACCCCAAAAACAGACTATCGAGTCCCAGATAATG	712		
Db	724	GAGCCTCTACAAAGTCACTTTTGTACCCCAAAAACAGACTATCGAGTCCCAGATAATG	783		
Qy	713	CTCTGCAATTTGCGCTCTATGGCAGGACTACAATGTCTTACACATAGCTTCTTGTGCT	772		
Db	784	CTCTGCAATTTGCGCTCTATGGCAGGACTACAATGTCTTACACATAGCTTCTTGTGCT	843		
Qy	773	ATGGGAAGGATCAGGCACCTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG	832		
Db	844	ATGGGAAGGATCAGGCACCTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG	903		
Qy	833	AAATTTCTCAGGGACCCATGCTTTTCATCTCTGGATATAAGAAAGGTAAGTGAACGTAAGTGACC	892		
Db	904	AAATTTCTCAGGGACCCATGCTTTTCATCTCTGGATATAAGAAAGGTAAGTGAACGTAAGTGACC	963		
Qy	893	TTTACAAGACCCCTCGCAGCAGAAAGATTTGAGATGACTCTTCCATTCACAGCAGTTTGAAA	952		
Db	964	TTTACAAGACCCCTCGCAGCAGAAAGATTTGAGATGACTCTTCCATTCACAGCAGTTTGAAA	1023		
Qy	953	TCCAGGATATTTGAAACTATCAACAATGCCATCAAAAGCATCTCTGGAGCTCTTCAACACCA	1012		
Db	1024	TCCAGGATATTTGAAACTATCAACAATGCCATCAAAAGCATCTCTGGAGCTCTTCAACACCA	1083		
Qy	1013	GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG	1072		
Db	1084	GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG	1143		
Qy	1073	ATTTTGGGGCATTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA	1132		
Db	1144	ATTTTGGGGCATTTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA	1203		
Qy	1133	AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAAGTTTCTGTGCTCAGCCTTGGAGG	1192		



**THIS PAGE BLANK (USPTO)**

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2005, 16:22:05 ; Search time 827.224 Seconds  
(without alignments)  
10283.394 Million cell updates/sec

Title: US-09-807-660C-7

Perfect score: 1437  
Sequence: 1 atggccctgtgtagtcagacag.....ctctctccactccaccta 1437

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1437	100.0	1437	3 AAD00207	Aad00207 Human sol
2	1437	100.0	1437	3 AAD00202	Aad00202 Coding re
3	1400	97.4	1464	3 AAD00209	Aad00209 Human sol
4	1400	97.4	1464	3 AAD00204	Aad00204 Coding re
5	1365	95.0	1365	3 AAD00206	Aad00206 Human sol
6	1365	95.0	1365	3 AAD00201	Aad00201 Fusion co
7	1319.2	91.8	1599	3 AAD00205	Aad00205 Human sol
8	1319.2	91.8	1599	3 AAD00200	Aad00200 Human sol
9	1319.2	91.8	1599	12 ADL24294	Adl24294 Human CD3
10	1319.2	91.8	1704	3 AAA96069	Aaa96069 Human ATP
11	1319.2	91.8	1704	10 ADJ57261	Adj57261 Human CD3
12	1319.2	91.8	1818	2 AAT38516	Aat38516 Human lym
13	1319.2	91.8	1818	2 AAT33966	Aat33966 DNA codin
14	1319.2	91.8	1818	11 ADI32149	Adi32149 Human CDN
15	1319.2	91.8	1818	12 ADK60414	Adk60414 Angiogene
16	1319.2	91.8	1818	12 ADK60715	Adk60715 Angiogene
17	1319.2	91.8	1818	12 ADP73338	Adp73338 CD39 lym
18	1319.2	91.8	2080	11 ADN5840	Adn5840 Human BEC
19	1319.2	91.8	2081	6 ABK83558	Abk83558 Human CDN
20	1319.2	91.8	2081	12 ADK60471	Adk60471 Angiogene

21	1319.2	91.8	2081	12 ADK60772	Adk60772 Angiogene
22	1319.2	91.8	2081	12 ADP73094	Adp73094 Angiogene
23	1319.2	91.8	2986	13 ABD32956	Abd32956 Human can
24	1319.2	91.8	3236	13 ABD32958	Abd32958 Human can
25	1319.2	91.8	3502	13 ABD32955	Abd32955 Human can
26	1319.2	91.8	4411	6 AAS94987	Aas94987 Human DNA
27	1305.2	90.8	3506	13 ABD32957	Abd32957 Human can
28	1287.4	89.6	3244	13 ACN42028	Actn42028 Human dia
29	1119.4	77.9	3165	13 ACN42029	Actn42029 Human dia
30	1039	72.3	1479	10 ADI62639	Adi62639 Human apo
31	835	58.1	2296	13 ABD32952	Abd32952 Mouse can
32	703.2	48.9	1488	13 ABD32954	Abd32954 Human can
c 33	640.2	44.6	704	12 ADK60271	Adk60271 Antisense
c 34	640.2	44.6	704	12 ADK60572	Adk60572 Antisense
c 35	640.2	44.6	704	12 ADP73195	Adp73195 Angiogene
c 36	640.2	44.6	6164	12 ADK60317	Adk60317 Angiogene
c 37	640.2	44.6	6164	12 ADK60618	Adk60618 Angiogene
c 38	640.2	44.6	6164	12 ADP73241	Adp73241 Angiogene
39	414	28.8	475	9 ACH37444	Ach37444 Human end
40	379	26.4	484	9 ACH35840	Ach35840 Human end
41	291	20.3	2797	3 AAA96067	Aaa96067 Human ect
42	291	20.3	2797	6 AAD31694	Aad31694 Human CD3
43	291	20.3	2797	6 ABK10350	Abk10350 DNA encod
44	291	20.3	2797	12 ADQ99443	Adq99443 Human CD3
45	291	20.3	2797	13 ADR69172	Adr69172 Human CD3

ALIGNMENTS

RESULT 1

AAD00207

ID AAD00207 standard; DNA; 1437 BP.

XX

AC AAD00207;

XX

DT 17-AUG-2000 (first entry)

XX

DE Human soluble CD39 fusion DNA construct, pIL2LsolCD39.

XX

KW Soluble CD39; solCD39; human; apyrase activity; platelet activation;  
unstable angina; myocardial infarction; stroke; coronary artery disease;  
atherosclerosis; peripheral vascular occlusion; thrombotic disorder; embolism;  
platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;  
coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;  
thrombus formation; occlusion; stenosis; restenosis; angiogenesis;  
anti-angiinal; cerebroprotective; antiarteriosclerotic; anticoagulant;  
cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 1..1437

FT /\*tag= a

FT /product= "Fusion protein of pIL2LsolCD39"

FT sig\_peptide 1..72

FT /\*tag= b

FT /note= "Human interleukin 2 (hIL2) leader sequence"

FT misc\_feature 73..108

FT /\*tag= c

FT /product= "Mature human interleukin 2 N-terminal end"

FT misc\_feature 109..117

FT /\*tag= d

FT misc\_feature 118..1434

FT /\*tag= e

FT /note= "Coding region of human soluble CD39 (solCD39)"

XX WO200023459-A1.

XX 27-APR-2000.

PD

XX

PF 13-OCT-1999; 99WO-US022955.  
XX  
PR 16-OCT-1998; 98US-0104585P.  
PR 06-NOV-1998; 98US-0107466P.  
PR 13-AUG-1999; 99US-0149010P.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Maliszewski CR, Gayle RB, Price VL, Gimpel SD;  
XX  
DR WPI; 2000-3339644/29.  
XX P-PSDB; AAY70914.  
DR  
XX New soluble CD39 polypeptides having apyrase activity, useful for  
PT inhibiting angiogenesis and treating unstable angina, myocardial  
PT infarction, stroke, coronary artery disease or injury.  
XX  
PS Claim 15a; Page 97-99; 122pp; English.  
XX  
CC The present DNA sequence is a fusion construct pIL2solCD39, comprising  
CC leader peptide of human interleukin 2 (hIL2), 12 amino acids from the  
CC mature N-terminus of hIL2 and soluble CD39 (solCD39) coding region,  
CC having apyrase activity. This produces high levels of solCD39 expression  
CC and activity in the transfected cells. Soluble CD39 is constructed by  
CC removing the N- and C-terminal transmembrane domains. It retains the  
CC capacity to metabolise ATP and ADP at relevant concentrations and the  
CC ability to block and reverse ADP-induced platelet activation and  
CC recruitment, including platelet aggregation. Soluble CD39 polypeptides  
CC are useful for inhibiting angiogenesis. It is useful for the treatment of  
CC unstable angina, myocardial infarction, stroke, coronary artery disease  
CC or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia,  
CC embolism, platelet-associated ischaemic disorders including lung,  
CC coronary and cerebral ischaemia, thrombotic disorders including coronary,  
CC peripheral and cerebral artery thrombosis, intracardiac and venous  
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary  
CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful  
CC for preventing thrombus formation or reformation, occlusion, reocclusion,  
CC stenosis or restenosis of blood vessels or stroke  
XX  
SQ Sequence 1437 BP; 411 A; 336 C; 335 G; 355 T; 0 U; 0 Other;

Query Match 100.0%; Score 1437; DB 3; Length 1437;  
Best Local Similarity 100.0%; Pred No. 0;  
Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCCCTGTGGATCGACAGGATGCAACTCCTCTCTGTGATTCGCACTAAGTCTTGCACTT 60  
DB 1 ATGGCCCTGTGGATCGACAGGATGCAACTCCTCTCTGTGATTCGCACTAAGTCTTGCACTT 60  
QY 61 GTCACAAACAGTGCACCTACTTCAAGTCTTACAAAGAAACACAGCTAACTAGTTCAACC 120  
DB 61 GTCACAAACAGTGCACCTACTTCAAGTCTTACAAAGAAACACAGCTAACTAGTTCAACC 120  
QY 121 CAGAACAAAGCATTTGCAGAAAACGTTAAGTATGGGATTTGCTGGATCGGGTCTTCTCT 180  
DB 121 CAGAACAAAGCATTTGCAGAAAACGTTAAGTATGGGATTTGCTGGATCGGGTCTTCTCT 180  
QY 181 CACACAAAGTTTATACATCTATAAGTGCCAGCAGAAAAGAGAAATGACACAGCGTGGTG 240  
DB 181 CACACAAAGTTTATACATCTATAAGTGCCAGCAGAAAAGAGAAATGACACAGCGTGGTG 240  
QY 241 CATCAAGTAGAAGATGCAGGGTTAAAGTCTCGGATCTCAAAATTTGTTCAAGAAAGTA 300  
DB 241 CATCAAGTAGAAGATGCAGGGTTAAAGTCTCGGATCTCAAAATTTGTTCAAGAAAGTA 300  
QY 301 AATGAAATAGGCATTTACCTGACTGATTTGCATGGAAGAGCTAGGGAAGTATTCCAAGG 360  
DB 301 AATGAAATAGGCATTTACCTGACTGATTTGCATGGAAGAGCTAGGGAAGTATTCCAAGG 360  
QY 361 TCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGCGAGCATGCGGTTGCTCAGG 420  
DB 361 TCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGCGAGCATGCGGTTGCTCAGG 420

RESULT 2  
AAD00202  
ID AAD00202 standard; DNA; 1437 BP.  
XX

QY 421 ATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCCTCAGCAAC 480  
DB |||||  
QY 421 ATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCCTCAGCAAC 480  
DB |||||  
QY 481 TACCCCTTTGACTTCCAGGGTCCAGGATCAATTACTGGCCAAAGAGAAAGTGCCTATGCG 540  
DB |||||  
QY 481 TACCCCTTTGACTTCCAGGGTCCAGGATCAATTACTGGCCAAAGAGAAAGTGCCTATGCG 540  
DB |||||  
QY 541 TGGATTACTATCAACTATCTGCTGGCAAAATTCAGTCAGAAAACAAGTGGTTCAGCAT 600  
DB |||||  
QY 541 TGGATTACTATCAACTATCTGCTGGCAAAATTCAGTCAGAAAACAAGTGGTTCAGCAT 600  
DB |||||  
QY 601 GTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTTGGACCTTGGGGAGCCTCT 660  
DB |||||  
QY 601 GTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTTGGACCTTGGGGAGCCTCT 660  
DB |||||  
QY 661 ACACAAGTCACCTTTTGTATACCCCAAAACAGACTATCGAGTCCCCAGATTAATGCTCTGCAA 720  
DB |||||  
QY 661 ACACAAGTCACCTTTTGTATACCCCAAAACAGACTATCGAGTCCCCAGATTAATGCTCTGCAA 720  
DB |||||  
QY 721 TTTGCGCTCTATGGCAAGGACTACAATGCTCTACACATAGCTTTCTTGCTATGGGAAG 780  
DB |||||  
QY 721 TTTGCGCTCTATGGCAAGGACTACAATGCTCTACACATAGCTTTCTTGCTATGGGAAG 780  
DB |||||  
QY 781 GATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTTCAGTTTGCAGTAAATGAAATTTCTC 840  
DB |||||  
QY 781 GATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTTCAGTTTGCAGTAAATGAAATTTCTC 840  
DB |||||  
QY 841 AGGGACCCATGCTTTTCATCTCGGATATAGAAGGTAGTGAACGTAAAGTCACTTTTCAAG 900  
DB |||||  
QY 841 AGGGACCCATGCTTTTCATCTCGGATATAGAAGGTAGTGAACGTAAAGTCACTTTTCAAG 900  
DB |||||  
QY 901 ACCCCTGCACCAAGAGATTGAGATGACTCTTCCATCCAGCAGTTTCAAAATCCAGGCT 960  
DB |||||  
QY 901 ACCCCTGCACCAAGAGATTGAGATGACTCTTCCATCCAGCAGTTTCAAAATCCAGGCT 960  
DB |||||  
QY 961 ATTGGAACACTCAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACACCAAGTACTGTC 1020  
DB |||||  
QY 961 ATTGGAACACTCAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACACCAAGTACTGTC 1020  
DB |||||  
QY 1021 CTTTACTCCAGTGTCCCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGATTTTGGG 1080  
DB |||||  
QY 1021 CTTTACTCCAGTGTCCCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGATTTTGGG 1080  
DB |||||  
QY 1081 GCATTTTCAGCTTTTACTTTGCTGATGAAGTTTAAACTTCACATCAGAGAAAGTCTCT 1140  
DB |||||  
QY 1081 GCATTTTCAGCTTTTACTTTGCTGATGAAGTTTAAACTTCACATCAGAGAAAGTCTCT 1140  
DB |||||  
QY 1141 CAGGAAAAGGTGACATGAGATGATGAAAAGTTCTGTGCTCAGCCTTGGGAGAGATAAAA 1200  
DB |||||  
QY 1141 CAGGAAAAGGTGACATGAGATGATGAAAAGTTCTGTGCTCAGCCTTGGGAGAGATAAAA 1200  
DB |||||  
QY 1201 ACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATATCTGCTTTTCTGGTACTAC 1260  
DB |||||  
QY 1201 ACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATATCTGCTTTTCTGGTACTAC 1260  
DB |||||  
QY 1261 ATTCTCTCCCTCTCTTCTGCAAGGCTATCATTTTCAGCTGATTTCTGGGAGCAGATCCAT 1320  
DB |||||  
QY 1261 ATTCTCTCCCTCTCTTCTGCAAGGCTATCATTTTCAGCTGATTTCTGGGAGCAGATCCAT 1320  
DB |||||  
QY 1321 TTTTATTTGGCAAGATCCAGGGCAGCGCGCTGGACTTTTGGGCTTACATGCTGAACCTG 1380  
DB |||||  
QY 1321 TTTTATTTGGCAAGATCCAGGGCAGCGCGCTGGACTTTTGGGCTTACATGCTGAACCTG 1380  
DB |||||  
QY 1381 ACCAATGATCCAGCTGAGCAACATTTGTCCACCTCTCTCCACCTCCACCTAA 1437  
DB |||||  
QY 1381 ACCAATGATCCAGCTGAGCAACATTTGTCCACCTCTCTCCACCTCCACCTAA 1437  
DB |||||

AC AAD00202;  
 XX 17-AUG-2000 (first entry)  
 XX Coding region of pIL2Lsol CD39.  
 XX Soluble CD39; ADP-induced platelet activation; platelet aggregation;  
 KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
 KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;  
 KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;  
 KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;  
 KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;  
 KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;  
 KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;  
 KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;  
 KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;  
 KW coronary ischaemia; vascular occlusion; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 XX Location/Qualifiers  
 FH 1. .1437  
 FT CDS  
 FT /\*tag= a  
 FT /product= "Fusion construct of pIL2Lsol CD39"  
 FT sig\_peptide  
 FT 1. .72  
 FT /\*tag= b  
 FT /note= "human IL2 leader sequence"  
 FT mat\_peptide  
 FT 73. .108  
 FT /\*tag= c  
 FT /product= "Mature human IL2 protein"  
 FT misc\_feature  
 FT 109. .117  
 FT /\*tag= c  
 FT /note= "a three amino acid linker"  
 FT mat\_peptide  
 FT 118. .1434  
 FT /\*tag= d  
 FT /product= "Soluble CD39 protein"  
 XX  
 XX WO200023094-A2.  
 XX  
 XX 27-APR-2000. 99WO-US023641.  
 XX  
 XX 13-OCT-1999; 99WO-US023641.  
 XX  
 XX 16-OCT-1998; 98US-0104585P.  
 XX 06-NOV-1998; 98US-0107466P.  
 XX 13-AUG-1999; 99US-0149010P.  
 XX  
 XX (IMMV ) IMMUNEX CORP.  
 XX (CORR ) CORNELL RES FOUND INC.  
 XX  
 XX Maliszewski CR, Gayle RB, Marcus AJ;  
 XX  
 XX WPI: 2000-339518/29.  
 XX P-PSDB; AAY70891.  
 XX  
 XX Inhibiting platelet activation and recruitment, useful for treating a  
 XX mammal suffering from unstable angina, myocardial infarction, stroke,  
 XX coronary artery disease or injury, comprises administering soluble CD39  
 XX polypeptides.  
 XX  
 XX Claim 11; Page 97-99; 118pp; English.  
 XX  
 XX The present sequence is coding region of pIL2SolCD39, a fusion construct  
 XX encoding sol(soluble)CD39 having apyrase activity. Fusion of 12 amino  
 XX acids from the N-terminus of mature human IL2 to the solCD39 coding  
 XX region results in high levels of both expression and activity in the  
 XX supernatants of transfected cells. This is used in the treatment of  
 XX unstable angina, myocardial infarction, stroke, coronary artery disease  
 XX or injury, atherosclerosis, peripheral vascular occlusion, preclampsia,  
 XX embolism, platelet-associated ischaemic disorder including lung  
 XX ischaemia, coronary ischaemia and cerebral ischaemia, thrombotic disorder  
 XX including coronary artery thrombosis, cerebral artery thrombosis,  
 XX intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis,

CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary  
 CC embolism (PE), transient ischaemic attack. Soluble CD39 is also useful  
 CC for preventing thrombus formation or reformation, occlusion, reocclusion,  
 CC stenosis or restenosis of blood vessels or stroke  
 XX  
 XX Sequence 1437 BP; 411 A; 336 C; 335 G; 355 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 1437; DB 3; Length 1437;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGGCCCTGTGATCGACAGGATGCAACTCTCTGCTTGCATTGCACATAGCTTTGACATT 60  
 DB 1 ATGGCCCTGTGATCGACAGGATGCAACTCTCTGCTTGCATTGCACATAGCTTTGACATT 60  
 QY 61 GTCAAAAACAGTGACCTTCTCAAGTTCTACAAAAGAAAACACAGCTAACTAGTTCAACC 120  
 DB 61 GTCAAAAACAGTGACCTTCTCAAGTTCTACAAAAGAAAACACAGCTAACTAGTTCAACC 120  
 QY 121 CAGAAACAAAGCATTCGCCAGAAAACGTTAAGTATGGGATTTGCTGGATGCGGGTTCTTCT 180  
 DB 121 CAGAAACAAAGCATTCGCCAGAAAACGTTAAGTATGGGATTTGCTGGATGCGGGTTCTTCT 180  
 QY 181 CACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAAATGACACAGCGGTGGTG 240  
 DB 181 CACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAAATGACACAGCGGTGGTG 240  
 QY 241 CATCAAGTAGAAGATGCAAGGTTAAAGTCTCTGCAATCTCAAAATTTGTTTCAGAAAGTA 300  
 DB 241 CATCAAGTAGAAGATGCAAGGTTAAAGTCTCTGCAATCTCAAAATTTGTTTCAGAAAGTA 300  
 QY 301 AATGAATAGGCATTTACCTGACTGATTCGATGGAAAGAGCTAGGGAAGTGTATTCACAGG 360  
 DB 301 AATGAATAGGCATTTACCTGACTGATTCGATGGAAAGAGCTAGGGAAGTGTATTCACAGG 360  
 QY 361 TCCAGACCCAAAGAGACACCCGTTTACCTGGAGGCCAGCGGAGGATGCGGTGTCTCAGG 420  
 DB 361 TCCAGACCCAAAGAGACACCCGTTTACCTGGAGGCCAGCGGAGGATGCGGTGTCTCAGG 420  
 QY 421 ATGGAAGTAGAAGTTGGCAGACAGGTTCTGGATGTGGAGAGAGGAGCCCTCAGCAAC 480  
 DB 421 ATGGAAGTAGAAGTTGGCAGACAGGTTCTGGATGTGGAGAGAGGAGCCCTCAGCAAC 480  
 QY 481 TACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGGCCAAAGAGGAAGTGCCTATGCG 540  
 DB 481 TACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGGCCAAAGAGGAAGTGCCTATGCG 540  
 QY 541 TGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTTCAGAAAAACAAGGTGTTTCAGCATA 600  
 DB 541 TGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTTCAGAAAAACAAGGTGTTTCAGCATA 600  
 QY 601 GTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGAGCTTTGGGGGAGCCCTCT 660  
 DB 601 GTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGAGCTTTGGGGGAGCCCTCT 660  
 QY 661 ACACAAGTCACCTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATGCTCTGCAA 720  
 DB 661 ACACAAGTCACCTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATGCTCTGCAA 720  
 QY 721 TTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTCTATGGGAAG 780  
 DB 721 TTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTCTATGGGAAG 780  
 QY 781 GATCAGCAGCTCTCGCAGAACTCGCCAGGACATTCAGGTTGCAAGTAATGAATTCCTC 840  
 DB 781 GATCAGCAGCTCTCGCAGAACTCGCCAGGACATTCAGGTTGCAAGTAATGAATTCCTC 840  
 QY 841 AGGACCCATCTCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAGTACCTTTACAAG 900  
 DB 841 AGGACCCATCTCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAGTACCTTTACAAG 900  
 QY 901 ACCCCCTGCACCAAGAGATTTGAGATGCTCTTCCATTTCCAGAGCTTTGAAATCCAGGT 960  
 DB 901 ACCCCCTGCACCAAGAGATTTGAGATGCTCTTCCATTTCCAGAGCTTTGAAATCCAGGT 960



QY 274 GGAATCTCAAAATTTGTTGTCAGAAAGTAAATGAAATAGGCATTTTACTGTACTGATGTCATG 333  
DB GGAATCTCAAAATTTGTTGTCAGAAAGTAAATGAAATAGGCATTTTACTGTACTGATGTCATG 360  
QY 334 GAAAGAGCTAGGGAAGTATCCAAAGGTCCTCAGCACCAGACCAAGACACCCGTTTACCTGGGA 393  
DB 361 GAAAGAGCTAGGGAAGTATCCAAAGGTCCTCAGCACCAGACCAAGACACCCGTTTACCTGGGA 420  
QY 394 GCCACGGCAGGATCGGTTGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTG 453  
DB 421 GCCACGGCAGGATCGGTTGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTG 480  
QY 454 GATGTGTTGGAGGAGGCTCAGCAACTACCCCTTTTGACTTCCAGGGTCCAGGATCATTT 513  
DB 481 GATGTGTTGGAGGAGGCTCAGCAACTACCCCTTTTGACTTCCAGGGTCCAGGATCATTT 540  
QY 514 ACTGCCAAGAGGAGGTCCTTATGCTGCTGATTTACTATCAACTATCTGTGGGCAATTC 573  
DB 541 ACTGCCAAGAGGAGGTCCTTATGCTGCTGATTTACTATCAACTATCTGTGGGCAATTC 600  
QY 574 AGTCAGAAAACAGGTGGTTTACGATAGTCCCATATGAAACCAATAATCAGGAAACCTTT 633  
DB 601 AGTCAGAAAACAGGTGGTTTACGATAGTCCCATATGAAACCAATAATCAGGAAACCTTT 660  
QY 634 GGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACCTTTTGTATCCCAAAACAGACT 693  
DB 661 GGAGCTTTGGACCTTTGGGGAGCCTCTACACAAGTCACCTTTTGTATCCCAAAACAGACT 720  
QY 694 ATCGAGTCCCAAGATAATGCTCTGCATTTTCCGCTCTATGGCAAGGACTACATGCTTAC 753  
DB 721 ATCGAGTCCCAAGATAATGCTCTGCATTTTCCGCTCTATGGCAAGGACTACATGCTTAC 780  
QY 754 ACACATAGTCTTGTGCTATGGGAGGATCAGGCACCTCTGCAGAAACTGGCCCAAGGAC 813  
DB 781 ACACATAGTCTTGTGCTATGGGAGGATCAGGCACCTCTGCAGAAACTGGCCCAAGGAC 840  
QY 814 ATTCAAGTTGCAAGTAATGAAATTTCTCAGGAGCCCATGCTTTTCATCTCGATATAGAAG 873  
DB 841 ATTCAAGTTGCAAGTAATGAAATTTCTCAGGAGCCCATGCTTTTCATCTCGATATAGAAG 900  
QY 874 TAGTGAAGTAAGTGACCTTTTACAAGACCCCTCGACCAAGAGATTTGAGATGACTCTT 933  
DB 901 TAGTGAAGTAAGTGACCTTTTACAAGACCCCTCGACCAAGAGATTTGAGATGACTCTT 960  
QY 934 CCAATTCACAGCAGTTTGAATCCAGGATATGGAATCTATCAACAATGCCATCAAGGATC 993  
DB 961 CCAATTCACAGCAGTTTGAATCCAGGATATGGAATCTATCAACAATGCCATCAAGGATC 1020  
QY 994 CTGGAGCTTTCAACACCAAGTTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTC 1053  
DB 1021 CTGGAGCTTTCAACACCAAGTTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTC 1080  
QY 1054 TTGCCACCACTCCAGGGGATTTTGGGGATTTTTCAGCTTTTACTTTGTGATGAAGTTT 1113  
DB 1081 TTGCCACCACTCCAGGGGATTTTGGGGATTTTTCAGCTTTTACTTTGTGATGAAGTTT 1140  
QY 1114 TTAACCTTGACATCAGAGAACTCTCTCAGGAAAGGTTGACTGAGATGATGAAGGATTC 1173  
DB 1141 TTAACCTTGACATCAGAGAACTCTCTCAGGAAAGGTTGACTGAGATGATGAAGGATTC 1200  
QY 1174 TGTGCTCAGCCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTG 1233  
DB 1201 TGTGCTCAGCCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTG 1260  
QY 1234 AGTGAATACTGTTTTTCTGGTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTC 1293  
DB 1261 AGTGAATACTGTTTTTCTGGTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTC 1320  
QY 1294 ACAGCTGATCTCTGGAGCACATTCATTTTCATTTGGCAAGATCCAGGGCAGCGCCGCG 1353  
DB 1321 ACAGCTGATCTCTGGAGCACATTCATTTTCATTTGGCAAGATCCAGGGCAGCGCCGCG 1380

QY 1354 TGGACTTTGGGCTACATCTGAACCTGACCAACATGATCCAGCTGAGCAACATTTGTC 1413  
DB TGGACTTTGGGCTACATCTGAACCTGACCAACATGATCCAGCTGAGCAACATTTGTC 1440  
QY 1414 ACACCTCTCTCCCACTCCACCTAA 1437  
DB 1441 ACACCTCTCTCCCACTCCACCTAA 1464  
RESULT 4  
AAD00204  
ID AAD00204 standard; DNA; 1464 BP.  
XX  
AC AAD00204;  
XX  
DT 17-AUG-2000 (first entry)  
XX  
DE Coding region of soluble CD39 expression plasmid.  
KW Soluble CD39; ADP-induced platelet activation; stroke; coronary artery disease;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; pre-eclampsia; embolism;  
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;  
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;  
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;  
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;  
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;  
KW occlusion; reocclusion; stenosis; restenosis; anti-angiogenic; cardiant;  
KW cerebroprotective; anti-arteriosclerotic; vasotrophic; anticoagulant;  
KW coronary ischaemia; vascular occlusion; solCD39 expression plasmid; ss.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1464  
FT /tag= b  
FT /product= "solCD39 expression plasmid protein"  
FT sig\_peptide 1..72  
FT /tag= a  
FT /note= "hUI2 leader sequence"  
FT mat\_peptide 73..108  
FT /tag= c  
FT /product= "Mature human IL2"  
FT /note= "First N-terminal 12 amino acids"  
FT misc\_feature 109..120  
FT /tag= d  
FT /label= linker  
FT misc\_feature 121..144  
FT /tag= e  
FT /note= "Flag tag"  
FT mat\_peptide 145..1461  
FT /tag= f  
FT /product= "Sol CD39"  
XX WO200023094-A2.  
PN  
XX 27-APR-2000.  
XX 13-OCT-1999; 99WO-US023641.  
XX 16-OCT-1998; 98US-0104585P.  
XX 06-NOV-1998; 98US-0107466P.  
XX 13-AUG-1999; 99US-0149010P.  
XX (IMMV ) IMMUNEX CORP.  
XX (CORR ) CORNELL RES FOUND INC.  
XX Maliszewski CR, Gayle RB, Marcus AJ;  
XX WPI; 2000-339518/29.  
XX P-FSDB; AAY70898.  
XX Inhibiting platelet activation and recruitment, useful for treating a

mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides.

Example 9; Page 107-109; 118pp; English.

The present sequence is the coding region of soluble CD39(solCD39) expression plasmid. This was used for the transient expression of solCD39 protein in mammalian expression systems. SolCD39 is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke

Sequence 1464 BP; 424 A; 340 C; 342 G; 358 T; 0 U; 0 Other;

Query Match 97.4%; Score 1400; DB 3; Length 1464;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1437; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

1 ATGGCCCTGGATCGACAGATGCAACTCCTCTGTGCAATGCACCTAAGTCTTGACATT 60  
1 ATGGCCCTGGATCGACAGATGCAACTCCTCTGTGCAATGCACCTAAGTCTTGACATT 60  
61 GTCAAAACAGTGCACCTACTCTCAAGTTCTACAAAGAAACACAGCTAAGTCTTC --- 116  
61 GTCAAAACAGTGCACCTACTCTCAAGTTCTACAAAGAAACACAGCTAAGTCTTCAGGA 120  
117 -----AACCAGAA CAAAGCATGTCGCAAGAAACGTTAAGTAT 153  
121 GACTACAAAGATGACGATGACAAACCCAGAACAAAGCATGTCGCAAGAAACGTTAAGTAT 180  
154 GGGATGTGCTGGATGCGGGTCTCTCACAAAGTTTATACATCTATTAAGTGGCCAGCA 213  
181 GGGATGTGCTGGATGCGGGTCTCTCACAAAGTTTATACATCTATTAAGTGGCCAGCA 240  
214 GAAAGAGAGATGACACAGCGGTGGTGCATCAAGTAGAAGAAATGCAGGGTTAAAGTCTCT 273  
241 GAAAGAGAGATGACACAGCGGTGGTGCATCAAGTAGAAGAAATGCAGGGTTAAAGTCTCT 300  
274 GGAATCTCAAAATTTGTTGAGAAAGTAAATGAAATAGGCAATTTACCTGATGATGATG 333  
301 GGAATCTCAAAATTTGTTGAGAAAGTAAATGAAATAGGCAATTTACCTGATGATGATG 360  
334 GAAAGAGCTAGGAGAGTATTCAGAGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGG 393  
361 GAAAGAGCTAGGAGAGTATTCAGAGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGG 420  
394 GCACGCGCAGCATGCGGTGGTCTCAGGATGCAAGTGAAGATGGCAGACAGGGTTCTTG 453  
421 GCCACGCGCAGCATGCGGTGGTCTCAGGATGCAAGTGAAGATGGCAGACAGGGTTCTTG 480  
454 GATGTGTGGAGAGGAGCCTCAGCAACTACCCCTTTGACATTCAGGGTGCAGGATCAT 513  
481 GATGTGTGGAGAGGAGCCTCAGCAACTACCCCTTTGACATTCAGGGTGCAGGATCAT 540  
514 ACTGGCCAGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 573  
541 ACTGGCCAGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
574 AGTCAGAAAAAAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 633  
601 AGTCAGAAAAAAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660  
634 GGAGCTTTGGACCTTGGGGAGGCTCTACAAAGTCACTTTTGTACCCCAAAACAGAGCT 693  
661 GGAGCTTTGGACCTTGGGGAGGCTCTACAAAGTCACTTTTGTACCCCAAAACAGAGCT 720

694 ATCGAGTCCCAGATAATGCTCTGCAATTTGCGCTCTATGGCAAGGACTACAAATGCTTAC 753  
721 ATCGAGTCCCAGATAATGCTCTGCAATTTGCGCTCTATGGCAAGGACTACAAATGCTTAC 780  
754 ACACATAGCTTCTGTGCTATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCCAAGGAC 813  
781 ACACATAGCTTCTGTGCTATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCCAAGGAC 840  
814 ATTCAAGTTCGAAGTAATGAATTTCTCAGGAGCCCTGCTTTCATCCTCGGATATAGAG 873  
841 ATTCAAGTTCGAAGTAATGAATTTCTCAGGAGCCCTGCTTTCATCCTCGGATATAGAG 900  
874 GTAGTGAACGTAAGTGACCTTTTACAAAGCCCTGCAACCAAGAGATTTGAGATGACTCTT 933  
901 GTAGTGAACGTAAGTGACCTTTTACAAAGCCCTGCTTTCATCCTCGGATATAGAG 960  
934 CCATTTCCAGCAGTTCGAAATCCAGGGTATTTGAAACTATCAACAATGCGATCAAAAGCAT 993  
961 CCATTTCCAGCAGTTCGAAATCCAGGGTATTTGAAACTATCAACAATGCGATCAAAAGCAT 1020  
994 CTGGAGCTTTCACACACAGTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTTC 1053  
1021 CTGGAGCTTTCACACACAGTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTTC 1080  
1054 TTGCCACCACTCCAGGGGATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTT 1113  
1081 TTGCCACCACTCCAGGGGATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTT 1140  
1114 TTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGATGATGATG 1173  
1141 TTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGATGATGATG 1200  
1174 TGTGCTCAGCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTG 1233  
1201 TGTGCTCAGCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTG 1260  
1234 AGTGAATCTGCTTTTCTGGTACCTACATCTCTCCCTCTCTCTCAGAGGCTATCATTTTC 1293  
1261 AGTGAATCTGCTTTTCTGGTACCTACATCTCTCCCTCTCTCTCAGAGGCTATCATTTTC 1320  
1294 ACAGCTGATTCCTGGAGCAGATTCATTTCAATTTGCAAGATCCAGGGCAGCAGCGCGC 1353  
1321 ACAGCTGATTCCTGGAGCAGATTCATTTCAATTTGCAAGATCCAGGGCAGCAGCGCGC 1380  
1354 TGGACTTTGGGCTACATGCTGAACTGACCAATGATCCCAATGATCCCAATGATCCCAATG 1413  
1381 TGGACTTTGGGCTACATGCTGAACTGACCAATGATCCCAATGATCCCAATGATCCCAATG 1440  
1414 ACACCTCTCTCCCACTCCACCTAA 1437  
1441 ACACCTCTCTCCCACTCCACCTAA 1464

RESULT 5

AAD00206

ID AAD00206 standard; DNA; 1365 BP.

XX AAD00206;

DT 17-AUG-2000 (first entry)

XX

Human soluble CD39 and IL2 N-terminus comprising fusion DNA construct.

XX

Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiodysplasia; antithrombotic; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.

OS Homo sapiens.  
XX Synthetic.  
FH Key  
FT Location/Qualifiers  
FT 1. .1365  
FT /tag= a  
FT /product= "Fusion protein of human Interleukin 2 (IL2) N-terminus and human soluble CD39 protein"  
FT misc\_feature  
FT 1. .45  
FT /tag= b  
FT /notes= "N-terminus of mature human interleukin 2 (IL2) "  
FT misc\_feature  
FT 45..1362  
FT /tag= c  
FT /notes= "Coding region of human soluble CD39 (solCD39) "  
XX WO200023459-A1.  
XX 27-APR-2000.  
XX 13-OCT-1999; 99WO-US022955.  
XX 16-OCT-1998; 98US-0104585P.  
XX 06-NOV-1998; 98US-0107466P.  
XX 13-AUG-1999; 99US-0149010P.  
XX (IMMV ) IMMUNEX CORP.  
XX Maliszewski CR, Gayle RB, Price VL, Gimpel SD;  
XX WPI, 2000-339644/29.  
XX P-PSDB; AAY0913.  
XX New soluble CD39 polypeptides having apyrase activity, useful for  
XX inhibiting angiogenesis and treating unstable angina, myocardial  
XX infarction, stroke, coronary artery disease or injury.  
XX Claim 11a; Page 93-95; 122pp; English.  
XX The present DNA sequence is a fusion construct, comprising the N-terminal  
XX region of mature human interleukin2 (IL2) and soluble CD39 (solCD39)  
XX coding region, having apyrase activity. This results in high levels of  
XX solCD39 expression and activity in the transfected cells. Soluble CD39 is  
XX constructed by removing the N- and C-terminal transmembrane domains. It  
XX retains the capacity to metabolise ATP and ADP at relevant concentrations  
XX and the ability to block and reverse ADP-induced platelet activation and  
XX recruitment, including platelet aggregation. Soluble CD39 polypeptides  
XX are useful for inhibiting angiogenesis. It is useful for the treatment of  
XX unstable angina, myocardial infarction, stroke, coronary artery disease  
XX or injury, atherosclerosis, peripheral vascular occlusion, pre-eclampsia,  
XX embolism, platelet-associated ischaemic disorders including lung,  
XX coronary and cerebral ischaemia, thrombotic disorders including coronary,  
XX peripheral and cerebral artery thrombosis, intracardiac and venous  
XX thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary  
XX embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful  
XX for preventing thrombus formation or reformation, occlusion, reocclusion,  
XX stenosis or restenosis of blood vessels or stroke  
SQ Sequence 1365 BP; 394 A; 317 C; 319 G; 335 T; 0 U; 0 Other;  
Query Match 95.0%; Score 1365; DB 3; Length 1365;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 73 GCACCTACTCAAGTTCTACAAAGAAACACAGCTAACTAGTTCAACCCAGAACAAAGCA 132  
DB 1 GCACCTACTCAAGTTCTACAAAGAAACACAGCTAACTAGTTCAACCCAGAACAAAGCA 60  
QY 133 TTGCCAGAAAACGTTAAAGTATGGGATGTGCTGGATGCGGGTCTTCTCACACAGTTTA 192  
DB 61 TTGCCAGAAAACGTTAAAGTATGGGATGTGCTGGATGCGGGTCTTCTCACACAGTTTA 120  
QY 193 TACATCTATAAGTGCCAGCAAGAAAGAGAAATGACACAGGCGTGGTCCATCAAGTAGAA 252  
|||||

DB 121 TACATCTATAAGTGCCAGCAAGAAAGAGAAATGACACAGGCGTGGTGCATCAAGTAGAA 180  
QY 253 GAATGACGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTTCAGAAAGTAAATGAATAGGC 312  
DB 181 GAAATGACGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTTCAGAAAGTAAATGAATAGGC 240  
QY 313 ATTTACCTGACTGATTTGATGGAAGAGCTAGGGAAGTGATTTCCAAAGGTCCAGCACCAA 372  
DB 241 ATTTACCTGACTGATTTGATGGAAGAGCTAGGGAAGTGATTTCCAAAGGTCCAGCACCAA 300  
QY 373 GAGACACCCGTTTACCTGGGAGCCACGCGAGCATCGGTTGCTCAGCATGGAAGTGA 432  
DB 301 GAGACACCCGTTTACCTGGGAGCCACGCGAGCATCGGTTGCTCAGCATGGAAGTGA 360  
QY 433 GAGTTGGCAGACAGGGTTCTGGATGTGTGAGAGAGCCCTCAGCAACTACCCCTTTGAC 492  
DB 361 GAGTTGGCAGACAGGGTTCTGGATGTGTGAGAGAGCCCTCAGCAACTACCCCTTTGAC 420  
QY 493 TTCCAGGTTGCCAGGATCATTTACTGGCCAAAGAGAGGTGCTATGGCTGGATTAATATC 552  
DB 421 TTCCAGGTTGCCAGGATCATTTACTGGCCAAAGAGAGGTGCTATGGCTGGATTAATATC 480  
QY 553 AACTATCTGCTGGCGCAATTCAGTCAGAAACAAAGGTGTTTTCAGCATAGTCCCATATGA 612  
DB 481 AACTATCTGCTGGCGCAATTCAGTCAGAAACAAAGGTGTTTTCAGCATAGTCCCATATGA 540  
QY 613 ACCAATATCAGGAAACCTTTTGGAGCTTTGGACCTTTGGGGAGCCCTTACACAAAGTCAC 672  
DB 541 ACCAATATCAGGAAACCTTTTGGAGCTTTGGAGCTTTGGGGAGCCCTTACACAAAGTCAC 600  
QY 673 TTTGTACCCCCAAAACCCAGACTATCGAGTCCCAAGATATGCTCTGCAATTTGCGCTCTAT 732  
DB 601 TTTGTACCCCCAAAACCCAGACTATCGAGTCCCAAGATATGCTCTGCAATTTGCGCTCTAT 660  
QY 733 GGCAAGNACTACAATGTCTACACATAGCTTCTGTGCTATGGGAAGATCAGGCACTC 792  
DB 661 GGCAAGNACTACAATGTCTACACATAGCTTCTGTGCTATGGGAAGATCAGGCACTC 720  
QY 793 TGGCAGAAACCTGGCCAAAGGACATTCAGTTGCCAAGTAAATGAATTTCTCAGGAGACCCATGC 852  
DB 721 TGGCAGAAACCTGGCCAAAGGACATTCAGTTGCCAAGTAAATGAATTTCTCAGGAGACCCATGC 780  
QY 853 TTTTCATCTGGATATAAGAGGTAGTGAACTAAGTGAACCTTTTACAGACCCCCCTGCACC 912  
DB 781 TTTTCATCTGGATATAAGAGGTAGTGAACTAAGTGAACCTTTTACAGACCCCCCTGCACC 840  
QY 913 AAGAGATTTGAGATGACTTCCATTCAGCAGATTTGAAATCCAGGGTATTTGGAAACTAT 972  
DB 841 AAGAGATTTGAGATGACTTCCATTCAGCAGATTTGAAATCCAGGGTATTTGGAAACTAT 900  
QY 973 CAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACACACAGTACTGCGCTTACTCCAG 1032  
DB 901 CAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACACACAGTACTGCGCTTACTCCAG 960  
QY 1033 TGTGCTTCAATGGGATTTTCTGCCACCACTCCAGGGGGATTTTGGGGCATTTTCAGCT 1092  
DB 961 TGTGCTTCAATGGGATTTTCTGCCACCACTCCAGGGGGATTTTGGGGCATTTTCAGCT 1020  
QY 1093 TTTTACTTTGTGATGAAGTTTAACTTGACATCAGAAAGTCTCTCAGAGAAAGGTG 1152  
DB 1021 TTTTACTTTGTGATGAAGTTTAACTTGACATCAGAAAGTCTCTCAGAGAAAGGTG 1080  
QY 1153 ACTCAGATGATGAAAAAGTTCTGTGCTCAGCTTGGGAGGAGATAAAAACATCTTACGCT 1212  
DB 1081 ACTCAGATGATGAAAAAGTTCTGTGCTCAGCTTGGGAGGAGATAAAAACATCTTACGCT 1140  
QY 1213 GGAGTAAAGGAGAGTACCTGAGTGAATCTGCTTTTCTGCTACCTACATTTCTCTCCCTC 1272  
DB 1141 GGAGTAAAGGAGAGTACCTGAGTGAATCTGCTTTTCTGCTACCTACATTTCTCTCCCTC 1200  
QY 1273 CTTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGGAGGACATCCATTTTCATTTGGCAAG 1332  
DB 1201 CTTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGGAGGACATCCATTTTCATTTGGCAAG 1260



QY 1333 ATCCAGGCGAGCAGCCGCGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1392  
|||||  
Db 1261 ATCCAGGCGAGCAGCCGCGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1320  
|||||  
QY 1393 CCAGCTGAGCAACCACTTTGCCACACCTCTCTCCCACTCCACCTAA 1437  
|||||  
Db 1321 CCAGCTGAGCAACCACTTTGCCACACCTCTCTCCCACTCCACCTAA 1365  
|||||

RESULT 6  
AAD00201  
ID AAD00201 standard; cDNA; 1365 BP.  
XX  
AC AAD00201;  
XX  
DT 17-AUG-2000 (first entry)  
XX  
DE Fusion construct of human soluble CD39 cDNA-1.  
XX  
KW Soluble CD39; ADP-induced platelet activation; platelet aggregation;  
unstable angina; myocardial infarction; stroke; coronary artery disease;  
atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;  
platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;  
cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;  
cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;  
peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;  
PE; pulmonary embolism; transient ischaemic attack; thrombus formation;  
occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant;  
cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;  
coronary ischaemia; vascular occlusion; ss.

OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
CDs 1. .1365  
FT /\*tag= a  
FT /product= "Human soluble CD39 protein"

XX W0200023094-A2.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US023641.

XX 16-OCT-1998; 98US-0104585P.

PR 06-NOV-1998; 98US-0107466P.

PR 13-AUG-1999; 99US-0149010P.

XX (IMV ) IMMUNEX CORP.

PA (CORR ) CORNELL RES FOUND INC.

XX Maliszewski CR, Gayle RB, Marcus AJ;

XX WPI; 2000-339518/29.

XX P-PSDB; AAY70890.

XX Inhibiting platelet activation and recruitment, useful for treating a

XX mammal suffering from unstable angina, myocardial infarction, stroke,

XX coronary artery disease or injury, comprises administering soluble CD39

XX polypeptides.

XX Claim 10; Page 93-95; 11pp; English.

XX The present cDNA sequence is a fusion construct encoding sol(soluble)CD39

XX having apyrase activity. Fusion of 12 amino acids from the N-terminus of

XX mature human II2 to the solCD39 coding region results in high levels of

XX both expression and activity in the supernatants of transfected cells.

CC cerebral artery thrombosis, intracardiac thrombosis, peripheral artery  
thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous  
thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.  
CC Soluble CD39 is also useful for preventing thrombus formation or  
CC reformation, occlusion, reocclusion, stenosis or restenosis of blood  
CC vessels or stroke  
XX  
SQ Sequence 1365 BP; 394 A; 317 C; 319 G; 335 T; 0 U; 0 Other;

Query Match 95.0%; Score 1365; DB 3; Length 1365;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 GCACCTACTTCAAGTTCTACAAAGAAACACACAGCTAACTAGTTCAACCCAGAACAAAGCA 132  
|||||  
Db 1 GCACCTACTTCAAGTTCTACAAAGAAACACACAGCTAACTAGTTCAACCCAGAACAAAGCA 60  
|||||  
QY 133 TTGCCAGAAAACGTTAAGTATGGGATTGTGTGGATGCGGGTTCTTCTCACAAAGTTTA 192  
|||||  
Db 61 TTGCCAGAAAACGTTAAGTATGGGATTGTGTGGATGCGGGTTCTTCTCACAAAGTTTA 120  
|||||  
QY 193 TACATCTATAAGTGGCCAGCAGAAAAGGAGATGACACAGGCGTGGTGCATCAAGTAGAA 252  
|||||  
Db 121 TACATCTATAAGTGGCCAGCAGAAAAGGAGATGACACAGGCGTGGTGCATCAAGTAGAA 180  
|||||  
QY 253 GAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTCAGAAAAGTAAATGAAATAGGC 312  
|||||  
Db 181 GAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTCAGAAAAGTAAATGAAATAGGC 240  
|||||  
QY 313 ATTTACCTGACTGATTGCAATGGAAGAGCTAGGGAAGTATTCAGAGTCCAGACACAA 372  
|||||  
Db 241 ATTTACCTGACTGATTGCAATGGAAGAGCTAGGGAAGTATTCAGAGTCCAGACACAA 300  
|||||  
QY 373 GAGACACCGGTTTACTGGGAGCCAGCGCAGCATGCGGTTGCTCAGGATGAAAAGTGA 432  
|||||  
Db 301 GAGACACCGGTTTACTGGGAGCCAGCGCAGCATGCGGTTGCTCAGGATGAAAAGTGA 360  
|||||  
QY 433 GAGTTGGCAGACAGGGTTCTGGATGCTGGAGAGAGAGCCTCAGCAACTACCCCTTTGAC 492  
|||||  
Db 361 GAGTTGGCAGACAGGGTTCTGGATGCTGGAGAGAGAGCCTCAGCAACTACCCCTTTGAC 420  
|||||  
QY 493 TTCCAGGGTGCAGGATCATTACTGGCCAAGAGAGTGCCTATGGCTGGATTACTATC 552  
|||||  
Db 421 TTCCAGGGTGCAGGATCATTACTGGCCAAGAGAGTGCCTATGGCTGGATTACTATC 480  
|||||  
QY 553 AACTATCTGCTGGGCAAAATTAGTCAGAAAACAAGGTGGTTCAGCATAGTCCCATATGA 612  
|||||  
Db 481 AACTATCTGCTGGGCAAAATTAGTCAGAAAACAAGGTGGTTCAGCATAGTCCCATATGA 540  
|||||  
QY 613 ACCAATATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTCTACACAAGTCACT 672  
|||||  
Db 541 ACCAATATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTCTACACAAGTCACT 600  
|||||  
QY 673 TTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATGCTCTGCAATTTCCCTCTAT 732  
|||||  
Db 601 TTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATGCTCTGCAATTTCCCTCTAT 660  
|||||  
QY 733 GCAAGGACTACAATGCTTACACATAGCTTTCTGTGCTATGGAGAGATCAGGCATC 792  
|||||  
Db 661 GCAAGGACTACAATGCTTACACATAGCTTTCTGTGCTATGGAGAGATCAGGCATC 720  
|||||  
QY 793 TGGCAGAAACTGGCCAAGGACATTCAGGTTTCAAGTAATGAAATTCCTCAGGGAACCCATGC 852  
|||||  
Db 721 TGGCAGAAACTGGCCAAGGACATTCAGGTTTCAAGTAATGAAATTCCTCAGGGAACCCATGC 780  
|||||  
QY 853 TTTTCATCTCTGGATATAAGAAAGTAGTGAACGTAAGTAGCTTTTACAAGACCCCTTCGACC 912  
|||||  
Db 781 TTTTCATCTCTGGATATAAGAAAGTAGTGAACGTAAGTAGCTTTTACAAGACCCCTTCGACC 840  
|||||  
QY 913 AAGAGATTGAGATGACTCTTCCATTCAGCAGTGTGGAATCCAGGTTATTCGAACTAT 972  
|||||  
Db 841 AAGAGATTGAGATGACTCTTCCATTCAGCAGTGTGGAATCCAGGTTATTCGAACTAT 900  
|||||



QY 973 CAACATGCGCATCAAGGATCTGGAGCTCTTCAACACGAGTTACTGCGCTTACTCCAG 1032  
Db 901 CAACATGCGCATCAAGGATCTGGAGCTCTTCAACACGAGTTACTGCGCTTACTCCAG 960  
QY 1033 TGTGCTTCAATGGGATTTCTTGCCACCACTCCAGGGGATTTGGGGCATTTTCAGCT 1092  
Db 961 TGTGCTTCAATGGGATTTCTTGCCACCACTCCAGGGGATTTGGGGCATTTTCAGCT 1020  
QY 1093 TTTTACTTTGTGATGAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAAGTGTG 1152  
Db 1021 TTTTACTTTGTGATGAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAAGTGTG 1080  
QY 1153 ACTGAGATGATGAAAAGTCTGTGCTCAGCTTGGAGGAGATGAAAACATCTTACGCT 1212  
Db 1081 ACTGAGATGATGAAAAGTCTGTGCTCAGCTTGGAGGAGATGAAAACATCTTACGCT 1140  
QY 1213 CGAGTAAGGAGAGTACCTGAGTGAATACTGCTTTCTGCTACCTACATCTCTCCCTC 1272  
Db 1141 GGAGTAAGGAGAGTACCTGAGTGAATACTGCTTTCTGCTACCTACATCTCTCCCTC 1200  
QY 1273 CTTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGGACACATCCATTTTCATTTGGCAAG 1332  
Db 1201 CTTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGGACACATCCATTTTCATTTGGCAAG 1260  
QY 1333 ATCCAGGGCAGGACGCCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1392  
Db 1261 ATCCAGGGCAGGACGCCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1320  
QY 1393 CCAGCTGAGCAACCATTTGCCACACCTCTCTCCCACTCCACCTAA 1437  
Db 1321 CCAGCTGAGCAACCATTTGCCACACCTCTCTCCCACTCCACCTAA 1365

RESULT 7

AAD00205  
ID AAD00205 standard; cDNA; 1599 BP.  
XX

AC AAD00205;

DT 17-AUG-2000 (first entry)

XX Human soluble CD39 protein encoding cDNA.

XX Soluble CD39; human; apyrase activity; platelet activation; inhibitor;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;  
KW platelet-associated ischaemic disorder; thrombotic disorder; reocclusion;  
KW coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;  
KW thrombus formation; occlusion; stenosis; restenosis; angiogenesis;  
KW antitanginal; cerebroprotective; antiarteriosclerotic; anticoagulant;  
KW cardiant; vasotropic; thrombolytic; ss.  
XX Homo sapiens.

XX Key Location/Qualifiers  
FH CDS 67..1599  
FT /\*tag= a  
FT /product= "Human soluble CD39 protein"  
FT /note= "Cell surface molecule"

XX WO200023459-A1.

XX 27-APR-2000.

XX 13-OCT-1999; 99WO-US022955.

XX 16-OCT-1998; 98US-0104585P.

XX 06-NOV-1998; 98US-0107466P.

XX 13-AUG-1999; 99US-0149010P.

XX (IMNV ) IMMUNEX CORP.

XX Maliszewski CR, Gayle RB, Price VL, GimpeI SB;

XX  
DR

XX WPI; 2000-339644/29.  
P-PSDB; AAY70910.  
PT New soluble CD39 polypeptides having apyrase activity, useful for  
PT inhibiting angiogenesis and treating unstable angina, myocardial  
PT infarction, stroke, coronary artery disease or injury.

XX Example 9; Page 85-87; 122pp; English.

XX The present sequence is the cDNA encoding the human soluble CD39 protein,  
CC a cell surface molecule, having apyrase activity. It is derived from a  
CC human B cell line cDNA library, referred to as Mp-1. Soluble CD39 is  
CC constructed by removing the N- and C-terminal transmembrane domains. It  
CC retains the capacity to metabolise ATP and ADP at relevant concentrations  
CC and the ability to block and reverse ADP-induced platelet activation and  
CC recruitment, including platelet aggregation. Soluble CD39 polypeptides  
CC are useful for inhibiting angiogenesis. It is useful for the treatment of  
CC unstable angina, myocardial infarction, stroke, coronary artery disease  
CC or injury, atherosclerosis, peripheral vascular occlusion, preclampsia,  
CC embolism, platelet-associated ischaemic disorders including lung,  
CC coronary and cerebral ischaemia, thrombotic disorders including coronary,  
CC peripheral and cerebral artery thrombosis, intracardiac and venous  
CC thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary  
CC embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful  
CC for preventing thrombus formation or reformation, occlusion, reocclusion,  
CC stenosis or restenosis of blood vessels or stroke

XX SQ Sequence 1599 BP; 446 A; 366 C; 382 G; 405 T; 0 U; 0 Other;

Query Match 91.8%; Score 1319.2; DB 3; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GTTCAACCCAGAACAAAGCATTTGCCAGAAACGTTTAACTATGGGATTTGCTGGATCGG 172  
Db 173 GGTGACCCAGAACAAAGCATTTGCCAGAAACGTTTAACTATGGGATTTGCTGGATCGG 232  
QY 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAGAAAGAGATGACACAG 232  
Db 233 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAGAAAGAGATGACACAG 292  
QY 233 CGTGGTGTCATCAAGTAGAAGATTCAGGGTTAAAGGTCCTTGAATCTCAAAATTTGTTTC 292  
Db 293 CGTGGTGTCATCAAGTAGAAGATTCAGGGTTAAAGGTCCTTGAATCTCAAAATTTGTTTC 352  
QY 293 AGAAGTAAATGAATAGGCAATTTACCTGACTGATTCGATGCGAAGAGCTAGGGAGTGA 352  
Db 353 AGAAGTAAATGAATAGGCAATTTACCTGACTGATTCGATGCGAAGAGCTAGGGAGTGA 412  
QY 353 TTCCAAGGTCCAGCAGCAACAGAGACACCCGTTTACCTGGGAGCCAGCGCATGCCGT 412  
Db 413 TTCCAAGGTCCAGCAGCCAGAGACACCCGTTTACCTGGGAGCCAGCGCATGCCGT 472  
QY 413 TGCTCAGGATGGAAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGAGCC 472  
Db 473 TGCTCAGGATGGAAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGAGCC 532  
QY 473 TCAGCAACTACCCCTTTTGACTTCCAGGGTGCCAGGATCATTTACTGGCCCAAGAGNAGTG 532  
Db 533 TCAGCAACTACCCCTTTTGACTTCCAGGGTGCCAGGATCATTTACTGGCCCAAGAGNAGTG 592  
QY 533 CCTATGGCTGGATTTACTATCAACTATCTCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTG 592  
Db 593 CCTATGGCTGGATTTACTATCAACTATCTCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTG 652  
QY 593 TCAGCATAGTCCCATATGAAAACCAATATCAGGAAACCTTTGGAGCTTTTGGACCTTGGGG 652  
Db 653 TCAGCATAGTCCCATATGAAAACCAATATCAGGAAACCTTTGGAGCTTTTGGACCTTGGGG 712  
QY 653 GAGCCTCTACCAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCAAGATATG 712  
Db 713 GAGCCTCTACCAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCAAGATATG 772

QY 713 CTCGTCAATTTCCGCTCTATGSCAAGGACTACAAATGCTACACACATAGCTTCTTGCT 772  
DB |||||  
QY 773 CTCGTCAATTTCCGCTCTATGSCAAGGACTACAAATGCTACACACATAGCTTCTTGCT 832  
DB |||||  
QY 773 ATGGGAAGGATCAGGCACCTCTGCGAGAAACTGCGCCAGGACATTCAGGTTGCAAGTAATG 832  
DB |||||  
QY 833 ATGGGAAGGATCAGGCACCTCTGCGAGAAACTGCGCCAGGACATTCAGGTTGCAAGTAATG 892  
DB |||||  
QY 833 AAATTTCTCAGGGACCCCATGCTTTTCATCTCGGATATAGGAAGGTAAGTGAACGTAAGTGACC 892  
DB |||||  
QY 893 AAATTTCTCAGGGACCCCATGCTTTTCATCTCGGATATAGGAAGGTAAGTGAACGTAAGTGACC 952  
DB |||||  
QY 893 TTTTACAGACCCCTCCACCAAGAGATTTGAGATGACTCTTCCATTCACGACGTTTGAA 952  
DB |||||  
QY 953 TTTTACAGACCCCTCCACCAAGAGATTTGAGATGACTCTTCCATTCACGACGTTTGAA 1012  
DB |||||  
QY 953 TCCAGGGTATTTGGAACATATCAACAATGCCATCAAAAGCATCTCTGGAGCTCTTCAACACCA 1012  
DB |||||  
QY 1013 TCCAGGGTATTTGGAACATATCAACAATGCCATCAAAAGCATCTCTGGAGCTCTTCAACACCA 1072  
DB |||||  
QY 1013 GTTACTGCCCTTACTCCAGTGCCCTTCAATGGGATTTTCTTGGCCACCATCTCCAGGGG 1072  
DB |||||  
QY 1073 GTTACTGCCCTTACTCCAGTGCCCTTCAATGGGATTTTCTTGGCCACCATCTCCAGGGG 1132  
DB |||||  
QY 1073 ATTTTGGGCAATTTTTCAGCTTTTACTTTGTGTGATGAAGTTTAAACTTTGACATCAGAGA 1132  
DB |||||  
QY 1133 ATTTTGGGCAATTTTTCAGCTTTTACTTTGTGTGATGAAGTTTAAACTTTGACATCAGAGA 1192  
DB |||||  
QY 1133 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTGAGCCTTTGGGAGG 1192  
DB |||||  
QY 1193 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTGAGCCTTTGGGAGG 1252  
DB |||||  
QY 1193 AGATAAAACATTTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTTCTG 1252  
DB |||||  
QY 1253 AGATAAAACATTTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTTCTG 1312  
DB |||||  
QY 1253 GTACCTACATCTCTCCCTCTTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGGAGC 1312  
DB |||||  
QY 1313 GTACCTACATCTCTCCCTCTTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGGAGC 1372  
DB |||||  
QY 1313 ACATCAATTTTCAVTTGGCAAGATCCAGGCGAGCGCGCTGGACTTTGGGCTACATGC 1372  
DB |||||  
QY 1373 ACATCAATTTTCAVTTGGCAAGATCCAGGCGAGCGCGCTGGACTTTGGGCTACATGC 1432  
DB |||||  
QY 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCTCCACTCCA 1432  
DB |||||  
QY 1433 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCTCCACTCCA 1492  
DB |||||  
QY 1433 CCTA 1436  
DB |||||  
QY 1493 CCTA 1496

RESULT 8  
AAD00200  
ID AAD00200 standard; cDNA; 1599 BP.  
XX  
XX AAD00200;  
XX AC  
XX AC  
XX AC  
XX AC  
XX 17-AUG-2000 (first entry)  
XX  
XX Human soluble CD39 cDNA.  
DE  
DE Soluble CD39; ADP-induced platelet activation; platelet aggregation;  
KW unstable angina; myocardial infarction; stroke; coronary artery disease;  
KW atherosclerosis; peripheral vascular occlusion; preclampsia; embolism;  
KW platelet-associated ischaemic disorder; lung ischaemia; thrombolytic;  
KW cerebral ischaemia; thrombotic disorder; coronary artery thrombosis;  
KW cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;  
KW peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT;  
KW PE; pulmonary embolism; transient ischaemic attack; thrombus formation;  
KW occlusion; reocclusion; stenosis; restenosis; antianginal; cardiac;

KW cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;  
KW coronary ischaemia; vascular occlusion; ss.  
XX Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 67..1599  
FT /\*tag= a  
FT /product= "Soluble CD39 protein"  
XX  
XX WO200023094-A2.  
XX PD 27-APR-2000.  
XX 13-OCT-1999; 99WO-US023641.  
XX 16-OCT-1998; 98US-0104585P.  
PR 06-NOV-1998; 98US-0107466P.  
PR 13-AUG-1999; 99US-0149010P.  
XX (IMMV ) IMMUNEX CORP.  
PA (CORR ) CORNELL RES FOUND INC.  
XX PI Maliszewski CR, Gayle RB, Marcus AJ;  
XX WPI: 2000-339518/29.  
DR P-PSDB; AAY70887.  
XX  
PT Inhibiting platelet activation and recruitment, useful for treating a  
PT mammal suffering from unstable angina, myocardial infarction, stroke,  
PT coronary artery disease or injury, comprises administering soluble CD39  
PT polypeptides.  
XX  
PS Example 10; Page 85-87; 118pp; English.  
XX  
CC The present cDNA sequence encodes soluble CD39 having apyrase activity.  
CC This was derived from a cDNA library prepared from a human B cell line  
CC referred to as MP-1. Soluble CD39 retains the capacity of wildtype CD39  
CC to metabolise ATP and ADP at physiologically relevant concentrations as  
CC well as the ability to block and reverse ADP-induced platelet activation  
CC and recruitment including platelet aggregation. This is used in the  
CC treatment of unstable angina, myocardial infarction, stroke, coronary  
CC artery disease or injury, atherosclerosis, peripheral vascular occlusion,  
CC preclampsia, embolism, platelet-associated ischaemic disorder including  
CC lung ischaemia, coronary ischaemia and cerebral ischaemia. a thrombotic  
CC disorder including coronary artery thrombosis, cerebral artery  
CC thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous  
CC thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT),  
CC pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also  
CC useful for preventing thrombus formation or reformation, occlusion,  
CC reocclusion, stenosis or restenosis of blood vessels or stroke  
XX  
SQ Sequence 1599 BP; 446 A; 366 C; 382 G; 405 T; 0 U; 0 Other;  
Query Match 91.8%; Score 1319.2; DB 3; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GTTCAACCCAGAACAAAGCATTCGCCAGAAAACGTTAAGTATGCGGATGTCGATGCGG 172  
DB |||||  
QY 173 GGTTCACCCAGAACAAAGCATTCGCCAGAAAACGTTAAGTATGCGGATGTCGATGCGG 232  
DB |||||  
QY 173 GTTCTTCTCACACAGTTTATACATCTATAAGTGTAAAGGTCCTCGAATCTCAAAATTTGTTTC 232  
DB |||||  
QY 233 GGTGTGTGATCAAGTAGAAGATGCAGGGTTAAAGGTCCTCGAATCTCAAAATTTGTTTC 292  
DB |||||  
QY 293 GGTGTGTGATCAAGTAGAAGATGCAGGGTTAAAGGTCCTCGAATCTCAAAATTTGTTTC 352  
DB |||||  
QY 293 AGAAAGTAATAAATAGGACATTTTACCTGACTGATTTGATGCAATGGAAGAGCTAGGGAAGTGA 352  
DB |||||  
QY 353 AGAAAGTAATAAATAGGACATTTTACCTGACTGATTTGATGCAATGGAAGAGCTAGGGAAGTGA 412  
DB |||||

353 TTCCAAAGTCCAGACCCAGAGACACCCGTTTAACTGGAGCCACGGCAGGCATGCCGT 412  
Db |||||  
413 TTCCAAAGTCCAGACCCAGAGACACCCGTTTAACTGGAGCCACGGCAGGCATGCCGT 472  
Qy  
413 TGCTCAGGATGGAAGTGAAGTGGGACAGACAGGGTCTGAGTGTGGAGAGAGCC 472  
Db |||||  
473 TGCTCAGGATGGAAGTGAAGTGGGACAGACAGGGTCTGAGTGTGGAGAGAGCC 532  
Qy  
473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTAATCTGGCCCAAGGAAGGTG 532  
Db |||||  
533 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTAATCTGGCCCAAGGAAGGTG 592  
Qy  
533 CTTATGGCTGGATTAATCAATCTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 592  
Db |||||  
593 CCTATGGCTGGATTAATCAATCTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 652  
Qy  
593 TCAGCATAGTCCCATATGAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG 652  
Db |||||  
653 TCAGCATAGTCCCATATGAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG 712  
Qy  
653 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATG 712  
Db |||||  
713 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATG 772  
Qy  
713 CTCTCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGTCT 772  
Db |||||  
773 CTCTCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGTCT 832  
Qy  
773 ATGGGAAGGATCAGGCATCTGGCAGAACTGGCCCAAGGACATTCAGGTGCAAGTAATG 832  
Db |||||  
833 ATGGGAAGGATCAGGCATCTGGCAGAACTGGCCCAAGGACATTCAGGTGCAAGTAATG 892  
Qy  
833 AAATTTCTCAGGACCCATGCTTTCTATCTGGATATAAGAGGTAGTGAACGTGAAGTACC 892  
Db |||||  
893 AAATTTCTCAGGACCCATGCTTTCTATCTGGATATAAGAGGTAGTGAACGTGAAGTACC 952  
Qy  
893 TTACAAGACCCCTGCAACCAAGAGATTGAGATGACTCTTCCATTCAGCAGATTGAAA 952  
Db |||||  
953 TTACAAGACCCCTGCAACCAAGAGATTGAGATGACTCTTCCATTCAGCAGATTGAAA 1012  
Qy  
953 TCCAGGATATGGAACCTATCAACATGCCATCAAGCATCTGAGCTCTTCAACACCA 1012  
Db |||||  
1013 TCCAGGATATGGAACCTATCAACATGCCATCAAGCATCTGAGCTCTTCAACACCA 1072  
Qy  
1013 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGCCACCACTCCAGGGGG 1072  
Db |||||  
1073 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGCCACCACTCCAGGGGG 1132  
Qy  
1073 ATTTTGGGGCAATTTTCACTTTTACTTTGTGATGAAGTTTAACTTGACATCAGAGA 1132  
Db |||||  
1133 ATTTTGGGGCAATTTTCACTTTTACTTTGTGATGAAGTTTAACTTGACATCAGAGA 1192  
Qy  
1133 AAGTCTCTCAGGAAAGGTGACTGATGATGAAAAAGTTCTGCTCAGCCTTGGAGG 1192  
Db |||||  
1193 AAGTCTCTCAGGAAAGGTGACTGATGATGAAAAAGTTCTGCTCAGCCTTGGAGG 1252  
Qy  
1193 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATCTGCTTTCTG 1252  
Db |||||  
1253 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATCTGCTTTCTG 1312  
Qy  
1253 GTACCTACATCTCTCCCTCTCTCTGCAAGGCTATCATTTACACAGCTGATTCCTGGAGC 1312  
Db |||||  
1313 GTACCTACATCTCTCCCTCTCTCTGCAAGGCTATCATTTACACAGCTGATTCCTGGAGC 1372  
Qy  
1313 ACATCCATTTCAATGGCAAGATCCAGGGCAGGACCGCGGTGAGCTTTGGGCTACATGC 1372  
Db |||||  
1373 ACATCCATTTCAATGGCAAGATCCAGGGCAGGACCGCGGTGAGCTTTGGGCTACATGC 1432  
Qy  
1373 TGAACCTCAGCAACATGATCCAGCTGAGCAACCATTTGCCACACCTCTCTCCCACTCCA 1432  
Db |||||  
1433 TGAACCTCAGCAACATGATCCAGCTGAGCAACCATTTGCCACACCTCTCTCCCACTCCA 1492

Qy 1433 CCTA 1436  
Db 1493 CCTA 1496  
RESULT 9  
ADL24294  
ID ADL24294 standard; DNA; 1599 BP.  
XX  
AC ADL24294;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human CD39 coding sequence.  
XX  
ds; Gene; cardiovascular disease; IL-17; interleukin; IL-18; 4-1BB; CD30;  
KW OX40; antagonist.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 67..1599  
FT /\*tag= a  
FT /product= "CD39"  
XX  
PN WO2004019866-A2.  
XX  
PD 11-MAR-2004.  
XX  
PF 21-AUG-2003; 2003WO-US026354.  
XX  
PR 28-AUG-2002; 2002US-0406418P.  
PR 12-AUG-2003; 2003US-0494457P.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Burton PB, Deisher TA;  
XX  
DR WPI; 2004-239107/22.  
DR P-PSDB; ADL24295.  
XX  
PT Use of IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists, for treating a  
PT cardiovascular disease, e.g. chronic immune myocarditis, congestive heart  
PT failure, aneurysm, angina, embolism, restenosis, ischemia or  
PT thrombocytopenic purpura.  
XX  
PS Disclosure; Page 130-132; 135pp; English.  
XX  
CC The present invention relates to a method of treating cardiovascular  
CC disease in a subject, comprising administering an IL-17, IL-18, 4-1BB,  
CC CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40  
CC antagonists are useful for treating cardiovascular disorders, e.g.  
CC (chronic immune) myocarditis, congestive heart failure, aneurysm,  
CC angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. The  
CC present sequence is a coding sequence used in the exemplification of the  
CC invention.  
XX  
SQ Sequence 1599 BP; 446 A; 366 C; 382 G; 405 T; 0 U; 0 Other;  
Query Match 91.8%; Score 1319.2; DB 12; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 113 GTTCAACCCAGAACAAAGCATTCGACAGAAACGTTTAAGTATGGATTGCTGGATCGG 172  
Db 173 GGTTCAGCCAGAACAAAGCATTCGACAGAAACGTTTAAGTATGGATTGCTGGATCGG 232  
Qy 173 GTTCTCTTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGAGAAATGACACAG 232  
Db 233 GTTCTCTTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGAGAAATGACACAG 292  
Qy 233 GCCTGGTGCATCAAGTAGAAGATGCGGGTTAAAGGTCTCTGGAATCTCAAAATTTGTT 292

293 GCGTGGTGCATCAAGTAGAAGAAATGCAGGGTTAAAGGTCCTGGAATCTCAAAAATTTGTTTC 352

293 AGAAGTAAATGAATAGGCAATTTACTGACTGATTTGCATGGAAGAGCTTAGGGAATGA 352

353 AGAAAGTAAATGAATAGGCAATTTACTGACTGATTTGCATGGAAGAGCTTAGGGAATGA 412

353 TTCCNAGGTCCTCAGCAGCAAGAGACACCCGCTTTACCTCTGGGAGCCACGGCAGGCAATCGGCT 412

413 TTCCNAGGTCCTCAGCAGCAAGAGACACCCGCTTTACCTCTGGGAGCCACGGCAGGCAATCGGCT 472

413 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTTGGATGTGGTGGAGAGAGCC 472

473 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTTGGATGTGGTGGAGAGAGCC 532

473 TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGCGCAAGAGAGGTTG 532

533 TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGCGCAAGAGAGGTTG 592

533 CCTATGGCTGGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 592

593 CCTATGGCTGGATTTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 652

593 TCAGCATAGTCCCCTATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 652

653 TCAGCATAGTCCCCTATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 712

653 GAGGCTCTACAAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCGCAGATAATG 712

713 GAGGCTCTACAAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCGCAGATAATG 772

713 CTCTGCAATTTGCGCTCTATGGAAGGACTACAAATGTCACACACATAGCTTCTGTGCT 772

773 CTCTGCAATTTGCGCTCTATGGAAGGACTACAAATGTCACACACATAGCTTCTGTGCT 832

773 ATGGGAAGTACAGGCACTCTGGCAGAACTGGCCAAAGCATTCAGGTTGCAAGTAATG 832

833 ATGGGAAGTACAGGCACTCTGGCAGAACTGGCCAAAGCATTCAGGTTGCAAGTAATG 892

833 AAATTTCTCAGGAGCCCATGCTTTTCACTCTGGATATAGAAGGTAGTGAAGTGAAGTACC 892

893 AAATTTCTCAGGAGCCCATGCTTTTCACTCTGGATATAGAAGGTAGTGAAGTGAAGTACC 952

893 TTTTACAGACCCCTGTCACCAAGAGATTTTCAGATGACTCTTCATTTCCAGCAGTTTGAAA 952

953 TTTTACAGACCCCTGTCACCAAGAGATTTTCAGATGACTCTTCATTTCCAGCAGTTTGAAA 1012

953 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAAGCATTCCTGGAGCTTCCAAACACCA 1012

1013 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAAGCATTCCTGGAGCTTCCAAACACCA 1072

1013 GTTACTGCCCTTACTCCAGTGCCTTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGG 1072

1073 GTTACTGCCCTTACTCCAGTGCCTTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGG 1132

1073 ATTTTGGGGCATTTTACGCTTTTACTTTCTGTGATGAAGTTTAAACTTCACATCAGAGA 1132

1133 ATTTTGGGGCATTTTACGCTTTTACTTTCTGTGATGAAGTTTAAACTTCACATCAGAGA 1192

1133 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTTCTGTGCTCAGCCTTTGGGAGG 1192

1193 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTTCTGTGCTCAGCCTTTGGGAGG 1252

1193 AGATAAAAAATCTTACGCTGGAGTAAAGAGAGTACCTGAGTGAATCTGCTTTTCTG 1252

1253 AGATAAAAAATCTTACGCTGGAGTAAAGAGAGTACCTGAGTGAATCTGCTTTTCTG 1312

1253 GTACTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAGAGCTGATTTCTCGGAGC 1312

1313 GTACTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAGAGCTGATTTCTCGGAGC 1372

1313 ACATCCATTTTCAITGGCAAGATCCAGGGCAGCAGCGCGGCTGGACTTTGGGTACATGC 1372

1373 ACATCCATTTTCAITGGCAAGATCCAGGGCAGCAGCGCGGCTGGACTTTGGGTACATGC 1432

QY 1373 TGAACTGACCAACATGATCCAGCTGAGCAACCAATTTGTCCACACCTCTCTCTCCACTCCA 1432

Db 1433 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCCACACCTCTCTCTCCACTCCA 1492

QY 1433 CCTA 1436

Db 1493 CCTA 1496

RESULT 10  
AAA96069  
ID AAA96069 standard; DNA; 1704 BP.  
XX  
AC AAA96069;  
XX  
DT 29-JAN-2001 (first entry)  
XX  
DE Human ATP diphosphohydrolase coding sequence.  
XX  
KW Drug resistance; ATP gradient; chemotherapeutic; antibiotic; herbicide;  
KW human; ATP diphosphohydrolase; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200052144-A1.  
XX  
PD 08-SEP-2000.  
XX  
PF 28-FEB-2000; 2000WO-US0053315.  
XX  
PR 03-MAR-1999; 99US-00261825.  
XX  
PA (TEXA ) UNIV TEXAS.  
XX  
PI Thomas CE, Windsor JB, Roux SJ, Lloyd AM, Hurley L;  
XX  
DR WPI; 2000-587306/55.  
XX  
PT Increasing or decreasing drug resistance in target bacteria, yeast, plant  
PT or mammalian cells comprises altering ATP gradient across biological  
PT membrane of target cell.  
XX  
PS Claim 14; Page; 85pp; English.  
XX  
CC The present invention relates to a method for increasing or decreasing  
CC drug resistance in target bacteria, yeast, plant or mammalian cells by  
CC altering the ATP gradient across the biological membrane of the target  
CC cell. The method is useful for modulating drug resistance of cells. It is  
CC useful for increasing the sensitivity of cells to chemotherapeutic and  
CC antibiotic agents and increasing resistance to herbicides. The present  
CC sequence is human ATP diphosphohydrolase coding sequence. This sequence  
CC encodes was used in the present invention to modulate drug resistance.  
CC Note: The present sequence is not shown in the specification, but is  
CC referred to via its GenBank accession number  
XX  
SQ Sequence 1704 BP; 468 A; 392 C; 403 G; 441 T; 0 U; 0 Other;

Query Match 91.8%; Score 1319.2; DB 3; Length 1704;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GTTCACCCAGCAACGATTCAGCAAGCAATTAAGTATGGGATTTGCTGGATGCCG 172

Db 137 GGTGACCCAGCAACGATTCAGCAAGCAATTAAGTATGGGATTTGCTGGATGCCG 196

QY 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAAGAAAGGAGAATGACACAG 232

Db 197 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAAGAAAGGAGAATGACACAG 256

QY 233 GCGTGGTGCATCAAGTAGAAGAAATGCAGGGTTAAAGGTCCTGGAATCTCAAAAATTTGTTTC 292

Db 257 GCGTGGTGCATCAAGTAGAAGAAATGCAGGGTTAAAGGTCCTGGAATCTCAAAAATTTGTTTC 316

QY 293 AGAAAGTAAATAGGAATGAGCATTTTAACTGACTGATTTGCAATGGAAGAGCTTAGGGAAGTGA 352  
DB 317 AGAAAGTAAATAGGAATGAGCATTTTAACTGACTGATTTGCAATGGAAGAGCTTAGGGAAGTGA 376  
QY 353 TTCCAAAGTCCCAAGCACCAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCGATCGGCT 412  
DB 377 TTCCAAAGTCCCAAGCACCAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCGATCGGCT 436  
QY 413 TGCTCAGGATGGAAGAGTTCGCGACAGACAGGGTTCTGAGTGTGGTGAGAGAGCC 472  
DB 437 TGCTCAGGATGGAAGTTCGCGACAGAGGGTTCTGAGTGTGGTGAGAGAGCC 496  
QY 473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTACTTGCCCAAGAGGAAGGTG 532  
DB 497 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTACTTGCCCAAGAGGAAGGTG 556  
QY 533 CCTATGGCTGGATTACTATCACTATCTCTGGGCAAAATTCAGTCAGAAACAAGGTGCT 592  
DB 557 CCTATGGCTGGATTACTATCACTATCTCTGGGCAAAATTCAGTCAGAAACAAGGTGCT 616  
QY 593 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTTGGGG 652  
DB 617 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTTGGGG 676  
QY 653 GAGCCTCTACAAAGTCACTTTTGTATACCCCAAAACAGACTATCGAGTCCCCAGATAATG 712  
DB 677 GAGCCTCTACAAAGTCACTTTTGTATACCCCAAAACAGACTATCGAGTCCCCAGATAATG 736  
QY 713 CTCTGCATTTTGCCTCTATGSCAAGGACTACAAATGTCTACACATAGCTTCTTGCTGT 772  
DB 737 CTCTGCATTTTGCCTCTATGSCAAGGACTACAAATGTCTACACATAGCTTCTTGCTGT 796  
QY 773 ATGGGAAGGATCAGGACCTCTGCGAGAACTCGCCAAAGGACATTCAGGTTCGAAGTAATG 832  
DB 797 ATGGGAAGGATCAGGACCTCTGCGAGAACTCGCCAAAGGACATTCAGGTTCGAAGTAATG 856  
QY 833 AAATTTCTCAGGACCCATCTTTTCACTCTGGATATAAGAAAGGTAGTGAACGTAAAGTGACC 892  
DB 857 AAATTTCTCAGGACCCATCTTTTCACTCTGGATATAAGAAAGGTAGTGAACGTAAAGTGACC 916  
QY 893 TTACAGAGCCCTGACCAAGAGATTGAGATGACTTCTTCATTCAGGATTTGAA 952  
DB 917 TTACAGAGCCCTGACCAAGAGATTGAGATGACTTCTTCATTCAGGATTTGAA 976  
QY 953 TCCAGGTATTGGAACCTATCAACATGCGCATCAAGCATCTGAGGCTTTCAACACCA 1012  
DB 977 TCCAGGTATTGGAACCTATCAACATGCGCATCAAGCATCTGAGGCTTTCAACACCA 1036  
QY 1013 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG 1072  
DB 1037 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG 1096  
QY 1073 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTAACTTGACATCAGAGA 1132  
DB 1097 ATTTTGGGGCATTTTTCAGCTTTTACTTTTGTGATGAAGTTTAACTTGACATCAGAGA 1156  
QY 1133 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGATAAAGTTCTGCTCAGCCCTCGGAGG 1192  
DB 1157 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGATAAAGTTCTGCTCAGCCCTCGGAGG 1216  
QY 1193 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATCTGCTTTTCTG 1252  
DB 1217 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATCTGCTTTTCTG 1276  
QY 1253 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTACAGCTGATTTCTGGAGC 1312  
DB 1277 GTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTACAGCTGATTTCTGGAGC 1336  
QY 1313 ACATCCATTTTCAATTCGCAAGATCCAGGCGAGCGCGCTGGACTTTGGCTACATGC 1372  
DB 1337 ACATCCATTTTCAATTCGCAAGATCCAGGCGAGCGCGCTGGACTTTGGCTACATGC 1396

QY 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCCAACCTCTCTCCACTCCA 1432  
DB 1397 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCCAACCTCTCTCCACTCCA 1456  
QY 1433 CCTA 1436  
DB 1457 CCTA 1460  
RESULT 11  
ADJ57261  
ID ADJ57261 standard; DNA; 1704 BP.  
XX  
AC ADJ57261;  
XX  
DT 06-MAY-2004 (first entry)  
XX Human CD39 polypeptide encoding DNA.  
XX  
KW CD39; nucleoside diphosphate; thrombolytic; anticoagulant;  
KW cardiovascular; cytostatic; antibacterial; immunosuppressive; vasotropic;  
KW cardiant; antianginal; antiarteriosclerotic; gynaecological;  
KW cerebroprotective; cancer; human ; apyrase; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT CDS 31..1563  
FT /\*tag= a  
FT /product= "CD39"  
XX  
PN WO2003070823-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 19-FEB-2003; 2003WO-US004845.  
XX  
PR 20-FEB-2002; 2002US-0358303P.  
XX  
PA (GEO ) GEN HOSPITAL CORP.  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
XX  
PI Elmaleh DR, Robson SC, Papisov MI;  
XX WPI; 2003-778966/73.  
DR P-PSDB; ADJ57262.  
XX  
PT New enzyme polymer conjugate used for treating abnormal levels of  
PT extracellular nucleotides or platelet aggregation, graft transplant,  
PT cardiovascular disease, cancer and sepsis.  
XX  
PS Disclosure; SEQ ID NO 1; 82pp; English.  
XX  
CC The invention relates to a conjugate (I) comprising an enzyme and a  
CC biodegradable polymer, where (i) enzymatic activity of the enzyme is  
CC higher relative to that of the enzyme in the absence of the biodegradable  
CC polymer, or (ii) the half life of the enzyme is longer than that of the  
CC enzyme in the absence of the polymer. The enzymatic activity (i) is at  
CC least 10 (preferably at least 100) times higher in the presence of the  
CC polymer. The enzyme is a multimeric, soluble and/or extracellular enzyme,  
CC preferably an apyrase, especially a soluble form of CD39 and catalyzes  
CC hydrolysis of nucleoside diphosphate. The conjugate can be used to treat  
CC diseases relating to abnormal levels of extracellular nucleotides or  
CC abnormal aggregation of platelets, particularly cardiovascular disease,  
CC cancer, sepsis or a disease related to graft transplant. (I) is also used  
CC for treating coronary artery disease or injury following myocardial  
CC infarction, unstable angina, atherosclerosis, pre-eclampsia, embolism,  
CC platelet associated ischaemic disorders including lung, coronary and  
CC cerebral ischaemia, reocclusion following thrombosis, thrombotic  
CC disorders, and thrombosis and coagulopathies associated with exposure to  
CC a foreign or injured tissue surface, in combination with angioplasty,  
CC carotid endarterectomy, anastomosis of vascular grafts and chronic  
CC cardiovascular devices. The present sequence represents a DNA encoding a



PI aggregation - using CD39 protein with ATP at: pncvplno:nyugotave activity,

XX Gene therapy of inflammatory or immunological stimulation of platelet  
PT aggregation - using CD39 protein with ATP di:phospho:hydrolase activity.



PT useful for preventing or alleviating thrombotic condition in mammalian  
 PT subject.  
 XX  
 PS Claim 3; Page 38; 65pp; English.  
 XX

CC Non-human transgenic or somatic recombinant mammals, whose cells contain  
 CC a heterologous DNA encoding a polypeptide (especially human CD39 protein)  
 CC having ATP-diphosphohydrolase activity under cellular activating  
 CC conditions is claimed. In particular the animal is a pig and its cells  
 CC (or tissues or organs) can be used for transplantation. DNA coding for  
 CC human CD39 is also useful for genetically modifying a mammalian cell to  
 CC render it less susceptible to an inflammatory or immunological stimulus  
 CC and platelet aggregation. The modified cells can be used to prevent or  
 CC alleviate a thrombotic condition. The present sequence encodes human CD39  
 CC protein and was disclosed in J.Immunol. 153 (8) (1994) 3574-3584  
 XX

SQ Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;

Query Match 91.8%; Score 1319.2; DB 2; Length 1818;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	113	GTTCAACCCAGAACAAAGCATTCGCCAGAAAACGTTAAGTATGGGATGTGCTGGATCGCG	172
Db	174	GGTTGACCCAGAACAAAGCATTCGCCAGAAAACGTTAAGTATGGGATGTGCTGGATCGCG	233
Qy	173	GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG	232
Db	234	GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG	293
Qy	233	GCCTGGTGCATCAAGTAGAAGATGACGGGTTAAAGTCTCGGAATCTCAAAATTTGTTTC	292
Db	294	GCCTGGTGCATCAAGTAGAAGATGACGGGTTAAAGTCTCGGAATCTCAAAATTTGTTTC	353
Qy	293	AGAAAGTAAATGAAATAGGCAITTAACCTGCACTGATTCGATGGAAGAGCTAGGGAAGTGA	352
Db	354	AGAAAGTAAATGAAATAGGCAITTAACCTGCACTGATTCGATGGAAGAGCTAGGGAAGTGA	413
Qy	353	TTCCAGGTTCCAGACCAAGACACACCCGTTTACCTGGGAGCCAGCGGATCGGCT	412
Db	414	TTCCAGGTTCCAGACCAAGACACCCGTTTACCTGGGAGCCAGCGGATCGGCT	473
Qy	413	TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGTTCTGGATGTGGTGAGAGGAGCC	472
Db	474	TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGTTCTGGATGTGGTGAGAGGAGCC	533
Qy	473	TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAATCTGCGCCAAAGAGGTTG	532
Db	534	TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAATCTGCGCCAAAGAGGTTG	593
Qy	533	CTATGGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAGAAAACAGGTGGT	592
Db	594	CTATGGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAGAAAACAGGTGGT	653
Qy	593	TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGAGCTTTGGACCTTTGGGG	652
Db	654	TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGAGCTTTGGACCTTTGGGG	713
Qy	653	GAGCCTCTACACAAGTCACATTTTGTATCCCAAAACACAGACTATCGAGTCCCCAGATAATG	712
Db	714	GAGCCTCTACACAAGTCACATTTTGTATCCCAAAACACAGACTATCGAGTCCCCAGATAATG	773
Qy	713	CTCTGCAATTTGCGCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTCTTGCT	772
Db	774	CTCTGCAATTTGCGCTCTATGGCAAGGACTACAAATGTCTACACATAGCTTCTTGCT	833
Qy	773	ATGGAGAGGATCAGGCACTCTGCGAGAACTTGCGCAAGGACATTCAGTTTGAAGTAATG	832
Db	834	ATGGAGAGGATCAGGCACTCTGCGAGAACTTGCGCAAGGACATTCAGTTTGAAGTAATG	893
Qy	833	AAATTTCTCAGGGACCCATGCTTTTCCTCGATATAGAAAGGTAGTGAACGTAAAGTGACC	892
Db	894	AAATTTCTCAGGGACCCATGCTTTTCCTCGATATAGAAAGGTAGTGAACGTAAAGTGACC	953

Qy	893	TTTACAAGACCCCTGACCAAGAGATTGAGATGACTCTTCATTTCCAGCAGTTTGAAA	952
Db	954	TTTACAAGACCCCTGACCAAGAGATTGAGATGACTCTTCATTTCCAGCAGTTTGAAA	1013
Qy	953	TCCAGGGTATTGGAAATATCAACAATGCCATCAAGCATCTCGGAGCTCTTCAACACCA	1012
Db	1014	TCCAGGGTATTGGAAATATCAACAATGCCATCAAGCATCTCGGAGCTCTTCAACACCA	1073
Qy	1013	GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGCACACATCCAGGGGG	1072
Db	1074	GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTCTTGCACACATCCAGGGGG	1133
Qy	1073	ATTTTGGGGCATTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA	1132
Db	1134	ATTTTGGGGCATTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTTGACATCAGAGA	1193
Qy	1133	AAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAGTTCTGTCTCAGCCTTGGGAGG	1192
Db	1194	AAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAGTTCTGTCTCAGCCTTGGGAGG	1253
Qy	1193	AGATAAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTCTG	1252
Db	1254	AGATAAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTCTG	1313
Qy	1253	GTACCTTACATTTCTCCCTCTCTTCTGCAAGGCTATCATTTTCAGCTGATTCCTGGGAGC	1312
Db	1314	GTACCTTACATTTCTCCCTCTCTTCTGCAAGGCTATCATTTTCAGCTGATTCCTGGGAGC	1373
Qy	1313	ACATCCATTTTCAATTTGGCAAGATCCAGGGCAGGAGCGCGGCTGGACTTTGGGTACATGC	1372
Db	1374	ACATCCATTTTCAATTTGGCAAGATCCAGGGCAGGAGCGCGGCTGGACTTTGGGTACATGC	1433
Qy	1373	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCATCCA	1432
Db	1434	TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCATCCA	1493
Qy	1433	CCCTA 1436	
Db	1494	CCTA 1497	

RESULT 14  
 ADI32149  
 ID ADI32149 standard; cDNA; 1818 BP.  
 XX  
 AC ADI32149;  
 DT  
 DX 17-JUN-2004 (first entry)  
 XX  
 DE Human cDNA #1475.  
 XX  
 KW Human; gene; ss; immunological response; immunopathological condition;  
 KW Crohn's disease; asthma; ulcerative colitis; hyperosinophilia;  
 KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;  
 KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;  
 KW osteopathic; antiarthritic; antirheumatic; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6607879-B1.  
 XX  
 PD 19-AUG-2003.  
 XX  
 PF 09-FEB-1998; 98US-00023655.  
 XX  
 PR 09-FEB-1998; 98US-00023655.  
 XX  
 PA (INCY-) INCYTE CORP.  
 XX  
 PI Cocks BG, Stuart SG, Seilhamer JJ;  
 XX  
 DX WPI; 2003-895307/82.



XX A composition comprising a plurality of cDNAs, useful for detecting  
 PT altered expression of genes in an immunological response or for  
 PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma  
 PT or osteoarthritis.

XX Claim 1; SEQ ID NO 1475; 50pp; English.

XX The invention relates to a composition comprising a plurality of cDNAs  
 CC for detecting the altered expression of genes in an immunological  
 CC response. The invention also relates to a method of diagnosing or  
 CC monitoring the treatment of an immunopathological condition in a sample,  
 CC comprising obtaining nucleic acids from a sample, contacting the nucleic  
 CC acids of the sample with an array comprising the plurality of cDNAs under  
 CC conditions to form one or more hybridisation complexes, detecting the  
 CC hybridisation complexes and comparing the levels of the detected  
 CC hybridisation complexes with the level of hybridisation complexes  
 CC detected in a non-diseased sample, where an altered level of the detected  
 CC hybridisation complexes correlates with the presence of an  
 CC immunopathological condition. Also disclosed are an expression profile  
 CC comprising a microarray and a plurality of detectable probes. The cDNAs  
 CC method for identifying a plurality of polynucleotide probes. The cDNAs  
 CC are useful as hybridisable array elements in a microarray for monitoring  
 CC the expression of target polynucleotides. The microarray can be used in  
 CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,  
 CC ulcerative colitis, hyperesoinophilia, irritable bowel syndrome,  
 CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in  
 CC identifying agents for the treatment of the diseases. The microarray may  
 CC also be used in drug discovery and development, toxicological and  
 CC carcinogenicity studies, forensics or pharmacogenomics. The composition  
 CC may also be used in purification of a subpopulation of mRNAs, cDNAs or  
 CC genomic fragments. This sequence represents a human cDNA of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification but was obtained in electronic format directly  
 CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;

Query Match 91.8%; Score 1319.2; DB 11; Length 1818;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GTTCAACCCAGAACAAAGCAATTCGACAAAACGTTAAGTATGGGATTTGCTGGATGCGG 172  
 DB 174 GGTTCACCCAGAACAAAGCAATTCGACAAAACGTTAAGTATGGGATTTGCTGGATGCGG 233  
 QY 173 GTTCTTCTCACACAGTTTATACATCTATAGTGGCCAGCAAGAAAGGAGATGACACAG 232  
 DB 234 GTTCTTCTCACACAGTTTATACATCTATAGTGGCCAGCAAGAAAGGAGATGACACAG 293  
 QY 233 CGGTGGTGCATCAAGTAGAAGATGACGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 292  
 DB 294 CGGTGGTGCATCAAGTAGAAGATGACGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 353  
 QY 293 AGAAAGTAAATGAATAGGATTTACCTGACTGATGATGAAAGAGAGCTAGGGAAGTGA 352  
 DB 354 AGAAAGTAAATGAATAGGATTTACCTGACTGATGATGAAAGAGAGCTAGGGAAGTGA 413  
 QY 353 TTCCAAGGTCACAGCACCAAGAGACACCGGTTTACCTGGGAGCCACGGCAGCATGCGGT 412  
 DB 414 TTCCAAGGTCACAGCACCAAGAGACACCGGTTTACCTGGGAGCCACGGCAGCATGCGGT 473  
 QY 413 TGCTCAGGATGGAAGTAGAAGTTGGCAGACAGAGGTTCTGGATGCTGGAGAGAGGCC 472  
 DB 474 TGCTCAGGATGGAAGTAGAAGTTGGCAGACAGAGGTTCTGGATGCTGGAGAGAGGCC 533  
 QY 473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGGATCATTAATCTGGCCAAAGAGGAAGTG 532  
 DB 534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGGATCATTAATCTGGCCAAAGAGGAAGTG 593  
 QY 533 CCTATGGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGT 592  
 DB 594 CCTATGGCTGGATTAATCACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGGT 653

QY 593 TCAGCATAGTCCCATATGAAACCAATAATCAGAAAAACCTTTGGAGCTTTTGGACCTTTGGGG 652  
 DB 654 TCAGCATAGTCCCATATGAAACCAATAATCAGAAAAACCTTTGGAGCTTTTGGACCTTTGGGG 713  
 QY 653 GAGCCTCTACACAAAGTCACTTTTGTACCCCAAAACAGACTATCAGTCCCAAGATAATG 712  
 DB 714 GAGCCTCTACACAAAGTCACTTTTGTACCCCAAAACAGACTATCAGTCCCAAGATAATG 773  
 QY 713 CTCTGCAATTTTGGCCTCTATGCAAGGACTACAAATGTCTACACATAGCTTTCTTGCTGT 772  
 DB 774 CTCTGCAATTTTGGCCTCTATGCAAGGACTACAAATGTCTACACATAGCTTTCTTGCTGT 833  
 QY 773 ATGGAAGGATCAGGCACTCTGGCAGAAAATGGCCAAAGACATTCAGGTTTGAAGTAATG 832  
 DB 834 ATGGAAGGATCAGGCACTCTGGCAGAAAATGGCCAAAGACATTCAGGTTTGAAGTAATG 893  
 QY 833 AAATTTCTCAGGAGCCCATGCTTTTCATCTCGATATAGAAGTAGTAGAAGTAAAGTACC 892  
 DB 894 AAATTTCTCAGGAGCCCATGCTTTTCATCTCGATATAGAAGTAGTAGAAGTAAAGTACC 953  
 QY 893 TTTCAAGACACCCCTGACCAAGAGATTTGAGATCACTTCTCCATTCCAGCAGTTTGAAGA 952  
 DB 954 TTTCAAGACACCCCTGACCAAGAGATTTGAGATCACTTCTCCATTCCAGCAGTTTGAAGA 1013  
 QY 953 TCCAGGGTATTTGGAAAATATCAACAATGCCATCAAAAGCATCCTGGAGCTCTTCAACACCA 1012  
 DB 1014 TCCAGGGTATTTGGAAAATATCAACAATGCCATCAAAAGCATCCTGGAGCTCTTCAACACCA 1073  
 QY 1013 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTGGCCACCACTCCAGGGGG 1072  
 DB 1074 GTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTGGCCACCACTCCAGGGGG 1133  
 QY 1073 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAGA 1132  
 DB 1134 ATTTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAGA 1193  
 QY 1133 AAGTCTCTCAGAAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGGAGG 1192  
 DB 1194 AAGTCTCTCAGAAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCCTTGGGAGG 1253  
 QY 1193 AGATAAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTTCTG 1252  
 DB 1254 AGATAAAAACATCTTACGCTGGAGTAAAGGAGAGTACTGAGTGAATACTGCTTTTCTG 1313  
 QY 1253 GTACTCATTTCTCTCCCTCTCTGCAAGGCTATCATTTTCAAGCTGATTTCTCTGGAGC 1312  
 DB 1314 GTACTCATTTCTCTCCCTCTCTGCAAGGCTATCATTTTCAAGCTGATTTCTCTGGAGC 1373  
 QY 1313 ACATCCATTTTCAATTTGGCAAGATCCAGGGCAGCGCGGCTGGACTTTGGGCTACATGC 1372  
 DB 1374 ACATCCATTTTCAATTTGGCAAGATCCAGGGCAGCGCGGCTGGACTTTGGGCTACATGC 1433  
 QY 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA 1432  
 DB 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA 1493  
 QY 1433 CCTA 1436  
 DB 1494 CCTA 1497

RESULT 15

ADK60414

ID ADK60414 standard; DNA; 1818 BP.

XX

XX ADK60414;

XX AC

DT 06-MAY-2004 (first entry)

XX

DE Angiogenesis differentially expressed gene #61.

XX

KW ds; vasotropic; antirheumatic; antiarthritic; hypotensive; antianginal;



Search completed: September 21, 2005, 17:05:32  
Job time : 832.224 secs

**THIS PAGE BLANK (USPTO)**

**THIS PAGE BLANK (USPTO)**

Result No.	Score	Query Match	Length	DB	ID	Description	
C	1	1063.6	74.0	1760	3	CR617781	full-length
	2	940.6	65.5	984	5	BX436692	EX136692 BX436692
	3	863	60.1	2410	3	AK029512	AK029512 Mus muscu
	4	863	60.1	4198	3	AK030601	AK030601 Mus muscu
	5	812.4	56.5	861	5	BX371889	BX371889 Mus muscu
	6	743.4	51.7	3563	3	AK028625	AK028625 Mus muscu
	7	730.2	50.8	1014	1	AL553150	AL553150 AL553150
	8	727	50.6	1066	5	BM906668	BM906668 AGENCOURT
	9	720.6	50.1	897	1	AL552123	AL552123 AL552123
	10	702.2	48.9	1025	5	BX402316	BX402316 BX402316
C	11	697.6	48.5	1023	1	AL547722	AL547722 AL547722
	12	656.8	45.7	952	5	BX327984	BX327984 BX327984
	13	652.6	45.4	1061	5	BM925184	BM925184 AGENCOURT
	14	645.2	44.9	808	2	BF664417	BF664417 602146163
	15	624.2	43.4	673	6	CB553235	CB553235 MMSP0076
	16	622.4	43.3	799	5	BX335123	BX335123 BX335123
	17	588.4	40.9	754	4	BI7171056	BI7171056 603059615
	18	584.8	40.7	608	2	AW965942	AW965942 EST378015
	19	584.2	40.7	820	4	BI822675	BI822675 603036008
	20	573.8	39.9	862	5	BP171342	BP171342 BP171342
C	21	561.2	39.1	656	5	BU947405	BU947405 1047f11.1y
	22	561	39.0	1112	1	AL576332	AL576332 AL576332
	23	556.2	38.7	805	5	BX381864	BX381864 BX381864
	24	520.2	36.2	884	5	BQ711179	BQ711179 AGENCOURT

113 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGCTGGATCGG 172

188 GGTGTGCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGCTGGATCGG 247

```
QY 173 GTTCTTCTCACACAGTTTATATCATCTATTAAGTGGCCAGACAGAAAGGAGATGACACAG 232
Db 248 GTTCTTCTCACACAGTTTATATCATCTATTAAGTGGCCAGACAGAAAGGAGATGACACAG 307
QY 233 GCGTGGTGCACTCAAGTAGAAGAAATGACAGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTC 292
Db 308 GCGTGGTGCACTCAAGTAGAAGAAATGACAGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTC 367
QY 293 AGAAAGTAAATGAAATAGGCAATTTACTGACTGATTTGCAATGGAAGAGAGCTAGGGAAGTGA 352
Db 368 AGAAAGTAAATGAAATAGGCAATTTACTGACTGATTTGCAATGGAAGAGAGCTAGGGAAGTGA 427
QY 353 TTTCCAGGTCCTCAGCAGCAGACACCCGTTTACCTGGGAGCCAGCGGAGGATCGCGT 412
Db 428 TTTCCAGGTCCTCAGCAGCAGACACCCGTTTACCTGGGAGCCAGCGGAGGATCGCGT 487
QY 413 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCC 472
Db 488 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCC 547
QY 473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGCGCAAGAGAGAAAGGTG 532
Db 548 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGCGCAAGAGAGAAAGGTG 607
QY 533 CCTATGGCTGATTAATCAACTATCTCTGGGCAATTCAGTCAGAAAACAAGGTGCT 592
Db 608 CCTATGGCTGATTAATCAACTATCTCTGGGCAATTCAGTCAGAAAACAAGGTGCT 667
QY 593 TCAGCATAGTCCCATATGAAACCAATAATCAGAAAACCTTTGGAGCTTTGGACCTTGGGG 652
Db 668 TCAGCATAGTCCCATATGAAACCAATAATCAGAAAACCTTTGGAGCTTTGGACCTTGGGG 727
QY 653 GAGCCTCTACACAGTCACTTTTGTATCCCAAAACAGACTATCGAGTCTCCCAAGATAATG 712
Db 728 GAGCCTCTACACAGTCACTTTTGTATCCCAAAACAGACTATCGAGTCTCCCAAGATAATG 787
QY 713 CTCTGCAATTTCCCTCTATGGAAGGACTTACATCTCTACACATAGCTTCTTGCT 772
Db 788 CTCTGCAATTTCCCTCTATGGAAGGACTTACATCTCTACACATAGCTTCTTGCT 847
QY 773 ATGGGAAGGATCAGGCACTCTGCGAGAACTGCGCAAGGACATTCAGGTTGCAAGTAATG 832
Db 848 ATGGGAAGGATCAGGCACTCTGCGAGAACTGCGCAAGGACATTCAGGTTGCAAGTAATG 894
QY 833 AAATTTCTCAGGAGCCCATGCTTTCTATCCCTGGATATAAGAAAGGTAGTGAAGTGAAGC 892
Db 895 ----- 894
QY 893 TTTTACAGAGCCCTGCACCAAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAA 952
Db 895 -----GCAATTTTGAA 905
QY 953 TCCAGGGTATTGGAACATATCAACAAATGCCATCAAGCATCTCGAGCTCTTCAACACCA 1012
Db 906 TCCAGGGTATTGGAACATATCAACAAATGCCATCAAGCATCTCGAGCTCTTCAACACCA 965
QY 1013 GTTACTGCCCTTACTCCAGTGTCCCTTCAATGGGATTTTCTTGGCAACCATCCAGGGGG 1072
Db 966 GTTACTGCCCTTACTCCAGTGTCCCTTCAATGGGATTTTCTTGGCAACCATCCAGGGGG 1025
QY 1073 ATTTTGGGGCATTTTCAGCTTTTACTTTGTGTGATGAAGTTTAAACTTCACATTCAGAGA 1132
Db 1026 ATTTTGGGGCATTTTCAGCTTTTACTTTGTGTGATGAAGTTTAAACTTCACATTCAGAGA 1085
QY 1133 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAGTTTCTGTGCTCAGCCCTTGGGAGG 1192
Db 1086 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAGTTTCTGTGCTCAGCCCTTGGGAGG 1145
QY 1193 AGATAAAAAATCTTACGCTGGAGTAAAGGAGAAAGTACTGAGTGAATACTGCTTTTCTG 1252
Db 1146 AGATAAAAAATCTTACGCTGGAGTAAAGGAGAAAGTACTGAGTGAATACTGCTTTTCTG 1205
```

```
QY 1253 GTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTTGGAGC 1312
Db 1206 GTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTACAGCTGATTTCTTGGAGC 1265
QY 1313 ACATCCATTTTCTTGGCAAGATCCAGGCGAGCGCCGGCTGGACTTTTGGGCTACATGC 1372
Db 1266 ACATCCATTTTCTTGGCAAGATCCAGGCGAGCGCCGGCTGGACTTTTGGGCTACATGC 1325
QY 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1432
Db 1326 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1385
QY 1433 CCTA 1436
Db 1386 CCTA 1389

BX436692 984 bp mRNA linear EST 04-MAY-2004
BX436692 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP003YK21
5-PRIME, mRNA sequence.
ACCESSION BX436692
VERSION BX436692
KEYWORDS BX436692.2 GI:47007879
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 984)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi:30779500.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5524.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?8=CS0CAP003AF11QPI&c=5524.f.
FEATURES
Location/Qualifiers
source 1..984
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP003YK21"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN
Query Match 65.5%; Score 940.6; DB 5; Length 984;
Best Local Similarity 97.9%; Pred. No. 2.9e-266;
Matches 949; Conservative 12; Mismatches 7; Indels 1; Gaps 1;
QY 113 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGTCTGGATCGCG 172
Db 17 GGTTCACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGTCTGGATCGCG 76
QY 173 GTTCTTCTCACACAGTTTATATCATCTATAAGTGGCCAGACAGAAAGGAGATGACACAG 232
Db 77 GTTCTTCTCACACAGTTTATATCATCTATAAGTGGCCAGACAGAAAGGAGATGACACAG 136
```

QY	233	GGGTGGTGCATCAAGTAGAAGATGAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC	292
Db	137	GGGTGGTGCATCAAGTAGAAGATGAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC	196
QY	293	AGAAAGTAATGAATAGGATGATTTACCTGACTGATTTGATGGAAGAGAGCTAGGAGTGA	352
Db	197	AGAAAGTAATGAATAGGATGATTTACCTGACTGATTTGATGGAAGAGAGCTAGGAGTGA	256
QY	353	TTTCAAGGTCCTCAGCAGCAGGAGACACCCGTTTACCTGGGAGCCACGGCAGGATCGCGT	412
Db	257	TTTCAAGGTCCTCAGCAGCAGGAGACACCCGTTTACCTGGGAGCCACGGCAGGATCGCGT	316
QY	413	TGCTCAGGATGGAAGTGAAGTGGGAGAGAGGTTCTGATGATGTTGGAGAGAGGCC	472
Db	317	TGCTCAGGATGGAAGTGAAGTGGGAGAGAGGTTCTGATGATGTTGGAGAGAGGCC	376
QY	473	TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCAATTAATGCTGGCCAGGAGGAGTG	532
Db	377	TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCAATTAATGCTGGCCAGGAGGAGTG	436
QY	533	CCTATGGCTGGATTACTCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT	592
Db	437	CCTATGGCTGGATTACTCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT	496
QY	593	TCAGCATAGTCCCATATGAACCAATATCAGAGAACCTTTGGAGCTTTGGACCTTTGGGG	652
Db	497	TCAGCATAGTCCCATATGAACCAATATCAGAGAACCTTTGGAGCTTTGGACCTTTGGGG	556
QY	653	GAGCCTCTACACAAGTCATTTGTTGACCCCAAAACAGACTATCAGTCCCGAGTAATG	712
Db	557	GAGCCTCTACACAAGTCATTTGTTGACCCCAAAACAGACTATCAGTCCCGAGTAATG	616
QY	713	CTCTGCAATTTGCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGCTGT	772
Db	617	CTCTGCAATTTGCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGCTGT	676
QY	773	ATGGAAGGATCAGGACCTCTGGCAGAACTGGCCAAAGACATTCAGGTTGCAAGTAATG	832
Db	677	ATGGAAGGATCAGGACCTCTGGCAGAACTGGCCAAAGACATTCAGGTTGCAAGTAATG	736
QY	833	AAATTTCTCAGGAGCCATCTTTCATCTGGATATAAGAGTGTAGTGAACCTAGTGACC	892
Db	737	AAATTTCTCAGGAGCCATCTTTCATCTGGATATAAGAGTGTAGTGAACCTAGTGAACC	796
QY	893	TTTACAAGACCCCTGACCAAGAGATTTGAGTCACTCTTCCATTCAGCAGATTTTGAAA	952
Db	797	TTTACAAGACCCCTGACCAAGAGATTTGAGTCACTCTTCCATTCAGCAGATTTTGAAA	856
QY	953	TCCAGGTTATTGGAACCTATCAACCAATGCCATCAAGCATCTGGAGCTCTTCAACACCA	1012
Db	857	TCCAGGTTATTGGAACCTATCAACCAATGCCATCAAGCATCTGGAGCTCTTCAAMACAA	916
QY	1013	GTTACTGCTTACTCCAGTGTGCTTCAATGGATTTCTTGGCCACCATCTCAGGGGG	1072
Db	917	GTTACTGCTTCAATTCCTGCTTCAATGGATTTCTTGGCCACCATCTCAGGGGG	975
QY	1073	ATTTTGGGG 1081	
Db	976	ATTTTGGGG 984	

RESULT 3	
AK029512	
LOCUS	AK029512
DEFINITION	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921511C05 product:reconucleoside triphosphate diphosphohydrolase 1, full insert sequence.
ACCESSION	AK029512
VERSION	AK029512.1 GI:26325463
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
MEDLINE	
PUBMED	
REFERENCE	
AUTHORS	The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	
PUBMED	
REFERENCE	
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES	Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/
SOURCE	Location/Qualifiers 1. . 2410 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J"





TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
JOURNAL Prepare full-length cDNA libraries for rapid discovery of new genes  
MEDLINE Genome Res. 10 (10), 1617-1630 (2000)  
PUBMED 20499374  
REFERENCE 11042159  
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M.,  
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,  
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
Fujiwara,S., Ishikawa,T., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,  
Okazaki,Y., Inoue,K., Ozawa,K., Tanaka,T., Muramatsu,S., Kawai,J.,  
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
JOURNAL sequencing pipeline with 384 multicapillary sequencer  
MEDLINE Genome Res. 10 (11), 1757-1771 (2000)  
PUBMED 20530913  
REFERENCE 11076861  
AUTHORS 4

TITLE The RIKEN Genome Exploration Research Group Phase II Team and the  
JOURNAL FANTOM Consortium.  
MEDLINE Functional annotation of a full-length mouse cDNA collection  
PUBMED Nature 409, 685-690 (2001)  
REFERENCE 11076861  
AUTHORS 4

TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research  
JOURNAL Group Phase I & II Team.  
MEDLINE Analysis of the mouse transcriptome based on functional annotation  
PUBMED Nature 420, 563-573 (2002)  
REFERENCE 11076861  
AUTHORS 4

TITLE Direct Submission  
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
MEDLINE Physical and Chemical Research (RIKEN), Laboratory for Genome  
PUBMED Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
REFERENCE RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
AUTHORS Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

TITLE CDNA library was prepared and sequenced in Mouse Genome  
JOURNAL Encyclopedia Project of Genome Exploration Research Group in Riken  
MEDLINE Genomic Sciences Center and Genome Science Laboratory in RIKEN  
PUBMED Division of Experimental Animal Research in Riken contributed to  
REFERENCE prepare mouse tissues.  
AUTHORS Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
Location/Qualifiers

FEATURES  
source  
1. .4198  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="PANTOM\_DB:5330437E10"  
/db\_xref="taxon:10090"  
/clone="5330437E10"  
/sex="male"  
/tissue type="pituitary gland"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev stage="adult"  
93. .1625  
/note="unnamed protein product; ectonucleoside  
triphosphate diphosphohydrolase 1 (MGD|MG1:102805,

GB|NM\_009848, evidence: BLASTN, 100%, match=2284)  
putative"  
/codon\_start=1  
/protein\_id="BAC27039.1"  
/db\_xref="GI:26326591"  
/translation="MEDIKSKVKRPFCSKNLIIILGPTSLILAVIALIIVGLTQNKPLP  
ENVYGVLDAGSSHTNLYIYKPAEKENDTGVQVLEBECQVKGPIISKYAOKTDEIG  
AYLAECMELSTELPTSKHQTPVYLGATAGMLRLMESBQSAVLAASVSLKSYSP  
QIFQAKIITQEGCAYGWIITNLLGRFTQESWLSLISQKQETFGALDLAGST  
QITFVPONTTIESPENSQPRLYGSDYTVYTHSLCYKQDQALWOKLAKDIOVSSGV  
LKDFPCNPGYEVNVNLSYCTPCTKREKPLPDPRIQGTQEQHQSLELPPNN  
SHCPYSQCAFNGVLPPLHSGFSAFYPFMDPFKVKAKNSVISOERKTIKPFCS  
KSWBETKYSYPSVREKYSFSGAYILSLQGYNFYDSSWEQIHFWMKTIKSNAG  
TVGMLNLTNMPAEQPLSPPLPHSTYIQLMVLFSLLVAIVAITGLFIYSKPSYFWE  
AV"  
polyA\_signal 4171. .4176  
/note="putative"  
polyA\_site 4198  
/note="putative"  
ORIGIN  
Query Match 60.1%; Score 863; DB 3; Length 4198;  
Best Local Similarity 79.8%; Pred. No. 4.3e-243;  
Matches 1058; Conservative 0; Mismatches 255; Indels 12; Gaps 3;  
QY 118 ACCGAGAACAAAGCATTCGCCAGAAACGTTAAGTATGGGATTGTCTGGATCGGGTCT 177  
Db 204 ACCGAGAACAAACCTTTGCCAGAAATGTTAAGTATGGGATTGTCTGGATCGGGTCA 263  
QY 178 TCTCACAAAGTTTATACATCTNTAAGTGGCCAGCAGAAAGAGAAATGACACAGCGTG 237  
Db 264 TCTCACAAACCTGTATCATCTACAAAGTGGCGGCCGAGAGAGAAATGACACAGCGTG 323  
QY 238 GTGCATCAAGTAGAAGATGAGAGTAAAGTCTCTGAATCTCAAAATTTGTTTCAGAAA 297  
Db 324 GTGCAGCTTAGAGGAATGCAAGTGAAGTCTCTGAATCTCAAAATTTGTTTCAGAAA 383  
QY 298 GTAAATGAATPAGGATTTACCTGACATGATTCATGGAAGAGCTAGGGAAGTGAATCCA 357  
Db 384 ACAGATGAATCGGTGCGTACCTGCGCAATGTCATGGAAGTCTCCACCGAACTGATACCA 443  
QY 358 AGGTCCAGCACCAGAGACACCCGTTTACCTGGGAGCCAGCGCAGGATCGGGTGTCTC 417  
Db 444 ACATCCAGCATCACAGACTCTCTGTCTACCTGGGAGCCACAGCAGGATCGGCTTGTCT 503  
QY 418 AGGATGAAAGTGAAGAGTTGGCAGACAGGGTCTCTGATGTGGTGGAGAGAGCCCTCAGC 477  
Db 504 AGAATGGAAGCGCAACATCGGCAGACAGGTCCTGCTGCAGTGTCAACAGCCTTAAG 563  
QY 478 AACTACCCCTTTGACTTTCCAGGGTCCAGGATCATTAATCTGCGCAAGAGAGAGTGCCTAT 537  
Db 564 AGCTACCCCTTTGACTTTCCAGGGTCCCAAGATCATCTGGAAGAGAGAGTGCCTAT 623  
QY 538 GGCTGGATTAATCAACTATCTCTGGGCAAAATTCAGTTCAGAAAACAAGGTGGTTCAGC 597  
Db 624 GGGTGGATTAATCAACTATCTCTGGGCAAGATTCATCTCAGGAACAGAGTTGGCTAAGC 683  
QY 598 ATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGAGCTTCGGGGAGCC 657  
Db 684 CTCATCTCA---GACAGTCAAGAACAGGAACCTTTGGCGCTTTGGAGTCTCGGGAGGCC 740  
QY 658 TCTACCAAGTCACTTTTGTACCCCAAAACACAGACTATCGAGTCCCAAGATAATGCTCTG 717  
Db 741 TCCACACAGATCACTTTGTCGTCGCCCAAAACACAGACTATAGAGTCCCAAGAAAATCTCTG 800  
QY 718 CAATTTCCCTCTATGAGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCTATGGG 777  
Db 801 CAATTTCCCTCTATGAGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCTATGGG 860  
QY 778 AAGGATCAGGACTCTCGCAGAACTCGCCCAAGGACATTCAGGTTCGAAGTAATGAATT 837  
Db 861 AAGGATCAGGCTCTCTCGCAGAACTCGCCCAAGGACATTCAGGTTCGAAGTGGTGGCGTC 920

Qy	838	CTCAGGACCCATGCTTTTCATCTCGGATATAAGAAAGGTAGTGAACGTAAGTGACCTTTTAC	897
Db	921	CTTAAAGACCCATGCTTTTAAACCCAGGATACGAGAAGGTTGTGAATGTAAAGTGAGCTCTAT	980
Qy	898	AAGACCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAATCCAG	957
Db	981	GGCACTCCCTGACCAAAAGATTGAAAAGAGCTACCATTTGATCAGTTTCGAATCCAG	1040
Qy	958	GGTATTGGAAATCATCAACAATGCATCAAGACATCTCGGAGCTCTTCAACACCGAGTTAC	1017
Db	1041	GGCACTGGAGACTACGAACAGTGCCACCAGAGCATCTTGAGCTCTTCAACAACAGCCAC	1100
Qy	1018	TGCCCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACCATCCAGGGGGATTTT	1077
Db	1101	TGCCCTTACTCCCACTGTGCTTCAATGGCGTCTTCTGCGCACCTCTCCATGGGAGTTTT	1160
Qy	1078	GGGCACTTTTTCAGCTTTTACTTTTGTCATGAAGTTTTTAACTTGACATCAGAGAA---	1133
Db	1161	GGGGCGTTTTTCTGCTTTCTACTTTGTGTGATGGATTTTTTTTAAAGGTAGCGAAAACAGT	1220
Qy	1134	--AGTCTCTCAGGAAAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCTTGGGAG	1191
Db	1221	GTCACTCTCAGGAGAAAATGACCGAGATAACAAAAAATTTTGCTCAAAATCTTGGGAA	1280
Qy	1192	GAGATAAAACATCTTACCGTGGGATTAAGGAGAAGTACCTGAGTGAATACTGCTTTTCT	1251
Db	1281	GAGACAAGACATCTTATCTCTTCAGTAAAGGAGAAGTACCTGAGTGAAGTACTGCTCTCG	1340
Qy	1252	GGTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTCAGAGTGAATCTCGGAG	1311
Db	1341	GGCGCTTACATCCTCTCTCTC--CTGCAAGGCTATAACTTCACAGACAGCTCTCGGAA	1397
Qy	1312	CACATCATTTTCATTGGCAAGATCCAGGCGAGCGCGGCTGGACTTTGGGCTACATG	1371
Db	1398	CAGATTCATTTTATGGGCAAGATCAAAAGACAGCAACGCGGGTGGACTTTGGGCTACATG	1457
Qy	1372	CTGAACCTGACCAACATGATCCAGCTTGAGCAACCATTTGTGCCACACCTCTCTCCCACTCC	1431
Db	1458	CTGAACTTGACCAACATGATCCAGCTTGACAGCGGTTGTCCCGGCTCTCCCTCACTCC	1517
Qy	1432	ACCTA 1436	
Db	1518	ACCTA 1522	

RESULT 5	861 bp	linear	EST 28-APR-2004
BOX371889/c	861 bp	linear	EST 28-APR-2004
LOCUS	861 bp	linear	EST 28-APR-2004
DEFINITION	861 bp	linear	EST 28-APR-2004
ACCESSION	861 bp	linear	EST 28-APR-2004
VERSION	861 bp	linear	EST 28-APR-2004
KEYWORDS	861 bp	linear	EST 28-APR-2004
SOURCE	861 bp	linear	EST 28-APR-2004
ORGANISM	861 bp	linear	EST 28-APR-2004
REFERENCE	861 bp	linear	EST 28-APR-2004
AUTHORS	861 bp	linear	EST 28-APR-2004
TITLE	861 bp	linear	EST 28-APR-2004
JOURNAL	861 bp	linear	EST 28-APR-2004
COMMENT	861 bp	linear	EST 28-APR-2004

http://www.genoscope.cns.fr/cdna?S=CSOBA10272A08\_CS02553\_1&c=5524.4.

FEATURES	source	Location/Qualifiers
	1. .861	
		/organism="Homo sapiens"
		/mol_type="mRNA"
		/db_xref="taxon:9606"
		/clone="CS01073YD08"
		/tissue_type="PLACENTA COT 25-NORMALIZED"
		/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
		/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN		
	Query Match	56.5%; Score 812.4; DB 5; Length 861;
	Best Local Similarity	99.2%; Pred. No. 2.3e-228;
	Matches 857; Conservative	0; Mismatches 3; Indels 4; Gaps 4
Qy	149	AGTATGGGATGTGCTGGATGCGGGTCTTCTCACACAAGTTTATACATCTATAAGTGGC 208
Db	861	AGTATGGGATGTGCTGNATCGGTTCTTCTCACACAAGTTTATACATCTATAAGTGGC 802
Qy	209	CAGCAGAAAAGGAGAAATGACAC-AGGCGTGGTGCATCAAGTAGAAGAAATCGAGGTTAAA 267
Db	801	CAGCAGAAAAGGAGAAATGACACNAGGCGTGGTGCATCAAGTAGAAGAAATCGAGGTTAAA 742
Qy	268	GGTCTCGGAATCTCAAAATTTGTTTCAGNAAGTAATGAATAGGCATTTTACCTGCACGTGAT 327
Db	741	GGTCTCGGAATCTCAAAATTTGTTTCAGAAAGTAAATGAATAGGCATTTTACCTGCACGTGAT 682
Qy	328	TGCATGAAAAGAGCTAGGGAAGTGATTCCAAAGGTCCAGCACCAGAGACACCCGTTTAC 387
Db	681	TGCATGAAAAGAGCTAGGGAAGTGATTCCAAAGGTCCAGCACCAGAGACACCCGTTTAC 622
Qy	388	CTGGAGCCACGGCAGGCATGCGGTTGCTCAGATGGAAAGTGAAGTTGGCAGACAGG 447
Db	621	CTGGAGCCACGGCAGGCATGCGGTTGCTCAGATGGAAAGTGAAGTTGGCAGACAGG 562
Qy	448	GTTCTGATGTGTGGAGAGAGCGCTCAGCAACTACCCCTTTGACTTCCAGGGTGCACAG 507
Db	561	GTTCTGATGTGTGGAGAGAGCGCTCAGCAACTACCCCTTTGACTTCCAGGGTGCACAG 502
Qy	508	ATCATTACTGCGCAAGAGGAAGTGCCCTATGGCTGGATTACTATCAACTATCTGCTGGGC 567
Db	501	ATCATTACTGCGCCAGAGGAAGTGCCCTATGGCTGGATTACTATCAACTATCTGCTGGGC 442
Qy	568	AAATTCTAGTCAGAAAACAAGGTGGTTCAGCATAGTCCCATATGAAACCAATAATCAGGAA 627
Db	441	AAATTCTAGTCAGAAAACAAGGTGGTTCAGCATAGTCCCATATGAAACCAATAATCAGGAA 382
Qy	628	ACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTCTACACAAGTCACCTTTTGTACCCCAAAC 687
Db	381	ACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTCTACACAAGTCACCTTTTGTACCCCAAAC 322
Qy	688	CAGACTATCAGTCCCCAGATAATGCTCTGCAATTTGCGCCTCTATGGCAAGGACTACAAT 747
Db	321	CAGACTATCAGTCCCCAGATAATGCTCTGCAATTTGCGCCTCTATGGCAAGGACTACAAT 262
Qy	748	GTCTACACATAGCTTCTTTGTGCTATGGGAAGGATCAGGCACCTCTGGCAGAAATCGGCC 807
Db	261	GTCTACACATAGCTTCTTTGTGCTATGGGAAGGATCAGGCACCTCTGGCAGAAATCGGCC 202
Qy	808	AAGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGGACCCAGTCTTTCATCTGGATAT 867
Db	201	AAGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGGACCCAGTCTTTCATCTGGATAT 142
Qy	868	AAGAAGGTAGTGAACGTAAGTGACCTTTTCAAGACCCCTTGCAACCAAGAGATTTGAGATG 927
Db	141	AAGAAGGTAGTGAACGTAAGTGACCTTTTCAAGACCCCTTGCAACCAAGAGATTTGAGATG 82
Qy	928	ACTCTTCATTCACGACGTTTGAATCCAGGGTATTTGGNAACCTATCAACCAATGCCATCAA 987





QY	713	CTCTGCAATTTGCCCTCTTATGGCAAGGACTTACAATGTCTACACACATAGCTTCTTGCTGCT	772
Db	771	CTCTGCAATTTGCCCTCTTATGGCAAGGACTTACAATGTCTACACACATAGCTTCTTGCTGCT	830
QY	773	ATGGGAAGGATCAGGCACCTCTGCGAGAACTGGCCAAAGGACATTGAGTTGCAAGTAATG	832
Db	831	ATGGGAAGGATCAGGCACCTCTGCGAGAACTGGCCAAAGGACATTGAGTTGCAAGTAATG	890
QY	833	AAATTTCTCAGGGACC	847
Db	891	AAATTTCTCAGGGACC	905
RESULT 8			
LOCUS	BM906668	1066 bp	mRNA linear EST 12-MAR-2002
DEFINITION	AGENCOURT_5621802 NIH_MGC_125	Homo sapiens	cdna clone IMAGE:5724619
ACCESSION	BM906668		
VERSION	BM906668.1	GI:19357047	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a>		
	Tissue Procurement: Invitrogen		
	cdna Library Preparation: Life Technologies, Inc.		
	cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	<a href="http://image.llnl.gov">http://image.llnl.gov</a>		
	Plate: LLAM12714 row: c column: 20		
	High quality sequence start: 2		
	High quality sequence stop: 664.		
FEATURES	Location/Qualifiers		
source	1..1066		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:5724619"		
	/lab_host="DH10B"		
	/clone_lib="NIH_MGC_125"		
	/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;		
	Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool		
	of three ovaries, from females ranging in age from 38 to		
	49 yo. Library is oligo-dr primed and directionally cloned		
	(EcoRV site is destroyed upon cloning). Average insert		
	size 2.1 kb, insert size range 1-3.5 kb. Library is		
	normalized and enriched for full-length clones and was		
	constructed by C. Gruber (Invitrogen). Research Genetics		
	tracking code 036."		

ORIGIN

Query Match	50.6%	Score 727;	DB 5;	Length 1066;
Best Local Similarity	93.6%	Pred. No. 4.6e-203;		
Matches 825;	Conservative 0;	Mismatches 45;	Indels 11;	Gaps 6;
Qy	113	GTTCAACCCAGAACAAAGCATTCGCAGAAAACGTTAAGTATGGGATTTGCTGGATGCGG	172	

QY	223	CGCTGGTGCATCAAGTAGAAGAAATCGAGGTTAAAGGCTCTCGAAATCTCAAAATTTGTTTC	292
Db	305	CGCTGGTGCATCAAGTAGAAGAAATCGAGGTTAAAGGCTCTCGAAATCTCAAAATTTGTTTC	364
QY	293	AGAAAGTAATGAATAGGCATTTACCTGACTGATTCGATGCGAAGAGCTAGGGAAGTGA	352
Db	365	AGAAAGTAATGAATAGGCATTTACCTGACTGATTCGATGCGAAGAGCTAGGGAAGTGA	424
QY	353	TTCCAAAGGTCCTCAGCAGCAACCCGTTTACCTGGAGCCACGGCAGGCGATCGCGT	412
Db	425	TTCCAAAGGTCCTCAGCAGCAACCCGTTTACCTGGAGCCACGGCAGGCGATCGCGT	484
QY	413	TGCTCAGGATGGAAGAGTTGGCAGACAGGGTTCTCGATGTGTGGAGAGAGCC	472
Db	485	TGCTCAGGATGGAAGAGTTGGCAGACAGGGTTCTCGATGTGTGGAGAGAGCC	544
QY	473	TCAGCAACTACCCCTTTCAGCTTCCAGGGTGCAGGATCAATTAATGCGCCAAAGGAGGTG	532
Db	545	TCAGCAACTACCCCTTTCAGCTTCCAGGGTGCAGGATCAATTAATGCGCCAAAGGAGGTG	604
QY	533	CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGTCAAGAAACAAGTGGT	592
Db	605	CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGTCAAGAAACAAGTGGT	664
QY	593	TCAGCATAGTCCCATATGAAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG	652
Db	665	TCAGCATAGTCCCATATGAAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG	724
QY	653	GAGCCTCTACACAGTCACTTTTGTACCCCAACCAAGGAGTATCAGTCCCGCCAGATTAATG	712
Db	725	GAGCCTCTACACAGTCACTTTTGTACCCCAACCAAGGAGTATCAGTCCCGCCAGATTAATG	784
QY	713	CTCTGCAATTTGCCCTCTTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGCTGCT	772
Db	785	CTCTGCAATTTGCCCTCTTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGCTGCT	844
QY	773	AT-GGGGAAGGATCAGGCACTCTGCGAGAAACTGG-CCAAAGGACATTCAGGTTGCAAGTAA	830
Db	845	ATGGGAAGGATCAGGCACTCTGCGAGAAACTGGCCCAAGGACCTTCAGGTTGCAAGTAA	904
QY	831	TGAATTTCTCAGGACCCATGC--TTTCATCTCGATATAGAGGTAGTGAACGTAA--	886
Db	905	TGAATTTCTCAGGACCCATGC--TTTCATCTCGATATAGAGGTAGTGAACGTAAAG	964
QY	887	-GTGACCTTTTACAAGACCCCTCGACCAAGAGATTGAGATGACTCTTCCATT--CCAGC	943
Db	965	GGACCTTTTACAAGACCCCTCGACCAAGAGATTGAGATGACTCTTCCATT--CCAGC	1024
QY	944	AGTTTGAAT--CCAGGATTTGGAACATATCAACAATGCC	982
Db	1025	AGTTTGAATCCCGGGTAATTGGAACTATTTCACNAAGGC	1065
RESULT 9			
LOCUS	AL552123	897 bp	mRNA linear EST 30-MAR-2004
DEFINITION	AL552123 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA		
ACCESSION	AL552123		
VERSION	AL552123.3	GI:45856912	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Li.W.B., Gruber.C., Jessee.J. and Polayes.D.		
JOURNAL	Full-length cDNA libraries and normalization		
COMMENT	Unpublished (2001)		
	On Feb 15, 2001 this sequence version replaced gi:31273939.		
	Contact: Genoscope		
	Genoscope - Centre National de Sequencage		
	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE		



353 TTCCAAAGTCCAGCACCAGAGACACCCGTTTACCTGGAGCCAGCGGATGCGGT 412  
428 TTCCAAAGTCCAGCACCAGAGACACCCGTTTACCTGGAGCCAGCGGATGCGGT 487  
413 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGTTCTGGATGTTGGAGAGGCC 472  
488 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGTTCTGGATGTTGGAGAGGCC 547  
473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAATGAGGAGGAGGTG 532  
548 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAATGAGGAGGAGGTG 607  
533 CCTATGGCTGGATTAATCAACTATCTGCTGGCAAAATTCAGTCAGAAAAACAAGTGGT 592  
608 CCTATGGCTGGATTAATCAACTATCTGCTGGCAAAATTCAGTCAGAAAAACAAGTGGT 667  
593 TCAGCATAGTCCCATATGAACCAATTAATCAGAAACCTTTGGAGCTTTGGACCTTGGG 652  
668 TCAGCATAGTCCCATATGAACCAATTAATCAGAAACCTTTGGAGCTTTGGACCTTGGG 727  
653 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 712  
728 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 787  
713 CTCTGCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTTGTGCT 772  
788 CTCTGCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTTGTGCT 847  
773 ATGGAAGGATCAGCACTCTGGCAGAACTGGCCAAAGGACATTTCAG 819  
848 ATGGAAGGATCAGCACTCTGGCAGAACTGGCCAAAGGACATTTCAG 894

RESULT 11  
AL547722  
LOCUS  
DEFINITION  
AL547722 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CS0D1017YB13 5-PRIME, mRNA sequence.  
AL547722  
ACCESSION  
AL547722.3 GI:45748162  
VERSION  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1023)  
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:31369551.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqre@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5524.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?c=CS0D1017CA07QPI&c=5524.f.  
Location/Qualifiers  
1..1023  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1017YB13"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was

FEATURES  
source

digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
Query Match 48.5%; Score 697.6; DB 1; Length 1023;  
Best Local Similarity 98.6%; Pred. No. 2.3e-194;  
Matches 697; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 113 GTTCAACCCAGAACAAAGCATTGCCAGAAACGTTTAAGTATGGGATTGTCTGGATGCGG 172  
DB 198 GGTTCACCCAGAACAAAGCATTGCCAGAAACGTTTAAGTATGGGATTGTCTGGATGCGG 247  
QY 173 GTTCTTCTCACACAAGTTTATACATCTATATAAGTGGCCAGAGAAAGAGAAATGACACAG 232  
DB 248 GTTCTTCTCACACAAGTTTATACATCTATATAAGTGGCCAGAGAAAGAGAAATGACACAG 307  
QY 233 GCGTGGTGATCNAAGTAGAAGATGCAGGGTTAAAGGTCCTGGATCTCAAAATTTGTTTC 292  
DB 308 GCGTGGTGATCNAAGTAGAAGATGCAGGGTTAAAGGTCCTGGATCTCAAAATTTGTTTC 367  
QY 293 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGCGAAGTGA 352  
DB 368 AGAAAGTAAATGAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGCGAAGTGA 427  
QY 353 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGCGATGCGGT 412  
DB 428 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGCGATGCGGT 487  
QY 413 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTTGGAGAGAGGCC 472  
DB 488 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTTGGAGAGAGGCC 547  
QY 473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAATGAGGAGGAGGTG 532  
DB 548 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCAATTAATGAGGAGGAGGTG 607  
QY 533 CCTATGGCTGGATTAATCAACTATCTGCTGGCAAAATTCAGTCAGAAAAACAAGTGGT 592  
DB 608 CCTATGGCTGGATTAATCAACTATCTGCTGGCAAAATTCAGTCAGAAAAACAAGTGGT 667  
QY 593 TCAGCATAGTCCCATATGAACCAATTAATCAGAAACCTTTGGAGCTTTGGACCTTGGG 652  
DB 668 TCAGCATAGTCCCATATGAACCAATTAATCAGAAACCTTTGGAGCTTTGGACCTTGGG 727  
QY 653 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 712  
DB 728 GAGCCTCTACACAAGTCACTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 787  
QY 713 CTCTGCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTTGTGCT 772  
DB 788 CTCTGCAATTTCCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTTGTGCT 847  
QY 773 ATGGAAGGATCAGCACTCTGGCAGAACTGGCCAAAGGACATTTCAG 819  
DB 848 ATGGAAGGATCAGCACTCTGGCAGAACTGGCCAAAGGACATTTCAG 894  
RESULT 12  
BX327984 952 bp mRNA linear EST 07-APR-2004  
BX327984 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CS0D1073YD08 5-PRIME, mRNA sequence.  
ACCESSION  
BX327984  
VERSION  
BX327984.1 GI:30332721  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 952)  
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)



COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5524.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?8=CS0BAG036ZD06_CS03404_1&c=5524.f		
FEATURES	source	Location/Qualifiers	
		1..952 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0D1073YD08" /tissue_type="PLACENTA COT 25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	
ORIGIN	Query Match 45.7%; Score 656.8; DB 5; Length 952; Best Local Similarity 98.7%; Pred. No. 2.6e-182; Matches 672; Conservative 0; Mismatches 8; Indels 1; Gaps 1;		
Qy	753	CACACATAGCTTCTTGTGCTATGGGAAGGATCAGGCACCTCTGGCAGAACTGGCCCAAGGA	812
Db	23	CACACATAGCTTCTTGTGCTATGGGAAGGATCAGGCACCTCTGGCAGAACTGGCCCAAGGA	82
Qy	813	CATTCAAGTTGCAAGTAATGAATAATTTCTCAGGGACCCATGCTTTCATCTCGGATATAAGAA	872
Db	83	CATTCAAGTTGCAAGTAATGAATAATTTCTCAGGGACCCATGCTTTCATCTCGGATATAAGAA	142
Qy	873	GGTAGTGAACGTAAGTGAACCTTTACAAGACCCCTCGACCAAGAGATTTGAGATGACTCT	932
Db	143	GGTAGTGAACGTAAGTGAACCTTTACAAGACCCCTCGACCAAGAGATTTGAGATGACTCT	202
Qy	933	TCCATTCCAGCAGTTTGAATTCAGGGTATTTGGAACCTATCAACATGATCCATCAAGCAT	992
Db	203	TCCATTCCAGCAGTTTGAATTCAGGGTATTTGGAACCTATCAACATGATCCATCAAGCAT	262
Qy	993	CTTGGAGCTCTTCAACACCAAGTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTT	1052
Db	263	CTTGGAGCTCTTCAACACCAAGTTACTGCCCTTACTCCAGTGTGCTTCAATGGGATTTT	322
Qy	1053	CTTTGCCACCACTCCAGGGGATTTTGGGGCATTTTCAGCTTTTATCTTTGTGTGATGAAGTT	1112
Db	323	CTTTGCCACCACTCCAGGGGATTTTGGGGCATTTTCAGCTTTTATCTTTGTGTGATGAAGTT	382
Qy	1113	TTTAACTTCACATCAGAGAAAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAGTT	1172
Db	383	TTTAACTTCACATCAGAGAAAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAGTT	442
Qy	1173	CTGTGCTCAGCCTTGGGAGGAGATAAAAACATCTTTACGCTGGAGTAAAGGAGAGTACCT	1232
Db	443	CTGTGCTCAGCCTTGGGAGGAGATAAAAACATCTTTACGCTGGAGTAAAGGAGAGTACCT	502
Qy	1233	GAGTGAATACGCTTTTCTGGTACCTACATTTCTCTCCCTCTCTCTGCAAGGCTATCATTT	1292
Db	503	GAGTGAATACGCTTTTCTGGTACCTACATTTCTCTCCCTCTCTCTGCAAGGCTATCATTT	562
Qy	1293	CACAGCTGATTTCTGGGAGCAGATCCATTTTCATTTGGCAAGATCCAGGCGACGCGCGG	1352
Db	563	CACAGCTGATTTCTGGGAGCAGATCCATTTTCATTTGGCAAGATCCAGGCGACGCGCGG	622
Qy	1353	CTGGACTTTTGGGTACATGCTGAACCTTGACCAACATGATCCCAAGCTGAGCAACCATTTGTC	1412
,			

Db	623	CTGGACTTTGGGCTACATGCTGAACCTGACCACTGATCCACGCTGAGCAACCATTTGT- 681
Qy	1413	CACACTCTCTCTCCCACTCCAC 1433
Db	682	CACACTGTCTTCTCCACTCCAC 702
RESULT 13		
BM925184	1061 bp	mRNA linear EST 12-MAR-2002
LOCUS	AGENCOURT_6627603	NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5762493
DEFINITION	5', mRNA sequence.	
ACCESSION	BM925184	
VERSION	BM925184.1	GI:19375563
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1061) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12812 row: m column: 22 High quality sequence start: 4 High quality sequence stop: 669.	
FEATURES	Location/Qualifiers	
	1..1061 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5762493" /lab_host="DH10B" /clone_lib="NIH_MGC_122" /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."	
ORIGIN		
Query Match 45.4%; Score 652.6; DB 5; Length 1061; Best Local Similarity 92.8%; Pred. No. 4.7e-181; Matches 773; Conservative 0; Mismatches 49; Indels 11; Gaps 8;		
Qy	382	GTTTACCTGGGAGCCACGGCAGGCATGCGGTTGCTCAGGATGGAAGTGAAGTTGGCA 441
Db	172	GTTTGACCCAGCAACAAAGCATTTGCCAGAAAAGTTAAGGATGGAAGTGAAGTTGGCA 231
Qy	442	GACAGGTTCTGGATGTGTGGAGAGGACCTCAGCACTACCCCTTTCACCTCCAGGCT 501
Db	232	GACAGGTTCTGGATGTGTGGAGAGGACCTCAGCACTACCCCTTTCACCTCCAGGCT 291
Qy	502	GCCAGGATCATTTACTGGCCAAAGAGAGTGGCTGCTGCTGATTACTATCAATCTATCTG 561
Db	292	GCCAGGATCATTTACTGGCCAAAGAGAGTGGCTGCTGCTGATTACTATCAATCTATCTG 351
Qy	562	CTGGGCAATTCAGTCCAGAAAACAAGGTGGTTTCAGCATAGTCCCATATGAAACCAATAAT 621



```
Db 352 CTGGGCAATTCACTCAGAAAAACAAGTGGTTCAGCATAGTCCCATATGAAACCAATAAT 411
Qy 622 CAGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAACTCACTTTGTACCC 681
Db 412 CAGAAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTCTACACAACTCACTTTGTACCC 471
Qy 682 CAAAACAGACTATCAGATCCCAAGATATGCTCTGCAATTTGCGCTCTATGGCAAGGAC 741
Db 472 CAAAACAGACTATCAGATCCCAAGATATGCTCTGCAATTTGCGCTCTATGGCAAGGAC 531
Qy 742 TACAATGTCTACACATAGCTTTCTGTGCTATGGGAAGGATCAGGACCTCTGGCAGAA 801
Db 532 TACAATGTCTACACATAGCTTTCTGTGCTATGGGAAGGATCAGGACCTCTGGCAGAA 591
Qy 802 CTGGCCAAGGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGACCCATGCTTTCACTCT 861
Db 592 CTGGCCAAGGACATTCAGGTTGCAAGTAATGAAATTTCTCAGGACCCATGCTTTCACTCT 651
Qy 862 GGNATATAAGAGTAGTGAACGTAACTGATGCTTTTACAGACCCCTTGCAACCAAGATTT 921
Db 652 GGNATATAAGAGTAGTGAACGTAACTGATGCTTTTACAGACCCCTTGCAACCAAGATTT 711
Qy 922 GAGATGACTCTTCCATTTCCAGCAGTTTGAATCCAGGGTATTTGGAACCTATCAACAATGC 981
Db 712 GAGATGACTCTTCCATTTCCAGCAGTTTGAATCCAGGGTATTTGGAACCTATCAACAATGC 771
Qy 982 CATCAAAGCATCTCGAGCTCTTCAACACAGTTACTGCCCTTACTCCCTCC - AGTGTGCCCT 1040
Db 772 CATCAAAGCATCTCGAGCTCTTCAACACAGTTACTGCCCTTACTCCCTCCAGTGTGCCCT 831
Qy 1041 CAATGGG--ATTTTCTTGGCACCACCTCCAGGGG--ATTTTGGGGCAATTTTCAAGC-TT 1095
Db 832 CAATGGGGATTTCTTGGGCCACCACTCCAGGGGGATTTTGGGGCAATTTTCAAGCTTTT 891
Qy 1096 TACTTTGTGATGAGTATTTTAACTTGACATCAGAG-CAACTCTCAGGAAAGG--T 1151
Db 892 TACTTTGGATGGATTTTAACTTGACATCAGAGCAATCCAGGAAAGTCCCTCAGGAAAGGGTG 951
Qy 1152 GACTGAGATGATG-AAAAAGTTCTGTGCTCAGCTTGGGAGGAGATATAAAACA 1203
Db 952 ACCTGGAATGATGAAAAAGTTCTGTGCTCACCCTTGGGGAGGAGATATAA 1004
```

```
RESULT 14
BF664417 808 bp mRNA linear EST 21-DEC-2000
LOCUS 602146163F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309839 5',
DEFINITION mRNA sequence.
ACCESSION BF664417
VERSION BF664417.1 GI:11938222
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 808)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1183 row: n column: 16
High quality sequence stop: 758.
Location/Qualifiers
1..808
/organism="Homo sapiens"
```

```
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4309839"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/Note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
```

ORIGIN

Query Match	44.9%;	Score 645.2;	DB 2;	Length 808;
Best Local Similarity	98.7%;	Pred. No. 6.6e-179;		
Matches 693;	Conservative 0;	Mismatches 3;	Indels 6;	Gaps 4;

Qy 676 GTACCCCAAAACACAGACTATGAGTCCCAAGATATGCTCTGCAATTTGCGCTCTATGGC 735  
Db 2 GTACCCCAAAACACAGACTATGAGTCCCAAGATATGCTCTGCAATTTGCGCTCTATGGC 61

Qy 736 AAGGACTACAATGTCTACACATAGCTTTCTGTGCTATGGGAAGGATCAGGACCTCTCG 795  
Db 62 AAGGACTACAATGTCTACACATAGCTTTCTGTGCTATGGGAAGGATCAGGACCTCTCG 121

Qy 796 CAGAACTGGCCAAAGCAATTCAGGTTGCAAGTAATGAAATTTCTCAGGACCCATGCTTT 855  
Db 122 CAGAACTGGCCAAAGCAATTCAGGTTGCAAGTAATGAAATTTCTCAGGACCCATGCTTT 181

Qy 856 CATCTGATATAGAAGGTAGTAACTGAGTAACTTCAAGACCCCTGCAACCAAG 915  
Db 182 CATCTGATATAGAAGGTAGTAACTGAGTAACTTCAAGACCCCTGCAACCAAG 241

Qy 916 AGATTGAGATGACTCTTCCATTTCCAGCAGTTTGAATCCAGGGTATTTGGAACCTATCAA 975  
Db 242 AGATTGAGATGACTCTTCCATTTCCAGCAGTTTGAATCCAGGGTATTTGGAACCTATCAA 299

Qy 976 CAATGCCATCAAAGCATCTCGAGCTTTCAACACCAAGTATCTGCCCTTACTCCAGTGT 1035  
Db 300 CAATGCCATCAAAGCATCTCGAGCTTTCAACACCAAGTATCTGCCCTTACTCCAGTGT 359

Qy 1036 GCCTTCAATGGATTTTCTGCCACCCTCCAGGGGATTTTGGGGCAATTTTCACTTTT 1095  
Db 360 GCCTTCAATGGATTTTCTGCCACCCTCCAGGGG--ATTGTTGGGGCAATTTTCACTTTT 417

Qy 1096 TACTTTGTGATGAAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACT 1155  
Db 418 TAC-TTGTGATGAAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACT 476

Qy 1156 GAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGGAGATATAAAACATCTTACCTGGA 1215  
Db 477 GAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGGAGATATAAAACATCTTACCTGGA 536

Qy 1216 GTAAGGAGAGTACCTGAGTGAATATCTGCTTTTCTGTGCTACATCTCTCCCTCTT 1275  
Db 537 GTAAGGAGAGTACCTGAGTGAATATCTGCTTTTCTGTGCTACATCTCTCCCTCTT 596

Qy 1276 CTGCAAGGCTATCATTTTCAACAGCTGATTTCTTGGGAGGACATCCATTTTCAATTTGGCAAGATC 1335  
Db 597 CTGCAAGGCTATCATTTTCAACAGCTGATTTCTTGGGAGGACATCCATTTTCA-TGGCAAGATC 655

Qy 1336 CAGGGCAGCAGCGCGCTGGACTTTTGGGCTTACATGCTGAAC 1377  
Db 656 CAGGGCAGCAGCGCGCTGGACTTTTGGGCTTACATGCTGAAC 697

RESULT 15  
CB553295  
LOCUS

673 bp mRNA linear EST 01-JUN-2003

DEFINITION	MMSP0076 A03 MMSP Macaca mulatta cdNA, mRNA sequence.
ACCESSION	CB553295
VERSION	CB553295.1 GI:31302490
KEYWORDS	EST.
SOURCE	Macaca mulatta (rhesus monkey)
ORGANISM	Macaca mulatta
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
TITLE	Cercopithecinæ; Macaca.
JOURNAL	1 (bases 1 to 673)
COMMENT	Katze,M.G., Bumgarner,R., Korth,M., Feldman,R., Amjadi,M. and Holzman,T.
	Expressed sequence tags from Rhesus macaque spleen
	Unpublished (2002)
	Contact: Holzman T
	Katze Lab
	University of Washington
	Box 358070, Seattle, WA 98195-8070, USA
	Tel: 206 732 6156
	Fax: 206 732 6055
	Email: ted@locke.hs.washington.edu
	Similar to GenBank entry S73813 S73813 CD39=lymphoid cell
	activation antigen [human, B lymphoblastoid cell line, MP-1, mRNA,
	1818 nt]. 4/1995
	Plate: MMSP0076 row: A column: 03.
FEATURES	Location/Qualifiers
source	1..673
	/organism="Macaca mulatta"
	/mol_type="mRNA"
	/db_xref="taxon:9544"
	/sex="male"
	/cell_type="monocytes"
	/dev_stage="adult"
	/clone_lib="MMSP"
	/notes="Organ: spleen"
ORIGIN	
Query Match	43.4%; Score 624.2; DB 6; Length 673;
Best Local Similarity	98.4%; Pred. No. 1e-172; Indels 3; Gaps 3;
Matches 662; Conservative	0; Mismatches 8;
Qy	725 GCCTCTATGGCAAGGACTCAATGTCTACACATAGCTTCTTGTG-CTATGGGAAGGAT 783
Db	1 GCCTCTATGGCAAGGACTCAATGTCTACACATAGCTTCTTGTGCTATGGGAAGGAT 60
Qy	784 CAGGCACTCTGGCAGAAAACCTGGCCAAAGGACATTCAGGTTGCCAAGTAATGAATTTCTCAGG 843
Db	61 CAGGCACTCTGGCAGAAAACCTGGCCAAAGGACATTCAGGTTGCCAAGTAATTCCTCAGG 120
Qy	844 GACCCATGCTTTCATCTGGATATAGAGGTAGTGAACGTAAGTGACCTTTACAAGACC 903
Db	121 GACCCATGCTTTCATCCGGATATAGAGGTAGTGAACGTAAGTGACCTTTACAAGACC 180
Qy	904 CCCTGCACCAAGAGATTGAGATGACTTTCATTCAGCAGTTCAGAGTTTGAATTCAGGGTATT 963
Db	181 CCCTGCACCAAGAGATTGAGATGACTTTCATTCAGCAGTTCAGAGTTTGAATTCAGGGTATT 240
Qy	964 GGAACCTATCAACAAATGCCATCAAAAGCATCCTGGAGCTTTTCAACACCAGTTTACTGCCCT 1023
Db	241 GGAACCTATCAACAAATGCCATCAAAAGCGTCTCTGGAGCTTTCACACACCAGTTTACTGCCCT 300
Qy	1024 TACTCCCGAGTGCCCTCAATGGATTTCCTGCCACCACTCCAGGGGATTTTGGGGCA 1083
Db	301 TACTCCCGAGTGCCCTCAATGGATTTCCTGCCACCACTCCAGGGGATTTTGGGGCA 360
Qy	1084 TTTTCAGCTTTTACTTTGTGATGAAGTTTAAACTTGACATCAGAGAAAGTCTCTCAG 1143
Db	361 TTTTCAGCTTTTACTTTGTGATGAATTTTAAACTTGACATCAGAGAAAGTCTCTCAG 420
Qy	1144 GAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGAGGAGATAAAAAACA 1203
Db	421 GAAAAGGTGACTGAGATGATGAAAAAGTTCTGTCTCAGCCTTGGAGGAGATAAAAAACA 480
Qy	1204 TCTTACGCTGGAGTAAAGGAGAACTACCTGAGTGAATACTGCTTTTCTGGTACCTACATT 1263
Db	481 TCTTACGCTGGAGTAAAGGAGAACTACCTGAGTGAATACTGCTTTTCTGGTACCTACATT 540
Qy	1264 CTCTCCCTCCTTCTGCAAGGCTATCA-TTTCAAGCTGATTCCTGGGAGCACATCCATT 1322
Db	541 CTCTCCCTACTTCTGCAAGGCTATCAATTTTCAAGCTGATTCCTGGGAGCACATCCATT 600
Qy	1323 CATTGGCAAGATCCAGGGCAGCGCCGGCT-GGACTTTGGGCTACATGCTGAACCTGA 1381
Db	601 CATTGGCAAGATCCAGGGCAGCGCCGGCTTTGGGCTACATGCTGAACCTGA 660
Qy	1382 CCAACATGATCCC 1394
Db	661 CCAACATGATCCC 673
Search completed: September 21, 2005, 23:22:06	
Job time : 5136.07 secs	

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2005, 16:29:41 ; Search time 257.45 Seconds  
(without alignments)  
9133.162 Million cell updates/sec

Title: US-09-807-660C-7  
Perfect score: 1437  
Sequence: 1 atggccctgtgtagcacag.....ctctctccactccacctaa 1437

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/prodata/1/ina/5A-COMB.seq: \*  
2: /cgn2\_6/prodata/1/ina/5B-COMB.seq: \*  
3: /cgn2\_6/prodata/1/ina/6A-COMB.seq: \*  
4: /cgn2\_6/prodata/1/ina/6B-COMB.seq: \*  
5: /cgn2\_6/prodata/1/ina/PCTUS-COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1319.2	91.8	1818	3	US-08-930-921-2
2	1319.2	91.8	1818	4	US-09-023-655-1475
3	1319.2	91.8	1818	4	US-09-781-796C-2
4	463.2	32.2	871	4	US-09-949-016-2106
5	291	20.3	2782	4	US-09-949-016-5457
6	291	20.3	2797	3	US-09-240-639-3
7	291	20.3	2797	4	US-09-908-510A-3
8	291	20.3	2797	4	US-09-905-744B-3
9	291	20.3	2797	4	US-10-107-660-3
10	291	20.3	2797	4	US-10-107-576-3
11	291	20.3	2797	4	US-09-905-732B-3
12	291	20.3	2797	4	US-09-923-304-3
13	291	20.3	2797	4	US-09-949-016-178
14	291	20.3	2797	4	US-09-905-743B-3
15	270.2	18.8	46885	4	US-09-949-016-13848
16	245.8	17.1	601	4	US-09-949-016-71601
17	220.8	15.4	1500	4	US-09-949-016-5688
18	167.8	11.7	364	4	US-09-513-999C-196
19	167	11.6	601	4	US-09-949-016-71600
20	140.4	9.8	601	4	US-09-949-016-71607
21	139	9.7	742	2	US-08-966-316-2
22	108	7.5	4928	1	US-08-345-913-1
23	108	7.5	4928	3	US-08-818-562-1
24	108	7.5	4928	3	US-09-628-445-1
25	108	7.5	5552	3	US-08-155-888-1
26	108	7.5	5585	2	US-08-303-221-1
27	108	7.5	5585	4	US-09-000-003A-1

28	107	7.4	6365	1	US-08-352-990-1	Sequence 1, Appli
29	96	6.7	601	4	US-09-949-016-71597	Sequence 71597, A
30	92.8	6.5	462	2	US-08-184-009-159	Sequence 159, App
31	92.8	6.5	462	2	US-08-458-356-159	Sequence 159, App
32	92.8	6.5	462	3	US-09-012-366-1	Sequence 1, Appli
33	92.8	6.5	462	3	US-08-460-736-159	Sequence 159, App
34	92.8	6.5	462	4	US-09-533-370-159	Sequence 159, App
35	92.8	6.5	462	4	US-09-663-667-159	Sequence 159, App
36	92.8	6.5	465	4	US-09-605-577-2	Sequence 2, Appli
37	92.8	6.5	604	6	5210029-2	Patent No. 5210029
38	92.8	6.5	604	6	5464939-1	Patent No. 5464939
39	92.8	6.5	604	6	5210029-2	Patent No. 5210029
40	92.8	6.5	604	6	5464939-1	Patent No. 5464939
41	92.8	6.5	801	4	US-09-023-655-1307	Sequence 1307, Ap
42	92.8	6.5	1540	1	US-07-932-915-1	Sequence 1, Appli
43	92.8	6.5	1540	5	PCT-US91-05026-1	Sequence 1, Appli
44	91.2	6.3	801	6	5314995-8	Patent No. 5314995
45	91.2	6.3	801	6	5314995-8	Patent No. 5314995

ALIGNMENTS

RESULT 1

US-08-930-921-2  
; Sequence 2, Application US/08930921B  
; Patent No. 6287837  
; GENERAL INFORMATION:  
; APPLICANT: BEAUDOIN, Adrien R.  
; APPLICANT: SEVIGNY, Jean  
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION  
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT  
; TITLE OF INVENTION: TECHNOLOGY  
; FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN  
; CURRENT APPLICATION NUMBER: US/08/930,921B  
; CURRENT FILING DATE: 1998-01-02  
; EARLIER APPLICATION NUMBER: PCT/CA96/00223  
; EARLIER FILING DATE: 1996-04-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1818  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: unknown  
US-08-930-921-2

Query Match		91.8%	Score 1319.2;	DB 3;	Length 1818;
Best Local Similarity		99.8%	Pred. No. 0;		
Matches 1321;		Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	113	GTTCACCCGAAACAAAGCATTGCCAGAAACGTTAAGTATGGATTCGCTGGATCGG	172		
Db	174	GGTTGACCCGAAACAAAGCATTGCCAGAAACGTTAAGTATGGATTCGCTGGATCGG	233		
Qy	173	GTTCCTCTCACACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAGAGAGATGACACAG	232		
Db	234	GTTCCTCTCACACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAGAGAGATGACACAG	293		
Qy	233	CGGTGGTGCAATCAAGTAGAAGAATGCAAGGGTTAAAGGTCCTGGAAATCTCAAAATTTGTC	292		
Db	294	CGGTGGTGCAATCAAGTAGAAGAATGCAAGGGTTAAAGGTCCTGGAAATCTCAAAATTTGTC	353		
Qy	293	AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTCGATGCAAGAGCTAGGGAAGTGA	352		
Db	354	AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTCGATGCAAGAGCTAGGGAAGTGA	413		
Qy	353	TTCCAAGGTCACGACCAACAGAGACACCCGTTTACCTGGGAGCCACGCGCATGCGGT	412		
Db	414	TTCCAAGGTCACGACCAACAGAGACACCCGTTTACCTGGGAGCCACGCGCATGCGGT	473		
Qy	413	TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGTTGGAGAGAGCC	472		

474 TGCTCAGGATGGAAGTGAAGAGTGGCAGACAGGGTTCGGATGTGGTGAGAGGAGCC 533  
 473 TCAGCAACTACCCCTTTGACTTCAGAGGTGCCAGGATCAATCTGCGCAAGAGAAAGGTG 532  
 534 TCAGCAACTACCCCTTTGACTTCAGAGGTGCCAGGATCAATCTGCGCAAGAGAAAGGTG 593  
 533 CCTATGGCTGGATTAATCACTATCTGCTGGCAAAATTCAGTCAGAAACAAGGTGTT 592  
 594 CCTATGGCTGGATTAATCACTATCTGCTGGCAAAATTCAGTCAGAAACAAGGTGTT 653  
 593 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG 652  
 654 TCAGCATAGTCCCATATGAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG 713  
 653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 712  
 714 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 773  
 713 CTCTGCNAATTCGCTCTATGGCAAGGACTACAAATGCTACACATAGCTTCTGTGCT 772  
 774 CTCTGCNAATTCGCTCTATGGCAAGGACTACAAATGCTACACATAGCTTCTGTGCT 833  
 773 ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 832  
 834 ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 893  
 833 AAATTTCTCAGGGACCCCATGCTTTTCACTCTGGATATAAGAAAGGTAGTGAAGTGACC 892  
 894 AAATTTCTCAGGGACCCCATGCTTTTCACTCTGGATATAAGAAAGGTAGTGAAGTGACC 953  
 893 TTTTACAAGACCCCTGACCAAGAGATTTGAGATGACTCTTCATTTCCAGCAGTTTGAA 952  
 954 TTTTACAAGACCCCTGACCAAGAGATTTGAGATGACTCTTCATTTCCAGCAGTTTGAA 1013  
 953 TCAGGGTATTTGGAACCTATCAACAATGCCATCAAGAGCTCTGGAGCTTCAACACCA 1012  
 1014 TCAGGGTATTTGGAACCTATCAACAATGCCATCAAGAGCTCTGGAGCTTCAACACCA 1073  
 1013 GTTACTGCCCTTACTCCAGTGTCCCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGG 1072  
 1074 GTTACTGCCCTTACTCCAGTGTCCCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGG 1133  
 1073 ATTTTGGGCAATTTTCACTTTTACTTTGATGAGTTTAACTTTGACATCAGAGA 1132  
 1134 ATTTTGGGCAATTTTCACTTTTACTTTGATGAGTTTAACTTTGACATCAGAGA 1193  
 1133 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAGTTTCTGTCTCAGCCTTTGGGAG 1192  
 1194 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAGTTTCTGTCTCAGCCTTTGGGAG 1253  
 1193 AGATAAAAAATCTTACGCTGGAGTAAAGAGAAAGTACCTGAGTGAATACTGCTTTCTG 1252  
 1254 AGATAAAAAATCTTACGCTGGAGTAAAGAGAAAGTACCTGAGTGAATACTGCTTTCTG 1313  
 1253 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGGAGC 1312  
 1314 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCAAGCTGATTTCTGGGAGC 1373  
 1313 ACATCCATTTTCTTGGCAAGATCCAGGCGAGCGCGGCTGGACTTTGGGCTACATGC 1372  
 1374 ACATCCATTTTCTTGGCAAGATCCAGGCGAGCGCGGCTGGACTTTGGGCTACATGC 1433  
 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1432  
 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1493  
 1433 CCTA 1436  
 1494 CCTA 1497

US-09-023-655-1475  
 ; Sequence 1475, Application US/09023655  
 ; Patent No. 6607879  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cocks, Benjamin G.  
 ; APPLICANT: Susan G. Stuart  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
 ; TITLE OF INVENTION: EXPRESSION  
 ; NUMBER OF SEQUENCES: 1508  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/023,655  
 ; FILING DATE: HEREWITH  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0001 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 1475:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1818 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GENBANK  
 ; CLONE: 9765255  
 ; US-09-023-655-1475

Query Match 91.8%; Score 1319.2; DB 4; Length 1818;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 113 GTTCAACCCAGAACAAAGCAATTCGCCAGAAAAAGTTAAGTATGGGATTTGCTGGATCGG 172  
 DB 174 GGTGACCCAGAACAAAGCAATTCGCCAGAAAAAGTTAAGTATGGGATTTGCTGGATCGG 233  
 QY 173 GTTCTTCTCACACAAAGTTTATACATCTATAAGTGGCCAGACAGAAAGGAGAAATGACACAG 232  
 DB 234 GTTCTTCTCACACAAAGTTTATACATCTATAAGTGGCCAGACAGAAAGGAGAAATGACACAG 293  
 QY 233 GCGTGGTGCATCAAGTAGAAGAAATGCAGGGTTAAAGGTCCTCGAATCTCAAAAATTTGTTTC 292  
 DB 294 GCGTGGTGCATCAAGTAGAAGAAATGCAGGGTTAAAGGTCCTCGAATCTCAAAAATTTGTTTC 353  
 QY 293 AGAAAGTAAATGAAATAGGCATTTTACCTGACATGATTTGATGAAAGAGCTAGGGAAAGTGA 352  
 DB 354 AGAAAGTAAATGAAATAGGCATTTTACCTGACATGATTTGATGAAAGAGCTAGGGAAAGTGA 413  
 QY 353 TTTCAGAGTCCCGACACCAAGAGACACCCGTTTACCTGGAGCCACCGGAGGATCGCTCGGT 412  
 DB 414 TTCCAGAGTCCCGACACCAAGAGACACCCGTTTACCTGGAGCCACCGGAGGATCGCTCGGT 473  
 QY 413 TGCTCAGGATGGAAGTGAAGAGTTTGGCAGACAGGGTTCTGGATGTGTGGAGAGAGCC 472

Db 474 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTCTGGATGTGGTGGAGAGAGCC 533  
Qy  
Db 473 TCAGCAACTACCCCTTTGACTTCACGGGTGCCAGGATCATTTACTTGCCCAAGAGAGGTG 532  
Db 534 TCAGCAACTACCCCTTTGACTTCACGGGTGCCAGGATCATTTACTTGCCCAAGAGAGGTG 593  
Qy 533 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTTCAGAAACAAGGTGT 592  
Db 594 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTTCAGAAACAAGGTGT 653  
Qy 593 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 652  
Db 654 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 713  
Qy 653 GAGCCTCTACACAAGTCACTTTTGTTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 712  
Db 714 GAGCCTCTACACAAGTCACTTTTGTTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 773  
Qy 713 CTCTGCAATTTGGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTGTGT 772  
Db 774 CTCTGCAATTTGGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTGTGT 833  
Qy 773 ATGGGAAGGATCAGGCACCTCTGGCAGAACTGGCCCAAGGACATTCAGGTTCGAAGTAATG 832  
Db 834 ATGGGAAGGATCAGGCACCTCTGGCAGAACTGGCCCAAGGACATTCAGGTTCGAAGTAATG 893  
Qy 833 AAATTTCTCAGGACCCCATGCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAAGTACC 892  
Db 894 AAATTTCTCAGGACCCCATGCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAAGTACC 953  
Qy 893 TTTTACAAGACCCCTGCAACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGA 952  
Db 954 TTTTACAAGACCCCTGCAACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGA 1013  
Qy 953 TCCAGGATTTGGAAACTATCAACATGCCATCAAGCATCTCTGAGCTTTCAACACCA 1012  
Db 1014 TCCAGGATTTGGAAACTATCAACATGCCATCAAGCATCTCTGAGCTTTCAACACCA 1073  
Qy 1013 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTCTTGCCACCCTCCAGGGGG 1072  
Db 1074 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTCTTGCCACCCTCCAGGGGG 1133  
Qy 1073 ATTTTGGGGCAATTTTTCAGCTTTTACTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1132  
Db 1134 ATTTTGGGGCAATTTTTCAGCTTTTACTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1193  
Qy 1133 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCTTGGGAGG 1192  
Db 1194 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCTTGGGAGG 1253  
Qy 1193 AGATAAAAACATTTTACGCTGGAGTAAAGGAGAAGTACTGAGTGAATCTGCTTTTCTG 1252  
Db 1254 AGATAAAAACATTTTACGCTGGAGTAAAGGAGAAGTACTGAGTGAATCTGCTTTTCTG 1313  
Qy 1253 GTACCTACATTTCTCCCTCTCTTCTGCAAGGCTATCATTTTACAGCTGATTCCTGGAGC 1312  
Db 1314 GTACCTACATTTCTCCCTCTCTTCTGCAAGGCTATCATTTTACAGCTGATTCCTGGAGC 1373  
Qy 1313 ACATCCATTTTCAATGGCAAGATCCAGGAGGAGGAGCCCGGTGGACTTTGGGCTACATGC 1372  
Db 1374 ACATCCATTTTCAATGGCAAGATCCAGGAGGAGGAGCCCGGTGGACTTTGGGCTACATGC 1433  
Qy 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATGTCACACCTCTCTCCCACTCCA 1432  
Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATGTCACACCTCTCTCCCACTCCA 1493  
Qy 1433 CCTA 1436  
Db 1494 CCTA 1497

US-09-781-796C-2  
; Sequence 2, Application US/09781796C  
; Patent No. 6800284  
; GENERAL INFORMATION:  
; APPLICANT: BEAUDOIN, Adrien R.  
; APPLICANT: SEVIGNY, Jean  
; APPLICANT: BACH, Fritz H.  
; APPLICANT: ROBSON, Simon  
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS OF PURIFICATION  
; THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT  
; TITLE OF INVENTION: TECHNOLOGY  
; FILE REFERENCE: 920333.90019  
; CURRENT APPLICATION NUMBER: US/09/781,796C  
; PRIOR FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 08/419,204  
; PRIOR FILING DATE: 1995-04-10  
; PRIOR APPLICATION NUMBER: CA96/00223  
; PRIOR FILING DATE: 1996-04-10  
; PRIOR APPLICATION NUMBER: 08/930,921  
; PRIOR FILING DATE: 1998-02-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1818  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-781-796C-2

Query Match 91.8%; Score 1319.2; DB 4; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 113 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTTAAGTATGGGATTTGCTGGATGCCG 172  
Db 174 GGTTCACCCAGAACAAAGCATTTGCCAGAAAACGTTTAAGTATGGGATTTGCTGGATGCCG 233  
Qy 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGAGAAATGACACAG 232  
Db 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGAGAAATGACACAG 293  
Qy 233 GCGTGGTGCATCAGTAGAAGTATGCAAGGTTAAAGGTCCTGGATCTCAAAATTTGTTTC 292  
Db 294 GCGTGGTGCATCAGTAGAAGTATGCAAGGTTAAAGGTCCTGGATCTCAAAATTTGTTTC 353  
Qy 293 AGAAAGTAAATGAAATAGGCAATTTACCTGACTGATTGATGCAAGAAAGAGCTAGGGAAGTGA 352  
Db 354 AGAAAGTAAATGAAATAGGCAATTTACCTGACTGATTGATGCAAGAAAGAGCTAGGGAAGTGA 413  
Qy 353 TTCCAAGGTCCCGACCAACAGAGACACCCGTTTACCTGGGAGCCACGGCAGCATGCCGT 412  
Db 414 TTCCAAGGTCCCGACCAACAGAGACACCCGTTTACCTGGGAGCCACGGCAGCATGCCGT 473  
Qy 413 TGCTCAGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCC 472  
Db 474 TGCTCAGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCC 533  
Qy 473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGCGCAAGAGGAAGGTG 532  
Db 534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTTACTGCGCAAGAGGAAGGTG 593  
Qy 533 CCTATGGCTGGATTACTATCAACTATCTGTGGGCAAAATTCAGTTCAGAAAAACAAGGTGT 592  
Db 594 CCTATGGCTGGATTACTATCAACTATCTGTGGGCAAAATTCAGTTCAGAAAAACAAGGTGT 653  
Qy 593 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 652  
Db 654 TCAGCATAGTCCCATATGAACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 713  
Qy 653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 712  
Db 714 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 773  
Qy 713 CTCTGCAATTTTGGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTTCTGTGT 772

```
Db 774 CTCTGCAATTTTCGCTCTATGGCAAGGACTACAAATGCTTACACACATAGCTTCTTGCT 833
Qy 773 ATGGGAAGGATCAGGCACTCTGCGAAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 832
Db 834 ATGGGAAGGATCAGGCACTCTGCGAAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 893
Qy 833 AAATTTCTCAGGGACCCATGCTTTCATCTCGGATATAAGAGGTAAGTAAGTAAAGTACC 892
Db 894 AAATTTCTCAGGGACCCATGCTTTCATCTCGGATATAAGAGGTAAGTAAGTAAAGTACC 953
Qy 893 TTTTACAAGACCCCTTCACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 952
Db 954 TTTTACAAGACCCCTTCACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 1013
Qy 953 TCAGGGTATGTGAAACTATCAACAATGCATCAAAAGCATCTCGAGACTCTTCAACACCA 1012
Db 1014 TCCAGGGTATGTGAAACTATCAACAATGCATCAAAAGCATCTCGAGACTCTTCAACACCA 1073
Qy 1013 GTTACTGCCCTTACTCCAGTGCTTCAATGGGATTTTCTTGCCACCACTCCAGGGG 1072
Db 1074 GTTACTGCCCTTACTCCAGTGCTTCAATGGGATTTTCTTGCCACCACTCCAGGGG 1133
Qy 1073 ATTTTGGGGCATTTTCAGCTTTTACTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1132
Db 1134 ATTTTGGGGCATTTTCAGCTTTTACTTTGTGATGAAGTTTAAACTTTGACATCAGAGA 1193
Qy 1133 AAGTCTCTCAGGAAAGGAGTCTGAGATGATGAAAAAGTTCTGTCTCAGCCTTGGGAGG 1192
Db 1194 AAGTCTCTCAGGAAAGGAGTCTGAGATGATGAAAAAGTTCTGTCTCAGCCTTGGGAGG 1253
Qy 1193 AGATAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATCTGCTTTCTG 1252
Db 1254 AGATAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATCTGCTTTCTG 1313
Qy 1253 GTACCTACATTTCTCCTCTCTCAAGGCTATCATTTTCAAGCTGATTTCTTGGGAGC 1312
Db 1314 GTACCTACATTTCTCCTCTCTCAAGGCTATCATTTTCAAGCTGATTTCTTGGGAGC 1373
Qy 1313 ACATCAATTTTCAATGGCAAGATCCAGGCGACGACGCGGCTGGACTTTGGGGTACATGC 1372
Db 1374 ACATCAATTTTCAATGGCAAGATCCAGGCGACGACGCGGCTGGACTTTGGGGTACATGC 1433
Qy 1373 TGAACCTGACCAATGATCCAGCTGAGCAACCACTTGCCACACTCTCTCCACTCCA 1432
Db 1434 TGAACCTGACCAATGATCCAGCTGAGCAACCACTTGCCACACTCTCTCCACTCCA 1493
Qy 1433 CCTA 1436
Db 1494 CCTA 1497

RESULT 4
US-09-949-016-2106
; Sequence 2106, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2106
; LENGTH: 871

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2106
Query Match 32.2%; Score 463.2; DB 4; Length 871;
Best Local Similarity 99.4%; Pred. No. 6.7e-144;
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 113 GTTCAACCCAGAACCAAGCATTGCCAGAAAAGCTTAAGTATATGGATTGCTGGATGCCG 172
Db 198 GGTTCACCCAGAACCAAGCATTGCCAGAAAAGCTTAAGTATATGGATTGCTGGATGCCG 257
Qy 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAAATGACACAG 232
Db 258 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAAATGACACAG 317
Qy 233 GCGTGGTGATCAAGTGTAGAAATCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 292
Db 318 GCGTGGTGATCAAGTGTAGAAATCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 377
Qy 293 AGAAAGTAATCAAAATAGGCATTTACCTGACTGATTTGCATGCAAAAGAGCTAGGAGTGA 352
Db 378 AGAAAGTAATCAAAATAGGCATTTACCTGACTGATTTGCATGCAAAAGAGCTAGGAGTGA 437
Qy 353 TTCCAAGGTCCAGACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGT 412
Db 438 TTCCAAGGTCCAGACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGT 497
Qy 413 TGCTCAGGATGAAAAGTGAAGATTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCC 472
Db 498 TGCTCAGGATGAAAAGTGAAGATTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCC 557
Qy 473 TCAGCAACTACCCCTTGTGACTTCCAGGGTGCCAGGATCATTAATGCGCAAGAGGAGGTG 532
Db 558 TCAGCAACTACCCCTTGTGACTTCCAGGGTGCCAGGATCATTAATGCGCAAGAGGAGGTG 617
Qy 533 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGA 580
Db 618 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGA 665

RESULT 5
US-09-949-016-5457
; Sequence 5457, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5457
; LENGTH: 2782

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5457
Query Match 20.3%; Score 291; DB 4; Length 2782;
Best Local Similarity 54.3%; Pred. No. 7e-86;
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

Qy 120 CCAGAACAAAGCATTGCCAGAAAAAGCTTAAGTATGGGATTTGCTGGATGCCGGTTCTTC 179
Db 219 CAAGCAAGAGGTCTCCCTCCAGGAGTGAAGTATGTTGCTGGATGCCGGTCTTC 278
```

```
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2106
Query Match 32.2%; Score 463.2; DB 4; Length 871;
Best Local Similarity 99.4%; Pred. No. 6.7e-144;
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 113 GTTCAACCCAGAACCAAGCATTGCCAGAAAAGCTTAAGTATATGGATTGCTGGATGCCG 172
Db 198 GGTTCACCCAGAACCAAGCATTGCCAGAAAAGCTTAAGTATATGGATTGCTGGATGCCG 257
Qy 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAAATGACACAG 232
Db 258 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGGAGAAATGACACAG 317
Qy 233 GCGTGGTGATCAAGTGTAGAAATCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 292
Db 318 GCGTGGTGATCAAGTGTAGAAATCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 377
Qy 293 AGAAAGTAATCAAAATAGGCATTTACCTGACTGATTTGCATGCAAAAGAGCTAGGAGTGA 352
Db 378 AGAAAGTAATCAAAATAGGCATTTACCTGACTGATTTGCATGCAAAAGAGCTAGGAGTGA 437
Qy 353 TTCCAAGGTCCAGACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGT 412
Db 438 TTCCAAGGTCCAGACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGT 497
Qy 413 TGCTCAGGATGAAAAGTGAAGATTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCC 472
Db 498 TGCTCAGGATGAAAAGTGAAGATTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCC 557
Qy 473 TCAGCAACTACCCCTTGTGACTTCCAGGGTGCCAGGATCATTAATGCGCAAGAGGAGGTG 532
Db 558 TCAGCAACTACCCCTTGTGACTTCCAGGGTGCCAGGATCATTAATGCGCAAGAGGAGGTG 617
Qy 533 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGA 580
Db 618 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGA 665

RESULT 5
US-09-949-016-5457
; Sequence 5457, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5457
; LENGTH: 2782

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5457
Query Match 20.3%; Score 291; DB 4; Length 2782;
Best Local Similarity 54.3%; Pred. No. 7e-86;
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

Qy 120 CCAGAACAAAGCATTGCCAGAAAAAGCTTAAGTATGGGATTTGCTGGATGCCGGTTCTTC 179
Db 219 CAAGCAAGAGGTCTCCCTCCAGGAGTGAAGTATGTTGCTGGATGCCGGTCTTC 278
```

QY	180	TCACACAAAGTTTATACATCTATTAAGTGGCCAGCACAAAAGAGAAATGACACAGGCGTGGT	239
DB	279	AAGAACCAACAGTCTACGTGTATCAATGGCCAGCACAAAAGAGAAATATACCGGAGTGGT	338
QY	240	GCATCAAGTAGAAGAAATGCAGGGTTAAAGGTCCTCGAATCTCAAAATTTGTTTCAGAAAAGT	299
DB	339	CAGTCAAACCTTCAAAATGTAGTGTGAAGGCTCTGGAAATCTCCAGCTATGGAATAACCC	398
QY	300	AAATGAAATAGGCATTTTACCTGACTGTATGTCATGAAAGAGCTAGGGAAGTGATTTCCAAAG	359
DB	399	CCAAGATGTCCCCAGAGCCTTTGAGGAGTGTATGCAAAAAGTCTAAGGGCAGGTTCCATC	458
QY	360	GTCCCAGCACCAAGAGACACCGTTTACCTGGAGCCAGGCAGGCATGCGGTTGCTCAG	419
DB	459	CCACCTCCACGGATCCACCCCATTCACCTGGAGCCACGGCTGGGATGCGCTTGCTCGAG	518
QY	420	GATGAAAAGTGAAGAGTTGGCGACACAGGGTCTCGATGTGTGGAGAGAGCCTCAGCAA	479
DB	519	GTTCGAAAATGAACACAGCAGCTATGAAGTCTCTTGAAGCATCCAAAGCTACTTCAAGTC	578
QY	480	CTACCCCTTTGACTTTCAGGFTGCCAGGATCATTTACTGGCCAAAGAGGAAGTGCTATGG	539
DB	579	CCAGCCCTTTCGACTTTAGGGTGTCTCAAAATCATTTCTGGGCAAGAAGGGGTATATGG	638
QY	540	CTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAACAGGTTGGTTCAGCAT	599
DB	639	ATGGATTACAGCAACTATTTAAATGGGAAATTTCTTGAGAGAAGAACCTGTGGCCACATGTG	698
QY	600	AGTCCCATATGAACCAATAATCAGAAAACTTTTGGAGCTTTTGGACCTTTGGGGAGCCTC	659
DB	699	GGTGC-----ACCGCATGGAGTGAACAACACGGTGCCCTGACCTTAGTGTGTGCTC	752
QY	660	TACACAAGTCACTTTTGTGACCCCAAAACACAGACTATCGAGTCCCCAGATAATGTCTGTCA	719
DB	753	CACCCAAATATCTTCGTGGCAGGAGAGAAGATGGATCTGAAACACCCAGCGACATCATGCA	812
QY	720	ATTTGCGCTCTATGCAAGGACTACAAATGCTCTACACATAGCTCTTGTGCTATGGAA	779
DB	813	GGTGTCCCTGTATGGCTACGTATACACGCTCTACACACACAGCTTCCAGTGTCTATGGCGG	872
QY	780	GGATCAGGCACTCTGGCAGAAAACGGCCAAAGACATTCAGGTGTGCAAGTAATGAAA--T	836
DB	873	GAATGAGGCTGAGAAGAAGTTTTCGGCAATGCTCTCTGCAAAATTCCTCTACCAAAAACCA	932
QY	837	TCTCAGGGAACCATGCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAGTGAACCTTTA	896
DB	933	TCTCAACAACTCCCTGTTTACCCTCGGATATAGCATCAGCTTCACCATGGGCCATGTATT	992
QY	897	CAAGNACCCCTGCAC-----CAAGAGATTTGAGATGACTCTTCCATTCAGACAGTTTGA	950
DB	993	TGATAGCCTGTGCACTGTGGACCCAGAGGCCAGAAAGTTATAACCCCAATGATGTCATCAC	1052
QY	951	AATCCAGGGTATGGAAACTATCAACAATGCCATCAAAAGCATCCTGGAGCTCTTCAACAC	1010
DB	1053	TTTTGAAGGAATCGGGNACCATCTCTGTGTGAAGGAGAGGTGGCTTCCATATTTGACTT	1112
QY	1011	CAGTTACTGCCCTTACTCCCAAG----TGGCCTTCAATGGGAATTTCTTGTGCCACCACTCCA	1067
DB	1113	CAAAAGCTTGCCATGATCAAGAAAACCTGTCTCTTTTGTGGGGTTTATCAGCCAAAAGATTAA	1172
QY	1068	GGGGGATTTTGGGCATTTTCAGCTTTTATCTTTGTGATGAAGTTTTTTAACTTGACATC	1127
DB	1173	AGGGCCATTTGTGGCTTTTGAGGATTTCTACTACACAGCCAGTGTCTTTAAATCT-.-TTC	1229
QY	1128	AGAGAAGTCTCTCAGGAAAAAGGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCGCTTG	1187
DB	1230	AGGTAGCTTTTCCCTGGACACTTCAACTCCAGCACCTGGAAATTTCTGCTCACAGAAATG	1289
QY	1188	GGAGGAGATAAAAACATCTTACGTGGAGTAAAGAGAAAGTACCTGAGTGAATACTGCTT	1247
DB	1290	GAGTCAGCTCCCACTGTGCTGCCCAAAATTTGATGAGTATATGCCCGCTCTTACTGCTT	1349

Qy	1248	TTCTGGTACCTACAGATTCTCTCCCTCCTTCTGCAAGGCTATCATTTACAGCTGATTCCTG	130
Db	1350	CTCAGCCAACCTACATCTACCACATTGTTTGTGAACGGTTACAAAATTACAGAGGAGACTTG	1409
Qy	1308	GGAGCACATCCATTTCATTGGCAAGATCCAGGGCAGCGAGCCGGCTGGACATTTTGGGCTA	1367
Db	1410	GCCCAAAATACACTTTGAAAAGAGTGGGAATAGCAGATAGCTGTGCTCTTGGCTA	1469
Qy	1368	CATGCTGAACCTGACCAACATGATCCAGCTGAGCAACCAATTG	1410
Db	1470	CATGCTCAGCTGACCAACAGATCCAGCTGAAAGGCCCTCTG	1512
RESULT 6			
US-09-240-639-3			
; Sequence 3, Application US/09240639			
; Patent No. 6350447			
; GENERAL INFORMATION:			
; APPLICANT: Chadwick, Brian Paul			
; APPLICANT: Frischauf, Anna-Maria			
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE			
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS			
; FILE REFERENCE: 9598-066			
; CURRENT APPLICATION NUMBER: US/09/240,639			
; CURRENT FILING DATE: 1998-01-29			
; NUMBER OF SEQ ID NOS: 29			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 3			
; LENGTH: 2797			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (83)..(1669)			
US-09-240-639-3			
Query Match 20.3%; Score 291; DB 3; Length 2797;			
Best Local Similarity 54.3%; Pred. No. 7e-86;			
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;			
Qy	120	CCAGAACAAAGCATTCGCAGAAAACGTTAAGTATGGATTGTGCTGGATGCGGGTCTTC	179
Db	220	CAAGCAAGAGGTCTCTCCTCCAGACTGAAGTATGTTGTGCTGGATGCCGGTCTTC	279
Qy	180	TCACAAAGTTTATACATCTATTAAGTGGCCAGCAGAAAAGGAGAATGACACAGCGCTGT	239
Db	280	AAGAACCAAGTCTACGTGTATCAATGGCCAGCAGAAAAGAGAAATAATACCGAGTGGT	339
Qy	240	GCATCAAGTAGAAGATGCAAGGTTAAAGTCTCGAAATCTCAAAATTTGTTCAGAAAGT	299
Db	340	CAGTCAAAACCTTCAAATGTAGTGTGAAGGCTCTGGAATCTCCAGCTATGGAATAACCC	399
Qy	300	AAATGAATAGGCATTTACTGACTGATTCATGGAAGAGCTAGGGAAGTGAATCCAAG	359
Db	400	CCAAGATGTCCCAGAGCCTTTGAGGAGTGATGCAAAAAGTCAAGGGCAGGTTCCATC	459
Qy	360	GTCCAGACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGATGCGGTGCTCAG	419
Db	460	CCACTCCACGGATCCACCCCATTCACCTGGAGGCCAGGCTGGGATGCGCTTGCTGAG	519
Qy	420	GATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGGAGCGCTCAGCA	479
Db	520	GTTGCAAAATGAACAGCAGCTAATCAAGTCTTTGAAAGCATCCAAGCTACTTCAAGTC	579
Qy	480	CTACCCCTTTGACTTCAGGGTGCAGGATCATTTACTGGCCAAGAGAGGTGCCTATGG	539
Db	580	CCAGCCCTTTGACTTTAGGGGTGCTCAAAATCATTTTCTGGGCAAGAAAGAGGGGTATATG	639
Qy	540	CTGGAATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAAGAAAACAAGGTGGTTCA	599
Db	640	ATGGAATTACGCCCACTATTTAATGGGAATTTCTCGGAGAGAGACCTGTGGCACATGTG	699
Qy	600	AGTCCCATATGAACCAATAATCAGGAAAACCTTTTGGAGCTTTTGGACCTTTGGGGGAGCCTC	659

```
Db 700 GGTGC-----ACCCGATGGAGTGGAAACCAAGGTCCTGGACTTAGTGGTGCCTC 753
Qy 660 TACACAAGTCACATTTGTATCCCAACACAGACTATCGAGTCCCAAGATAATGCTCTGCA 719
Db 754 CACCCAAATCTCTGTGGCAGGAGAGATGGATCTGAAACACAGCGACATCATGCA 813
Qy 720 ATTTCGGCTCTATGGCAGAGACTACAAATGTCACACATAGCTTCTTTGTGCTATGGAA 779
Db 814 GGTGTCCCTGTATGGCTATACACGCTCTACACACAGCTTCCAGTGTCTATGGCG 873
Qy 780 GGATCAGGCACTCGGCCAGAACTGGCCAGAGCAATTCAGGTTCGAAATGAATGAAA--T 836
Db 874 GAATGAGGCTGAGAGAAATTTCTGGCAATGCTCTCGCAATTCCTTACCAAAACCA 933
Qy 837 TCTCAGGACCCATGCTTTTCATCTCGATATAAGAAAGGTAGTGAACGTAAGTGACCTTTA 896
Db 934 TCTCACCACCTCTGTACCTCGGATATAGCATCAGCTTCACCATGGGCCATGTATT 993
Qy 897 CAAGACCCCTGCAC-----CAAGAGATTTGAGATGACTCTTCCATTCAGCAGTTTGA 950
Db 994 TGATAGCTGTGACCTGTGGACAGAGGCCAGAAAGTTATAACCCCAATGATGTCATCAC 1053
Qy 951 AATCCAGGGTATTGGAAACTATCAACAAATGCCATCAAGCATCTCGAGCTCTTCAACAC 1010
Db 1054 TTTTGAAGAACTGGGACCCATCTCTGTGTAGGAGAGGTGGCTTCATATTGACTT 1113
Qy 1011 CAGTTACTGCCCTTACTTCCAG---TGTGCTTTCAATGGGATTTCTTGCACCACTCCA 1067
Db 1114 CAAAGCTTGGCATGATCAAGAAACCTGTTCTTTTGTATGGGTTTATCAGCCAAAGATTAA 1173
Qy 1068 GGGGGATTGGGGCATTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTGCATC 1127
Db 1174 AGGGCCATTTTGTGGCTTTTTCAGGATTTCTACTACACAGCCAGTGTCTTAAATCT---TTC 1230
Qy 1128 AGAGAAAGTCTCTCAGAAAGGTGACTGAGATGATGAAAGTCTGTGCTCAGCCTTG 1187
Db 1231 AGGTAGCTTTTCCCTGGACACTTCACTCAGACCTGGAATTTCTGCTCAGAAATTG 1290
Qy 1188 GSAGGAGATAAAACATCTTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATCTGCTT 1247
Db 1291 GAGTCAGCTCCCACTGCTGCTCCCAAAATTTGTAGAGTATATGCGCGCTTACTGCTT 1350
Qy 1248 TTTCTGTTACTACATTTCTCCCTCTCTCTGCAAGGCTATCATTTTCAGCTGATTTCTTG 1307
Db 1351 CTCAGCCAACTACATCTACCACTTGTGTGAAACGGTTACAAATTCACAGAGGAGACTTG 1410
Qy 1308 GGAGCACATCCATTTCAATGGCAAGATCCAGGCGAGCGCGCTGGAATTTTGGGCTA 1367
Db 1411 GCCCCAAATACATTTTGAAAGAAAGTGGGGAATAGCAGATAGCTGTCTCTTGGCTA 1470
Qy 1368 CATGCTGAACCTGACCAACATGATCCCGCTGAGCAACCATTTG 1410
Db 1471 CATGCTCAGCTGACCAACAGATCCCGCTGAAAGCCCTCTG 1513
```

RESULT 7

```
US-09-908-510A-3
; Sequence 3, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischaut, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/361205
; CURRENT APPLICATION NUMBER: US/09/908,510A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
```

```
; LENGTH: 2797
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (83)..(1669)
; OTHER INFORMATION:
US-09-908-510A-3
```

```
Query Match 20.3%; Score 291; DB 4; Length 2797;
Best Local Similarity 54.3%; Pred. No. 7e-86;
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;
```

```
Qy 120 CCAGACAAAGCATTTGCCAGAAACGTTTAAGTATGGATTGCTGGATGCGGTTCTTC 179
Db 220 CAAAGCAAGAGTCTCCCTCCAGGACTGAAGTATGTTGCTGGATGCCGGTCTTC 279
Qy 180 TCACACAAAGTTTATACATCTATAAGTGGCCAGACAGAAAAGAGAAATGACACAGGCGTGT 239
Db 280 AAGAACCACAGTCTACGTGTATCAATGGCCAGCAGAAAAGAGAAATATACCGAGTGT 339
Qy 240 GCATCAAGTAGAAGAAATGACGGGTAAAGGTCCTGGAATCTCAAAATTTTGTTCAGAAAT 299
Db 340 CAGTCAAAACCTTCAAAATGTAGTGTGAAAAGGCTCTGGAATCTCCAGCTATGGAATAAACCC 399
Qy 300 AATGAAATAGGCATTTACCTGACTGATTCATGCAAGAGCTAGGAAAGTATTCCTCAAG 359
Db 400 CCAAGATGTCCACAGAGCCTTTGAGAGTGTATGCAAAAAGTCAAGGGGCGAGTTCCATC 459
Qy 360 GTCCAGACACCAAGAGACACACCCGTTTACCTGGGAGCCACGGCAGGCTATGCTGCTAG 419
Db 460 CCACCTCCAGGATCCACCCCATTTCACTGGAGCCAGGCTGGGATGCGTTCGTGAG 519
Qy 420 GATGAAAGTAGAAGTGTGGCAGACAGGTTCTGATGTGGTGGAGAGAGCCTCAGCAA 479
Db 520 GTTGCAAAATGAAACAGCAGCTAATGAAGTCTTGAAGCATCCAAAGCTACTTCAAGTC 579
Qy 480 CTACCCCTTTGACTTCCAGGTCAGGATCAATTAAGTCTGCAAGAGAGTGCCTATGCG 539
Db 580 CCAGCCCTTTGACTTTAGGGGTGCTCAAAATCAATTTCTGGGCAAGAAAGGGGTATATGG 639
Qy 540 CTGGATTACTACAACTATCTGCTGGCAAAATTCAGTTCAGAAAAACAAGTGTGTTCAAGCAT 599
Db 640 ATGGATTACAGCAACTATTTAATGGAAATTTCTGGAGAGAAACCTGTGACACATGTG 699
Qy 600 AGTCCCATATGAAACCAATATACAGAAACCTTTTGGAGCTTTTGGACCTTTGGGGGAGCCTC 659
Db 700 GGTGC-----ACCCGCAATGGAGTGGAAACCAAGGTCCTGGAATTAAGTGGTGCCTC 753
Qy 660 TACACAAGTCACTTTTGTACCCCAAAACCAAGACTATCGAGTCCCCAGATAATGCTCTGCA 719
Db 754 CACCCAAATATCTCTGTCGGCAGAGAGAAAGTGAATCTGAAACACAGCGACATCATGCA 813
Qy 720 ATTTGCGCTCTATGCAAGGACTACAAATGCTACACACATAGCTTCTTGTGCTATGGGAA 779
Db 814 GGTGTCCCTGTATGGCTAGTATACAGCTCTACACACAGCTTCCAGTGTCTATGGCG 873
Qy 780 GGATCAGGCACTCTGCGCAGAAACTGGCCAGAGCAATTCAGGTTCGAAATGAATGAAA--T 836
Db 874 GAATGAGGCTGAGAAAGATTTCTGCAATGCTCTCTGCAAGAAATTCCTTACCAAAACCA 933
Qy 837 TCTCAGGACCCATGCTTTTCATCTCGATATAAGAGGTAGTGAAGTAAAGTGAACCTTTA 896
Db 934 TCTCACCACCTCTGTACCTCGGATATAGCATCAGCTTCACCATGGGCCATGTATT 993
Qy 897 CAAGACCCCTGCAC-----CAAGAGATTTGAGATGACTCTTCCATTCAGCAGTTTGA 950
Db 994 TGATAGCTGTGACCTGTGGACAGAGGCCAGAAAGTTATAACCCCAATGATGTCATCAC 1053
Qy 951 AATCCAGGGTATTGGAAACTATCAACAAATGCCATCAAGCATCTCGAGCTCTTCAACAC 1010
Db 1054 TTTTGAAGAACTGGGACCCATCTCTGTGTAGGAGAGGTGGCTTCATATTGACTT 1113
```



QY 1011 CAGTTACTGCCCTTACTCCAG---TGTGCTTCAATGGGATTTTCTTGGCCACCCTCA 1067  
Db 1114 CAAAGCTTGGCATGATCAAGAAACCTGTTCTTTGATGGGTTTATCAGCCCAAGATTAA 1173  
QY 1068 GGGGATTTTGGGCAATTTTCAAGCTTTTACTTTTGTGATGAGTTTAAACTTCACATC 1127  
Db 1174 AGGGCAATTTTGGCTTTTGGAGATTCTTACACAGCCATGCTTTTAAATCT---TTC 1230  
QY 1128 AGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCCTG 1187  
Db 1231 AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTTGAATTTCTGTCTACAGAAATG 1290  
QY 1188 GGAGAGATAAAACATCTTACGTGGAGTAAAGGAGAAAGTACCTGAGTGAATCTGCTT 1247  
Db 1291 GAGTCAGCTCCCACTGCTCTCCCAAAATTTGATGAGGTATATGCCCGCTCTTACTGCTT 1350  
QY 1248 TTCTGGTACTACATTTCTCTCCCTCTCTCTGCAAGCTATCATTTTACAGCTGATTCCTG 1307  
Db 1351 CTCAGCCAACTACATCTACCACTTGTGTTGTGAACGTTTACAATTTACACAGGAGACTTG 1410  
QY 1308 GGAGCACATCCATTTTCAATTTGGCAAGATCCAGGCGACGACGCGGCTGGACTTTGGGCTA 1367  
Db 1411 GCCCAATACACTTTTGAAGAAAGTGGGAAATAGCAGCATAGCTTGTCTCTTTGGCTA 1470  
QY 1368 CATGCTGAACCTGACCAACATGATCCCACTGAGCTGAGCAACCATTTG 1410  
Db 1471 CATGCTCAGCTGACCAACCATGATCCCACTGAGCTGAAAGCCCTCTG 1513

RESULT 8  
US-09-905-744B-3  
; Sequence 3, Application US/09905744B  
; Patent No. 6780410  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; TITLE OF INVENTION: ACIDS  
; FILE REFERENCE: 28110/36120A  
; CURRENT APPLICATION NUMBER: US/09/905,744B  
; PRIORITY FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
; OTHER INFORMATION:  
US-09-905-744B-3

Query Match 20.3%; Score 291; DB 4; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 7e-86;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

QY 120 CCAGAACAAAGATTGCCAGAAACCGTTAAGTATGGGATTTGTCTGGATGCGGGTTCTTC 179  
Db 220 CAAGCAAGAGTCTCCCTCCAGGACTGAAGTATGGTATTTGTGCTGGATGCGGGTCTTC 279  
QY 180 TCACACAAAGTTTATACATCTATAGTGGCGCAGAGAAAGGAGATGACACAGCGGTGGT 239  
Db 280 AAGAACCAACAGCTTACGTTGATCAATGGCCAGCAGAGAAAGAGAAATAATACCGAGTGGT 339  
QY 240 GCATCAAGTAGAAGAAATCAGGGTTAAAGGCTCTGGAATCTCAAAATTTGTTTCAGAAAGT 299  
Db 340 CAGTCAACCTTCAAAATGTAGTGAAGGCTCTGGAATCTCCAGTATGGAATTAACCC 399  
QY 300 AAATGAAATAGGCATTTTACCTGACTGATTGATGGAAGAGCTAGGGAAGTGTATCCAA 359

Db 400 CCAAGATGTCCCCAGAGAGCTTTGAGGAGTGTATGCAAAAAAGTCAAGGGGAGGTTCCATC 459  
QY 360 GTCCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACCGCAGGCATCTGCGTGTCTCAG 419  
Db 460 CCACCTCCACGGATCCACCCCATTCACCTGGAGCCACGGCTGGGATGCGCTTGTCTAG 519  
QY 420 GATGAAAGTGAAGATTGGCAGACAGGGTCTTGGATGTGTGGAGAGAGGCTCAGCAAA 479  
Db 520 GTTGCAAAATGAAACAGCAGCATTAAGTCTTTGAAAGCATCCAAAGCTACTTCAAGTC 579  
QY 480 CTACCCCTTTTACCTTCCAGGGTGCAGGATCATTTACTGGCCCAAGAGGAGGTCCTATGG 539  
Db 580 CAGCCCTTTTACCTTTAGGGTGTCTCAAAATCATTTCTGGCAAGAGAGGGGTATATGG 639  
QY 540 CTGATTTACTATCACTATCTGTGGGCAAAATTCAGTCAAGAAAAAAGGTGGTTTCAGCAT 599  
Db 640 ATGGATTTACGCCAACTATTTAATGGGAAATTTCTTGGAGAAAGAACCTGTGGCAGATGTG 599  
QY 600 AGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTTGGACCTTTGGGGGAGCCTC 659  
Db 700 GGTGC-----ACCGCATGGAGTGGAAACCAACGGGTGCGCTTGGACTTAGGTGTGCTC 753  
QY 660 TACACAGTCACTTTTGTACCCCAAAACCAAGCTATCGAGTCCCAGATTAATGCTCTGCA 719  
Db 754 CACCAAAATATCTTCTGTGGCAGGAGAGATGGATCTGAACACCGACATCATGCA 813  
QY 720 ATTTGCGCTCTATGGCAAGGACTCAATGTCTACACACATAGCTTCTTGTGTATGGGAA 779  
Db 814 GGTGCTCTGTATGGCTACGTATACCGCTCTACACACAGCTTCCAGTCTCAGTGTATGGCG 873  
QY 780 GGATCAGCACTCTGGCAGAAACCTGGCCAAAGACATTCAGGTTCGCAAGTAAATGAAA---T 836  
Db 874 GAATGAGCTCAGAAAGATTTCTTGGCAATCTCTCTGCAGAAATCTCTCTACCAAAACCA 933  
QY 837 TCTCAGGACCCATGCTTTTCACTCTGGATATAAGAGGTAGTGAACGTAAAGTGAACCTTTA 896  
Db 934 TCTCACCAAATCCCTGTTTACCCCTCGGATATATAGCATCAGCTTTCACCTGGGCGCATGTAT 993  
QY 897 CAAGACCCCTGACAC-----CAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGA 950  
Db 994 TGATAGCTGTGCACTGTGGACAGAGCCAGAAAGTTTAAACCCATGATGTATCATCAC 1053  
QY 951 AATCCAGGGTATGGAACATTAACAATGCCATCAAGACATCTCTGGAGCTCTTCAACAC 1010  
Db 1054 TTTTGAAGGAACCTGGGACCCATCTCTGTGTGAAGAGAGGTGGCTTCCATATTTGACTT 1113  
QY 1011 CAGTTACTGCCCTTACTCCCAG---TGTGCTTCAATGGGATTTTCTTGGCCACCCTCCA 1067  
Db 1114 CAAAGCTTGGCCATGATCAAGAAACCTGTCTTTTGTGATGGGTTTATCAGCCCAAGATTAA 1173  
QY 1068 GGGGATTTTGGGCAATTTTTCAGCTTTTACTTTTGTGATGAAGTTTAAACTTGCACATC 1127  
Db 1174 AGGGCAATTTTGGCTTTTGGAGATTTCTACTACACAGCCAGTGTCTTAAATCT---TTC 1230  
QY 1128 AGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCCTG 1187  
Db 1231 AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTGGAATTTCTGCTCAGAGAAATG 1290  
QY 1188 GGAGGAGATAAAACATCTTACGCTGGAGTAAAGAGAGTACCTGAGTGAATCTGCTT 1247  
Db 1291 GAGTCAGCTCCCACTGCTGCTCCCAAAATTTGATGAGGTATATGCCCGCTCTTACTGCTT 1350  
QY 1248 TTCTGGTACCTTACATTTCTCTCCCTCTCTTCAAGGCTATCATTTTACAGCTGATTTCTG 1307  
Db 1351 CTAGCCAACTACATCTACCACTTGTGTTGTGAACGTTTACAATTTACAGAGGAGACTTG 1410  
QY 1308 GGAGCACATCCATTTCAATTTGGCAAGATCCAGGCGACGACCGGCTGGACTTTGGGCTA 1367  
Db 1411 GCCCAATACACTTTTGAAGAAAGTGGGAAATAGCAGCATAGCTTGTCTCTTTGGCTA 1470  
QY 1368 CATGCTGAACCTGACCAACATGATCCCACTGAGCTGAGCAACCATTTG 1410  
Db 1471 CATGCTCAGCTGACCAACCATGATCCCACTGAGCTGAAAGCCCTCTG 1513

RESULT 9  
US-10-107-660-3  
; Sequence 3, Application US/10107660  
; Patent No. 6780977  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischaut, Anna-Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE  
; FILE REFERENCE: 9598-066  
; CURRENT APPLICATION NUMBER: US/10/107,660  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: US/09/240,639  
; PRIOR FILING DATE: 1998-01-29  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
US-10-107-660-3

Query Match 20.3%; Score 291; DB 4; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 7e-86;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

QY 120 CCAGAACAAAGCATTCGCCAGAAACGTTAAGTAGTGGATTGTGCTGGATGCGGGTCTTC 179  
DB 220 CAAGCAAGAGGTCCTCCCTCCAGGACTGAAGTAGTGTATTTGCTGGATGCGGGTCTTC 279  
QY 180 TCACACAAGTTTATACATCTATTAAGTGGCCAGCAGAAAAAGGAAATGACACAGCGGTGGT 239  
DB 280 AAGAACACAGCTACGCTGTATCAATGGCCAGCAGAAAAAGAAATATACCGAGTGT 339  
QY 240 GCATCAAGTAGAAGATGACAGGGTTAAAGTCTCTGGAATCTCAAAATTTGTTCAAGAAAT 299  
DB 340 CAGTCAAAACCTTCAAAATGTAGTGAAGGCTCTGGAATCTCAGCTATGGAATTAACCC 399  
QY 300 AAATGAATAGGATTTTACCTGACTGATTCGATGGAAGAGCTAGGGAAGTATCCAAAG 359  
DB 400 CCAAGATGTCACAGAGCCTTTGAGAGTGTATGCAAAAAGTCAAGGGCAGGTTCCATC 459  
QY 360 GTCCAGCACAAGAGACACCCCGTTTACCTGGAGCCACGGCAGGATGCGGTTGCTCAG 419  
DB 460 CCACCTCCAGGATCCACCCCATTCACCTGGAGCCACGGCTGGGATGCGCTTGTGAG 519  
QY 420 GATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCCTCAGCAA 479  
DB 520 GTTGCAAAATGAAACAGCAGCTAATGAAGTCTTGAAGCATCCAAAGCTACTTCAAGTC 579  
QY 480 CTACCCCTTTGACTTCAGGTCGCCAGGATCATTATGCGCCAGAGAGGAGTCCCTATGG 539  
DB 580 CCAGCCCTTTGACTTTAGGGGTGCTCAAAATCATTTCTGGGCAAGAGAGGGGTATATGG 639  
QY 540 CTGGATTACTATCAACTATCTCTGGGCAAAATTCAGTCAGAAAAAAGGTGGTTTCAGCAT 599  
DB 640 ATGATTAACAGCCAACTATTATTAATGGAAATTTCTGGAGAGAACTGTGGCAGATGTG 699  
QY 600 AGTCCCATATGAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGGGAGCCTC 659  
DB 700 GGTGC-----ACCCGATGGAGTGAACACACGGGTGCGCTGGACTTAGGTGGTGCCTC 753  
QY 660 TACCAAGTCACTTTGTATCCCAACCAACAGACTATCGAGTCCCCAGATAATCTCTGCA 719  
DB 754 CACCAAAATATCTTGTGGCAGAGAGAGATGGATCTTGAACACCAAGCAATCATGCA 813  
QY 720 ATTTGCGCTCTATGGCAAGGACTACATGTCTACACATAGCTTCTTTGTGCTATGGAA 779

DB 814 GGTGTCCTGTATGGCTACGTATACACGCTCTACACACACAGCTTCCAGTGTCTATGGCCG 873  
QY 780 GGATCAGGCACCTCTGSCAGAAACTGSCCAAGGACATTCAGGTTGCAAGTAATGAAA---T 836  
DB 874 GAATGAGGCTGAGAAAGTTTCTGGCAATGCTCTCTGCAGAAATTCCTCTACAAAACCA 933  
QY 837 TCTCAGGGACCCATGCTTTTCATCCTCGATATAGAAGGTAGTGAAGTGAAGTGAACCTTTA 896  
DB 934 TCTCACCATCTCTGTATACCTCGGATTTATAGCATCAGCTTCCACCATGGCCATGATTT 993  
QY 897 CAAAGCCCTCTGCAC-----CAAGAGATTTGAGATGACTCTTTCATTTCCAGCAGTTGA 950  
DB 994 TGATAGCCTGTGCACTGTGGACCCAGAGGCGCAAGAGTTATAACCCCAATGATGTCATC 1053  
QY 951 AATCAGGGTATTTGAAACTATCAACAATGCCATCAAGCATCCTGGAGCTCTTCAACAC 1010  
DB 1054 TTTTGAAGGAACCTGGGACCCATCTCTGTGAAGGAGAGGTGGCTTCCATATTTGACTTT 1113  
QY 1011 CAGTTACTGCCCTTACTTCCCAG---TGTGCTTCAATGGGATTTTCTTGGCCACCACTCCA 1067  
DB 1114 CAAAGCTTGCCATGATCAAGAAACCTGTCTTTTGTGGGTTTATCAGSCCAAGATTAA 1173  
QY 1068 GGGGATTTTGGGCAATTTTCAGCTTTTACCTTTGTGATGAAGTTTAAACTTGCATC 1127  
DB 1174 AGGGCCATTTGTGGCTTTTGCAGGATTTCTACTACACAGCCAGTGTCTTAAATCT---TTC 1230  
QY 1128 AGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTG 1187  
DB 1231 AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTGGAAATTTCTGCTCAGAAATTTG 1290  
QY 1188 GGAGGAGATAAAAACATCTTACGCTGGAGTAAAGGAGAGTAGTACCTGAGTGAATACTGCTT 1247  
DB 1291 GAGTCAGCTCCACGCTGCTCTCCCAAAATTTGATGAGGTATATGCCGCTCTTACTGCTT 1350  
QY 1248 TTCTGGTACCTACATTTCTCTCCCTCTCTGCAAGGTATCATTTTCACAGCTGATTCCTG 1307  
DB 1351 CTCAGCCAACTACATCTACCACTTGTGTGAACGGTTACAAATTCACAGAGGAGACTTG 1410  
QY 1308 GGAGCACATCCATTTCAITGGCAAGATCCAGGGCAGCGCGCTGCACTTTGGGCTA 1367  
DB 1411 GCCCAAAATACACTTTGAAAAAGAGTGGGGAAATAGCAGCATAGCTGTCTCTTGGCTA 1470  
QY 1368 CATGCTGAACCTTGACCAACATGATCCAGCTGAGCAACCACTTG 1410  
DB 1471 CATGCTAGCCTGACCAACCACTCCAGCTCCAGCTGAAAGCCCTCTG 1513

RESULT 10  
US-10-107-576-3  
; Sequence 3, Application US/10107576  
; Patent No. 6783959  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischaut, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; FILE REFERENCE: 28110/36120H  
; CURRENT APPLICATION NUMBER: US/10/107,576  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
; OTHER INFORMATION:  
US-10-107-576-3

Query Match		20.3%;	Score 291;	DB 4;	Length 2797;
Best Local Similarity		54.3%;	Pred. No. 7e-86;		
Matches 707;		Conservative 0;	Mismatches 575;	Indels 21;	Gaps 5;
Qy	120	CCAGAACAAAGCATTCGCCAGAAAAACGTTAAGTATGGATTGTGCTGGATGCGGGTCTTTC	179		
Db	220	CAAGCAAGAGTCCCTCCCTCCAGGACTGAAGTATGGTATTGTGCTGGATGCCGGTCTTTC	279		
Qy	180	TCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAAGGAGAATGACACAGCGGTGGT	239		
Db	280	AAGAACCACAGCTACGTGTATCAATGGCCAGACAGAAAAAGAGAATAATACCGAGTGGT	339		
Qy	240	GCATCAAGTAGAAGATGACAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTCAGAAAGT	299		
Db	340	CAGTCAAACTTTCAATGTAGTGTGAAGGGCTCTGGAATCTCCAGCTATGGAATAAACCC	399		
Qy	300	AAATGAAATAGGCATTTACCTGACTGATTGCATGGAAGAGCTAGGGAAGTCAATCCCAAG	359		
Db	400	CCAAGATGTCCCAGAGCCTTTGAGGAGTGTATGCANAAAGTCAAGGGCAGGTCCCATC	459		
Qy	360	GTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGATCGCGTTGCTCAG	419		
Db	460	CCACCTCCACGGATCCACCCCATTCACCTGGGAGCCACGGCTGGGATGCGCTTGCCTGAG	519		
Qy	420	GATGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGTGGAGAGAGCCTCAGCAA	479		
Db	520	GTGCAAAATGAACAGCAGCTAATGAAGTCTTGAAGCATCCAAAGCTACTTCAAGTC	579		
Qy	480	CTPACCCCTTTGACTTCCAGGGTCCAGGATCAATTAAGTCTGCAAGAGGAGGTGCTATGG	539		
Db	580	CCAGCCCTTTGACTTTAGGGTGTCAATCAATTTCTGGCAAGAAAGGGGTATATGG	639		
Qy	540	CTGGATTACTATCAACTACTCTGCTGGCAAAATTCAGTCAGAAAAACAAGTGGTTTCAGCAT	599		
Db	640	ATGGATTACAGCAACTATTTAATGGAAATTTCTCGGAGAAGACCTGTGCGCATGTG	699		
Qy	600	AGTCCCATATGAACCAATATACAGAAACCTTTGGAGCTTTGGACCTTGGGGAGCCTC	659		
Db	700	GGTGC-----ACCCGCATGGAGTGGAAACCAACGGGTGCCCTGGACTTTAGGTGGTGCCTC	753		
Qy	660	TACACAAGTCACTTTTGTACCCCAAAACACAGACTATCGAGTCCCAGATAATGCTCTGCA	719		
Db	754	CACCAAAATATCTTCTGTGGCAGGAGAAGATGGATCTGAACACCAAGGACATCATGCA	813		
Qy	720	ATTTGCGCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCTATGGAA	779		
Db	814	GGTGTCCCTGTATGCTACGTATACACGCTCTACACACAGCTTCCAGTGTATGGCG	873		
Qy	780	GGATCAGGCACTCTGGCAGAACTGGCCAAAGACATTCAGGTTCGAAGTAATGAAA---T	836		
Db	874	GAATGAGGCTGAGAAGAAGTTTCTGGCAATGCTCCTGCAGAATTCCTCTACCAAAAACCA	933		
Qy	837	TCTCAGGACCCATGCTTTTCATCCTGGATATAAGNAGGTAGTGAACGTAAAGTACCTTTA	896		
Db	934	TCTCACCATCCCTGTTACCTTCGGATTTATAGCATCAGCTTCACCATGGGCCATGTATT	993		
Qy	897	CAAGACCCCTGECAC-----CAAGAGATTTGAGATGACTCTTCATTCACGACAGTTGA	950		
Db	994	TGATAGCTGTGCACTGTGGACGAGGCCAGAAAGTTATAACCCCATGATGTCATCAC	1053		
Qy	951	AATCAGGGTATTTGAAACTATCAACAATGCCATCAAAAGCATCTCTGGAGCTTCTTCAACAC	1010		
Db	1054	TTTTGAAGAACTGGGGACCCATCTCTGTGTAAGGAGAAGGTGGCTTCCATATTGACTT	1113		
Qy	1011	CAGTTACTGCCCTTACTCCAG---TGTGCTTCAATGGGATTTTCTTGCCACCACTCCA	1067		
Db	1114	CAAGCTTGCATGATCAAGAAACCTGTTCTTTTGTATGGGTTTATACGCCAAAGATTAA	1173		
Qy	1068	GGGGGATTTGGGGCATTTTCAGCTTTTATCTTTTGTGATGAAGTTTAAACTTGCATC	1127		
Db	1174	AGGGCCATTTGTGGCTTTTTCAGGATTTCTACTACACGCCAGTGTCTTAAATCT---TTC	1230		
Qy	1128	AGAGAAAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTTCTGTGCTCAGCCTTG	1187		

Db	1231	AGBTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTTGAATTTCTGCTCACAGAAATG	1290		
Qy	1188	GGAGGAGATAAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTT	1247		
Db	1291	GAGTCAGCTCCCACTGCTGCTCCCAAAATTTGATGAGGTATATGCCCGCTCTTACTGCTT	1350		
Qy	1248	TTCTGGTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTTCACAGCTGATTCCTG	1307		
Db	1351	CTCAGCCAACTACATCTACCACTTGTGTAACGTTTACAAATTCACAGAGGAGACTTG	1410		
Qy	1308	GGAGCACATCCATTTTCATTTGGCAAGATCCAGGGCAGCAGCCGCGCTGGACTTTGGGCTA	1367		
Db	1411	GCCCAAAATACACTTTGAAAAAGAGTGGGAATAGCAGCATAGCCTGGTCTCTTTGGCTA	1470		
Qy	1368	CATGCTGAACCTGACCAACATGATCCCACTGAGCAACCATTTG	1410		
Db	1471	CATGCTAGCCTGACCAACCAAGATCCCACTGAAAAGCCCTCTG	1513		
RESULT 11					
US-09-905-732B-3					
; Sequence 3, Application US/09905732B					
; Patent No. 6787328					
; GENERAL INFORMATION:					
; APPLICANT: Chadwick, Brian Paul					
; APPLICANT: Frieschaut, Anna Maria					
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND					
; FILE REFERENCE: 28110/361208					
; CURRENT APPLICATION NUMBER: US/09/905,732B					
; PRIOR FILING DATE: 2001-07-13					
; PRIOR APPLICATION NUMBER: 09/240,639					
; PRIOR FILING DATE: 1999-01-29					
; NUMBER OF SEQ ID NOS: 32					
; SOFTWARE: PatentIn version 3.1					
; SEQ ID NO 3					
; LENGTH: 2797					
; TYPE: DNA					
; ORGANISM: Homo Sapiens					
; FEATURE:					
; NAME/KEY: CDS					
; LOCATION: (83)..(1669)					
; OTHER INFORMATION:					
US-09-905-732B-3					
Query Match					
Best Local Similarity 20.3%; Score 291; DB 4; Length 2797;					
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;					
Qy	120	CCAGAACAAAGCATTCGCCAGAAAAACGTTAAGTATGGATTGTGCTGGATGCGGGTCTTTC	179		
Db	220	CAAGCAAGAGTCCCTCCCTCCAGGACTGAAGTATGGTATTGTGCTGGATGCCGGTCTTTC	279		
Qy	180	TCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAAGGAGAATGACACAGCGGTGGT	239		
Db	280	AAGAACCACAGCTTACGTGTATCAATGGCCAGCAGAAAAAGAGAATAATACCGAGTGGT	339		
Qy	240	GCATCAAGTAGAAGATGACAGGGTTAAAGGTTAAAGTCTTCAAAATTTGTTTCAGAAAGT	299		
Db	340	CAGTCAAACTTTCAAAATGTAGTGTGAAGGGCTCTGGAATCTCCAGCTATGGAATAAACCC	399		
Qy	300	AAATGAAATAGGCATTTACCTGACTGATTGCATGGAAGAGCTAGGGAAGTCAATCCCAAG	359		
Db	400	CCAAGATGTCCCAGAGCCTTTGAGGAGTGTATGCANAAAGTCAAGGGCAGGTCCCATC	459		
Qy	360	GTCCAGCACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGATCGCGTTGCTCAG	419		
Db	460	CCACCTCCACGGATCCACCCCATTCACCTGGGAGCCACGGCTGGGATGCGCTTGCCTGAG	519		
Qy	420	GATGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGTGGAGAGAGCCTCAGCAA	479		
Db	520	GTGCAAAATGAACAGCAGCTAATGAAGTCTTGAAGCATCCAAAGCTACTTCAAGTC	579		
Qy	480	CTPACCCCTTTGACTTCCAGGGTCCAGGATCAATTAAGTCTGCAAGAGGAGGTGCTATGG	539		
Db	580	CCAGCCCTTTGACTTTAGGGTGTCAATCAATTTCTGGCAAGAAAGGGGTATATGG	639		
Qy	540	CTGGATTACTATCAACTACTCTGCTGGCAAAATTCAGTCAGAAAAACAAGTGGTTTCAGCAT	599		
Db	640	ATGGATTACAGCAACTATTTAATGGAAATTTCTCGGAGAAGACCTGTGCGCATGTG	699		
Qy	600	AGTCCCATATGAACCAATATACAGAAACCTTTGGAGCTTTGGACCTTGGGGAGCCTC	659		
Db	700	GGTGC-----ACCCGCATGGAGTGGAAACCAACGGGTGCCCTGGACTTTAGGTGGTGCCTC	753		
Qy	660	TACACAAGTCACTTTTGTACCCCAAAACACAGACTATCGAGTCCCAGATAATGCTCTGCA	719		
Db	754	CACCAAAATATCTTCTGTGGCAGGAGAAGATGGATCTGAACACCAAGGACATCATGCA	813		
Qy	720	ATTTGCGCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCTATGGAA	779		
Db	814	GGTGTCCCTGTATGCTACGTATACACGCTCTACACACAGCTTCCAGTGTATGGCG	873		
Qy	780	GGATCAGGCACTCTGGCAGAACTGGCCAAAGACATTCAGGTTCGAAGTAATGAAA---T	836		
Db	874	GAATGAGGCTGAGAAGAAGTTTCTGGCAATGCTCCTGCAGAATTCCTCTACCAAAAACCA	933		
Qy	837	TCTCAGGACCCATGCTTTTCATCCTGGATATAAGNAGGTAGTGAACGTAAAGTACCTTTA	896		
Db	934	TCTCACCATCCCTGTTACCTTCGGATTTATAGCATCAGCTTCACCATGGGCCATGTATT	993		
Qy	897	CAAGACCCCTGECAC-----CAAGAGATTTGAGATGACTCTTCATTCACGACAGTTGA	950		
Db	994	TGATAGCTGTGCACTGTGGACGAGGCCAGAAAGTTATAACCCCATGATGTCATCAC	1053		
Qy	951	AATCAGGGTATTTGAAACTATCAACAATGCCATCAAAAGCATCTCTGGAGCTTCTTCAACAC	1010		
Db	1054	TTTTGAAGAACTGGGGACCCATCTCTGTGTAAGGAGAAGGTGGCTTCCATATTGACTT	1113		
Qy	1011	CAGTTACTGCCCTTACTCCAG---TGTGCTTCAATGGGATTTTCTTGCCACCACTCCA	1067		
Db	1114	CAAGCTTGCATGATCAAGAAACCTGTTCTTTTGTATGGGTTTATACGCCAAAGATTAA	1173		
Qy	1068	GGGGGATTTGGGGCATTTTCAGCTTTTATCTTTTGTGATGAAGTTTAAACTTGCATC	1127		
Db	1174	AGGGCCATTTGTGGCTTTTTCAGGATTTCTACTACACGCCAGTGTCTTAAATCT---TTC	1230		
Qy	1128	AGAGAAAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTTCTGTGCTCAGCCTTG	1187		



```
QY 951 AATCCAGGGTATTGGAAACTATCAACAATGCCATCAAGCATCTCTGGAGCTCTTCAACAC 1010
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1054 TTTTGAAGAACTGGGGACCCATCTCTGTGTGAAGGAAGGTGGCTTCCATATTTGACTT 1113
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1011 CAGTTACTGCTTACTCCAG---TGTGCTTCAATGGATTTCTTGGCCACCACTCA 1067
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1114 CAAAGCTTCCCATGATCAAGAAACCTGTCTTTGATGGGTATATCAAGCCAAAGATTAA 1173
QY 1068 GGGGATTTTGGGCATTTTACGCTTTTACCTTTGTGATGAAGTTTAAACCTTGACATC 1127
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1174 AGGGCAATTTTGGCTTTTTCAGGATTTCTACTACAGCCAGTGTCTTAAATCT---TTC 1230
QY 1128 AGAGAAAGTCTCTAGGAAAGGTGACTGAGATGATGAAGTATCTGTGCTCAGCCTTG 1187
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1231 AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTGGAAATTTCTGCTCACAGAAATG 1290
QY 1188 GGAGGAGATAAAACATCTTACGCTGGAGTAAGGAAGTACCTGAGTGAATATGCTT 1247
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1291 GAGTCAGCTCCACCTGCTGCTCCCAATTTGATGAGGTATATGCCCGCTCTTACTGCTT 1350
QY 1248 TTCTGGTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTTCAAGCTGATTCTCTG 1307
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1351 CTCAGCCAACTACATCTACCCTTCTTGTGAACGGTTACAAATTTCAAGAGGAGACTTG 1410
QY 1308 GGAGCACATTCATTTGCAAGATCCAGGCGAGCGCCGCTGGACTTTGGGGCTA 1367
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1411 GCCCAAAATACACTTTGAAAAAGAGTGGGAATAGCAGCATAGCTGCTCTCTTGGCTA 1470
QY 1368 CATGCTGAACCTGACCAATGATCCAGCTGAGCAACCATTTG 1410
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1471 CATGCTCAGCTGACCAACCAAGATCCAGCTGAAAAAGCCCTCTG 1513
```

RESULT 13

```
US-09-949-016-178
; Sequence 178, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 2797
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-178
```

```
Query Match 20.3%; Score 291; DB 4; Length 2797;
Best Local Similarity 54.3%; Pred. No. 7e-86;
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

QY 120 CCAGAACAAAGCATTTGCCAGAAAAAGTTAAGTATGGGATTTGCTGGATCGGGTTCTTC 179
Db 220 CAAGCAAGAGTCTCTCCCTCCAGNCTGAAGTATGTTATTTGCTGGATCGGGTTCTTC 279

QY 180 TCACACAAAGTTTATACATCTAAGTGGCCAGCAGAAAAAGGAGAAATGACACAGCGGTGT 239
Db 280 AAGAACCAACAGTCTACGTGTATCAATGSCCAGCAGAAAAAGGAAATATAACCGAGTGT 339

QY 240 GCATCAAGTAGAAGATCCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTTCAGAAAGT 299
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
Db 340 CAGTCAAAACCTTTCAAAATGTAGTGTGAAGGCTCTGGAATCTCCAGCTATGGAATAAACCC 399
QY 300 AAATGAAATAGGCATTTTACCTGACTGATTGCATGGAAGAGCTAGGGAAGTGAATTTCCAAAG 359
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1400 CCAAGATGTCCTCCAGAGCCTTTGAGGAGTGTATGCAAAAAGTCAAGGGCAGGTTCCATC 459
QY 360 GTCCAGACCAAGAGACACCCGTTTACTGGAGGCCACGGCAGCATGCGGTGCTCAG 419
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1460 CCACCTCCAGCGATCCACCCCATTTCACTGGAGGCCACGGCTGGGATGCGCTTCTGCTGAG 519
QY 420 GATGGAAGTCAAGAGTTGGCAGACAGGGTCTCGATGTGTGGAGAGGAGCCTCAGCAA 479
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1520 GTTGCAAAATGAACACAGCAGCTAATGAAGTCTTTGAAAGCATCCAAGCTACTTCAAGTC 579
QY 480 CTACCCCTTTGACTTTCCAGGGTGCAGGATCAATTAATCTGCGCAAGAGGAGGTCCTATGG 539
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1580 CCAGCCCTTTGACTTTAGGGGTGCTCAATCATTTCTGGGCAAGAAAGGGGTATATGG 639
QY 540 CTGATTAATCAATCAATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGGTGTTGAGCAT 599
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1640 ATGATTAACAGCAACTATTTAATGGGAAAATTTCTGGAGAAAGAACCTGTGGCACAATGTG 699
QY 600 AGTCCCATATGAACCAATATCAAGGAACCTTTGGAGCTTTGGACCTTTGGGGAGCCTC 659
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1700 GGTGC-----ACCCGATGAGGTGGAACCAACGGGTGCTTGGACTTTAGGTGGTCTC 753
QY 660 TACACAAAGTCACTTTTGTACCCCAAAACCAAGCTATCGAGTCCCCAGATAATGCTCTGCA 719
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1754 CACCAAAATATCTTCTGGCAGGAGAGAGATGATCTGAAACACCAAGGACATATGCA 813
QY 720 ATTTGGCTCTATGGCAAGGACTCAATGTCTACACATAGCTTTTGTGCTATGGAA 779
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1814 GGTGTCTGTATGGCTACGTATACAGCTCTACACACACAGCTTCCAGTGTCTATGGCG 873
QY 780 GGATCAGGCACTCTGGCAGAAAACCTGGCCCAAGGACATTCAGGTTCGAGTGAATGAA---T 836
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1874 GAATGAGGCTGAGAAGAGTTTCTGGCAATGCTCTCGCAAAATTTCTCTCAAAAACCA 933
QY 837 TCTCAGGACCCATGCTTTTCACTCTGGATATAAGAAAGGTAGTGAACGTAAGTACCTTTA 896
Db 934 TCTCACCANTCTCTTACCTCGGGATTTATGATCAGCTTCCACCTGGGCCATGTATT 993
QY 897 CAAGACCCCTTGAC-----CAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGA 950
Db 994 TGATAGCTGTGCACTGTGGACACAGAGCCAGAAAGTTATAACCCCAATGATGTCATCAC 1053
QY 951 AATCCAGGGTATTGGAAACTATCAACAATGCCATCAAGCATCTGGAGCTTCTCAACAC 1010
Db 1054 TTTTGAAGGAACTGGGGACCCATCTCTGTGTAAAGGAAGGTGGCTTCCATATTTGACTT 1113
QY 1011 CAGTTACTGCTCTTACTCCAG---TGTGCTTCAATGGGATTTTCTTGGCCACCACTCCA 1067
Db 1114 CAAAGCTTGCCATGATCAAGAAACCTGTCTTTTGTATGGGGTTTATCAGCCAAAGATTAA 1173
QY 1068 GGGGATTTTGGGCATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAAACTTTGACATC 1127
Db 1174 AGGCCCATTTTGTGGCTTTTTCAGGATTTCTACTACAGCCAGTGTCTTTAAATCT---TTC 1230
QY 1128 AGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTG 1187
Db 1231 AGGTAGCTTTTCCCTGGACACCTTTCAACTCCAGCACCTGGAAATTTCTGCTCACAGAAATG 1290
QY 1188 GGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTT 1247
Db 1291 GAGTCAGCTCCACTGCTGCTCCCAATTTTGTAGAGGTATATGCCCGCTCTTACTGCTT 1350
QY 1248 TTCTGGTACCTACATTTCTCTCCCTCTCTTCTGCAAGGCTATCATTTTCAAGCTGATTCTGT 1307
Db 1351 CTAGCCCAACTACATCTACCATTTGTTGTGTAACGGTTACAAATTTCAAGAGGAGACTTG 1410
QY 1308 GGAGCACATTCATTTGCAAGATCCAGGCGAGCGCCGCTGGACTTTGGGGCTA 1367
Db 1411 GCCCAAAATACACTTTGAAAAAGAGTGGGAATAGCAGCATAGCTGCTCTCTTGGCTA 1470
```

QY 1368 CATGCTGAACCTACCAACATGATCCAGCTGAGCAACCATTTG 1410  
Db 1471 CATGCTCAGCCTGACCAACAGATCCAGCTGAAGCCCTCTG 1513

RESULT 14

US-09-905-743B-3  
; Sequence 3, Application US/09905743B  
; Patent No. 6828423  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND ACIDS  
; FILE REFERENCE: 28110/36120C  
; CURRENT APPLICATION NUMBER: US/09/905,743B  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1669)  
; OTHER INFORMATION:  
US-09-905-743B-3

Query Match 20.3%; Score 291; DB 4; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 7e-86;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;  
QY 120 CCAGAACAAAGCATTCGCAAGAAACGTTAAGTAGTGGATTGTCTCGATGCGGGTTCTTC 179  
Db 220 CAAGCAGAGGTCTCTCCAGACTGAAGTAGTATGTATGTGCTGATGCGGGTCTTC 279  
QY 180 TCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAGGAAATGACACAGGCGTGT 239  
Db 280 AAGAACACACAGTCTACGTGTATCAATGGCCAGCAGAAAGAAATAATACCGAGTGT 339  
QY 240 GCATCAAGTAGAAGATGACGGGTTAAAGTCTCTGGAATCTCAAAATTTGTTCCAGAAAGT 299  
Db 340 CAGTCAAACTTCAAAATGTAGTGTGAAGGCTCTGGAATCTCAGCTATGGAATAACCC 399  
QY 300 AAATGAAATAGGATTTACCTGACTGATTCATGGAAGAGAGCTAGGGAAGTATTCGAAG 359  
Db 400 CCAAGATGTCCTCCAGAGCCTTTGAGGAGTGTATGCAAAAGTCAAGGGGAGGTTCATC 459  
QY 360 GTCCAGACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGATCGGTTGCTCAG 419  
Db 460 CCACCTCCAGGATCCACCCCATTCACCTGGAGCCACGGCTGGATGCGCTTGCTGAG 519  
QY 420 GATGGAAGTAGAGATTGGCAGACAGGTTCTGGATGTGGTGGAGAGAGCCTCAGCA 479  
Db 520 GTTGCAAAATGAAACAGCAGCTAATGAAGTCTTGAAGCATCCAAAGCTACTTCAAGTC 579  
QY 480 CTACCCCTTTGACTTCCAGGCTCCAGGATCATTTACTGGCCAAGAGGAGGCTTATGG 539  
Db 580 CCAGCCCTTTGACTTTTAGGGGTGCTCAATCATTTCTGGCAGAGAGAGGGGTATATGG 639  
QY 540 CTGGATTACTATCAACTATCTCTGGGCAAAATTCAGTCAAGAAACAAAGGTGTTTACAGCAT 599  
Db 640 ATGGATTACAGCAACTATTATTAATGGAAATTTCTGGAGAAACCTGTGGCAGCATGTG 699  
QY 600 AGTCCCATATGAACCAATTAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGGAGCCTC 659  
Db 700 GGTGTC-----ACCCGATGGAGTGGAAACCAAGGCTGCGCTAGTGTAGTGGTCCCT 753  
QY 660 TACACAAGTCACCTTTTGTAGCCCAAAACAGACTATCGAGTCCCGCAGATAATGCTGTGCA 719

Db 754 CACCCAAATATCTCTTCGTGGCAGGAGAGATGATCTGAAACACAGCGACATCATGCA 813  
QY 720 ATTTCCGCTCTATGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGTATGGGAA 779  
Db 814 GGTGTCCCTGTATGGCTACGTATACACGCTCTACACACACAGCTTCCAGTGTCTATGGCG 873  
QY 780 GGATCAGGCACCTCTCGCAGAAACTGCGCAAGGACATTCAGGTTGCAAGTAATGAAA---T 836  
Db 874 GAATGAGGCTGAGAAGAAGTTTCTGCAATGCTCTCTGAGAAATTCCTTACCAAAACCA 933  
QY 837 TCTCAGGACCCATCTTTTCATCTCTGGATATAAGAGGTAGTGAACGTAAGTGAOCCTTTA 896  
Db 934 TCTCACCATCTCTGTACCTCGGATTTATAGCATCAGCTTCCACATGGGCCATGTATT 993  
QY 897 CAAAGACCCCTGCAC-----CAAGAGATTTGAGATGACTCTTCCATTCACGACGATTGA 950  
Db 994 TGATAGCCTGTGCACTGTGGACAGAGGCCAGAAAGTTATTAACCCCAATGATGTCAATC 1053  
QY 951 AATCCAGGCTATTGGAAGACTATCAACAATGCCATCAAGCATCCTGGAGCTCTTCAACAC 1010  
Db 1054 TTTTGAAGAACTGGGACCCCATCTCTGTGTAAGAGAGGTGGCTTCCATATTTGACTTT 1113  
QY 1011 CAGTTACTGCCCTTACTCCACG---TGTCCTTCAATGGGATTTTCTTGGCCACCACTCCA 1067  
Db 1114 CAAAGCTTGCCATGATCAAGAAACCTGTTCTTTTGATGGGTTTATCAGCCAAAGATTAA 1173  
QY 1068 GGGGATTTGGGCACTTTTCAGCTTTTCTCTTTGATGAAGTTTAACTTGAATCTGACATC 1127  
Db 1174 AGGGCCATTTGTGGCTTTTGCAGGATTTCTACTACACAGCAGTGTCTTAAATCT---TTC 1230  
QY 1128 AGAGAAAGTCTCTCAGGAAAGGTGCTGAGATGATGAAAGATTTCTGTGCTCAGCCTTG 1187  
Db 1231 AGTAGCTTTTCCCTGGACACCTTCACTCCAGCACCTGGAATTTCTGCTCAGAGATTG 1290  
QY 1188 GGAGGAGATAAAACATCTTACGCTGGAGTAAAGAGAGTACCTGAGTGAATACTGCTT 1247  
Db 1291 GAGTCAGCTCCCACTGCTGCTCCCAAAATTTGATGAGGTATATGCCGCTCTTACTGCTT 1350  
QY 1248 TTCTGGTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCACAGCTGATTCCTG 1307  
Db 1351 CTCAGCCAACTACATCTACCACCTTGTGTTGTAACGGTTACAAAATTCACAGAGGAGACTTG 1410  
QY 1308 GGAGCACATCCATTTTCATTTGGCAAGATCCAGGGCAGCGCGCTGGACTTTTGGGCTA 1367  
Db 1411 GCCCAATACACTTTGAAAAGAGAGTGGGGAATAGCAGCATAGCCTGCTCTCTTGGCTA 1470  
QY 1368 CATGTGAACCTGACCAACATGATCCAGCTGAGCAACCATTTG 1410  
Db 1471 CATGCTCAGCTGACCAACAGATCCAGCTGAAAGCCCTCTG 1513

RESULT 15

US-09-949-016-13848  
; Sequence 13848, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13848  
; LENGTH: 46885

```
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(46885)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13848

Query Match      18.8%; Score 270.2; DB 4; Length 46885;
Best Local Similarity 98.9%; Pred. No. 5.2e-78;
Matches 272; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      813 CATTGAGTTGCAAGTAATGAAATTCACGGGACCCATGCTTTTCATCCTGGATATAAGAA 872
Db      26315 CATTGAGTTGCAAGTAATGAAATTCACGGGACCCATGCTTTTCATCCTGGATATAAGAA 26374

Qy      873 GGTAGTGAACGTAAGTGACCTTTACAAGACCCCTGCACCAAGAGATTGTGAGATGACTCT 932
Db      26375 GGTAGTGAACGTAAGTGACCTTTACAAGACCCCTGCACCAAGAGATTGTGAGATGACTCT 26434

Qy      933 TCATTCCAGCAGTTTGAAATCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCAT 992
Db      26435 TCATTCCAGCAGTTTGAAATCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCAT 26494

Qy      993 CCTGAGCTCTTCAACACACAGTTACTGCCCTTACTCCAGTGTCCTTCAATGGGATTTT 1052
Db      26495 CCTGAGCTCTTCAACACACAGTTACTGCCCTTACTCCAGTGTCCTTCAATGGGATTTT 26554

Qy      1053 CTTGCCACCACTCCAGGGGATTTTGGGGCATTTT 1087
Db      26555 CTTGCCACCACTCCAGGGGATTTTGGGGTAAGTT 26589
```

Search completed: September 21, 2005, 23:30:35  
Job time : 262.45 secs

**THIS PAGE BLANK (USPTO)**

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: September 21, 2005, 20:35:18 ; Search time 1041.08 Seconds  
(without alignments)  
9228.876 Million cell updates/sec

Title: US-09-807-660C-7  
Perfect score: 1437  
Sequence: 1 atggccctgtgtagcag.....ctctctccactccaccta 1437

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7400704 seqs, 3343079526 residues

Total number of hits satisfying chosen parameters: 14801408

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	1437	100.0	1437 9	US-09-835-147-7 Sequence 7, Appli
2	1400	97.4	1464 9	US-09-835-147-25 Sequence 25, Appli
3	1365	95.0	1365 9	US-09-835-147-5 Sequence 5, Appli
4	1319.2	91.8	1599 9	US-09-835-147-1 Sequence 1, Appli
5	1319.2	91.8	1599 19	US-10-646-308-29 Sequence 29, Appli
6	1319.2	91.8	1818 18	US-10-641-643-1475 Sequence 1475, Ap
7	1319.2	91.8	1818 22	US-10-934-998-290 Sequence 290, App

8	1319.2	91.8	2081	22	US-10-934-998-46	Sequence 46, Appl	
9	1319.2	91.8	4411	16	US-10-240-965-242	Sequence 242, App	
c	10	640.2	704	22	US-10-934-998-147	Sequence 147, App	
c	11	640.2	6164	22	US-10-934-998-193	Sequence 193, App	
	12	414	28.8	475	10	US-09-918-995-24656	Sequence 24656, A
	13	379	26.4	484	10	US-09-918-995-23052	Sequence 23052, A
c	14	335.8	23.4	703	16	US-10-002-631C-275	Sequence 275, App
	15	291	20.3	2797	9	US-09-923-304-3	Sequence 3, Appli
	16	291	20.3	2797	22	US-11-076-982-2	Sequence 296, App
	17	287.6	20.0	1494	24	US-11-076-982-2	Sequence 2, App
	18	270.2	18.8	304	16	US-10-029-386-23310	Sequence 23310, A
	19	270.2	18.8	534	16	US-10-029-386-9610	Sequence 9610, A
	20	260.8	18.1	1485	24	US-11-076-982-4	Sequence 4, Appli
	21	260.8	18.1	2261	9	US-09-823-356-21	Sequence 21, Appli
	22	199.2	13.9	2122	21	US-10-498-788-72	Sequence 72, Appl
	23	199.2	13.9	2126	13	US-10-052-586-495	Sequence 495, App
	24	199.2	13.9	2126	14	US-10-174-590-495	Sequence 495, App
	25	199.2	13.9	2126	14	US-10-176-758-495	Sequence 495, App
	26	199.2	13.9	2126	14	US-10-175-737-495	Sequence 495, App
	27	199.2	13.9	2126	14	US-10-174-581-495	Sequence 495, App
	28	199.2	13.9	2126	14	US-10-176-483-495	Sequence 495, App
	29	199.2	13.9	2126	14	US-10-176-749-495	Sequence 495, App
	30	199.2	13.9	2126	14	US-10-176-914-495	Sequence 495, App
	31	199.2	13.9	2126	14	US-10-176-915-495	Sequence 495, App
	32	199.2	13.9	2126	14	US-10-173-706-495	Sequence 495, App
	33	199.2	13.9	2126	14	US-10-175-738-495	Sequence 495, App
	34	199.2	13.9	2126	14	US-10-175-752-495	Sequence 495, App
	35	199.2	13.9	2126	14	US-10-176-482-495	Sequence 495, App
	36	199.2	13.9	2126	14	US-10-176-757-495	Sequence 495, App
	37	199.2	13.9	2126	14	US-10-176-913-495	Sequence 495, App
	38	199.2	13.9	2126	14	US-10-180-552-495	Sequence 495, App
	39	199.2	13.9	2126	14	US-10-180-557-495	Sequence 495, App
	40	199.2	13.9	2126	14	US-10-173-700-495	Sequence 495, App
	41	199.2	13.9	2126	14	US-10-174-572-495	Sequence 495, App
	42	199.2	13.9	2126	14	US-10-174-579-495	Sequence 495, App
	43	199.2	13.9	2126	14	US-10-174-582-495	Sequence 495, App
	44	199.2	13.9	2126	14	US-10-174-588-495	Sequence 495, App
	45	199.2	13.9	2126	14	US-10-175-739-495	Sequence 495, App

ALIGNMENTS

RESULT 1  
US-09-835-147-7  
; Sequence 7, Application US/09835147  
; Patent No. US2002002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Maliszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835.147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 1437  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion  
; OTHER INFORMATION: construct of human CD39

		NAME/KEY: CDS		LOCATION: (1)..(1434)		US-09-835-147-7	
		Query Match		100.0%; Score 1437; DB 9; Length 1437;			
		Best Local Similarity		100.0%; Pred. No. 0;			
		Matches 1437; Conservative		0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGCCCTGTGGATCGACAGGATGCAACTCTCTGTGCAATGTCATTAAGTCTTGCACTT	60				
DB	1	ATGGCCCTGTGGATCGACAGGATGCAACTCTCTGTGCAATGTCATTAAGTCTTGCACTT	60				
QY	61	GTCAAAAACAGTGCACCTACTCTCAAGTCTTACAAAAGAAAACACAGCTAACTAGTTCACACC	120				
DB	61	GTCAAAAACAGTGCACCTACTCTCAAGTCTTACAAAAGAAAACACAGCTAACTAGTTCACACC	120				
QY	121	CAGAACAAAGCATTGGCCAGAAAAACGTTAAGTATGGGATTTGTCTGGATGCGGGTCTTCTCT	180				
DB	121	CAGAACAAAGCATTGGCCAGAAAAACGTTAAGTATGGGATTTGTCTGGATGCGGGTCTTCTCT	180				
QY	181	CACAAAGTTTATACATCTATTAAGTGGCCAGCAGAAAAGAGAAATGACACAGCGTGGTG	240				
DB	181	CACAAAGTTTATACATCTATTAAGTGGCCAGCAGAAAAGAGAAATGACACAGCGTGGTG	240				
QY	241	CATCAAGTAGAAGAAATGCAGGGTTAAAGTCTCGGAATCTCAAAATTTGTTCAAGAAAGTA	300				
DB	241	CATCAAGTAGAAGAAATGCAGGGTTAAAGTCTCGGAATCTCAAAATTTGTTCAAGAAAGTA	300				
QY	301	AATGAAATAGGCATTTACCTGACTGATTGTCATGGAAGAGCTAGGGAAGTGAATTCOAAGG	360				
DB	301	AATGAAATAGGCATTTACCTGACTGATTGTCATGGAAGAGCTAGGGAAGTGAATTCOAAGG	360				
QY	361	TCCAGACCAAGAGACACCCGTTTACCTGGAGGCCACGCGGCAATGCGGTTGCTCAGG	420				
DB	361	TCCAGACCAAGAGACACCCGTTTACCTGGAGGCCACGCGGCAATGCGGTTGCTCAGG	420				
QY	421	ATGGAAGTGAAGAGTTGGCAGACAGGTTCTGGATGTGTGGAGAGGAGCCTCAGCAAC	480				
DB	421	ATGGAAGTGAAGAGTTGGCAGACAGGTTCTGGATGTGTGGAGAGGAGCCTCAGCAAC	480				
QY	481	TACCCCTTTGACTTCCAGGGTGCAGGATCATTTACTTGGCCAAAGGAAGTGCTTATGGC	540				
DB	481	TACCCCTTTGACTTCCAGGGTGCAGGATCATTTACTTGGCCAAAGGAAGTGCTTATGGC	540				
QY	541	TGGAATTAATCAACTATCTGTCTGGGCAAAATTCAGTCAGAAAACAAGTGGTTTCAGCAT	600				
DB	541	TGGAATTAATCAACTATCTGTCTGGGCAAAATTCAGTCAGAAAACAAGTGGTTTCAGCAT	600				
QY	601	GTCCCATATGAAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTGGGGAGCCTCT	660				
DB	601	GTCCCATATGAAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTGGGGAGCCTCT	660				
QY	661	ACAAAGTCACTTTTGTACCCCAAAACCCAGACTATCGAGTCCCCAGATAATGCTCTGCAA	720				
DB	661	ACAAAGTCACTTTTGTACCCCAAAACCCAGACTATCGAGTCCCCAGATAATGCTCTGCAA	720				
QY	721	TTTGGCCTCTATGGCAAGGACTCAATGTCTACACATAGCTTCTTGCTATGGGAAG	780				
DB	721	TTTGGCCTCTATGGCAAGGACTCAATGTCTACACATAGCTTCTTGCTATGGGAAG	780				
QY	781	GATCAGGCACTCTGGCAGAACTGGCCAGGACATTGAGTTGCAAGTAATGAAATTTCTC	840				
DB	781	GATCAGGCACTCTGGCAGAACTGGCCAGGACATTGAGTTGCAAGTAATGAAATTTCTC	840				
QY	841	AGGGAACCATGCTTTTCACTCTGGATATAAGAAAGTAGTGAACGTAAGTGACCTTTTACAAG	900				
DB	841	AGGGAACCATGCTTTTCACTCTGGATATAAGAAAGTAGTGAACGTAAGTGACCTTTTACAAG	900				
QY	901	ACCCCTGCAACCAAGAGATTGATGACTCTTCCATTCAGCAGATTGAAATCCAGGTT	960				
DB	901	ACCCCTGCAACCAAGAGATTGATGACTCTTCCATTCAGCAGATTGAAATCCAGGTT	960				
QY	961	ATTGGAAACTATCAACAAATGCCATCAAGCATCCTGGAGCTCTTCAACACCAAGTTACTGC	1020				
DB	961	ATTGGAAACTATCAACAAATGCCATCAAGCATCCTGGAGCTCTTCAACACCAAGTTACTGC	1020				
QY	1021	CCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGATTTTGGG	1080				
DB	1021	CCTTACTCCAGTGTGCTTCAATGGGATTTTCTTGGCCACCACTCCAGGGGATTTTGGG	1080				
QY	1081	GCATTTTTCAGCTTTTACTTTTGTGTGATGAAGTTTAAACTTCACATCAGAGAAAGTCTCT	1140				
DB	1081	GCATTTTTCAGCTTTTACTTTTGTGTGATGAAGTTTAAACTTCACATCAGAGAAAGTCTCT	1140				
QY	1141	CAGGAAAAAGGTGACTGAGATGATGAAAAAGTTTCTGTGCTCAGCCTTGGGAGGAGATAAAA	1200				
DB	1141	CAGGAAAAAGGTGACTGAGATGATGAAAAAGTTTCTGTGCTCAGCCTTGGGAGGAGATAAAA	1200				
QY	1201	ACATCTTACGCTGGAGTAAAGGAGAACTACCTGAGTGAATACTGCTTTTCTGGTACCTAC	1260				
DB	1201	ACATCTTACGCTGGAGTAAAGGAGAACTACCTGAGTGAATACTGCTTTTCTGGTACCTAC	1260				
QY	1261	ATTCTCTCCCTCTTCTCAAGGCTATCATTTTTCACAGCTGATTTCTTGGGAGCACATCCAT	1320				
DB	1261	ATTCTCTCCCTCTTCTCAAGGCTATCATTTTTCACAGCTGATTTCTTGGGAGCACATCCAT	1320				
QY	1321	TTTATTGGCAAGATCCAGGCGACGCGCGCTGGACTTTGGGCTTACATGCTGAACCTG	1380				
DB	1321	TTTATTGGCAAGATCCAGGCGACGCGCGCTGGACTTTGGGCTTACATGCTGAACCTG	1380				
QY	1381	ACCAACATGATCCAGCTGAGCAACCATTTGTCCACCTCTCTCCCACTCCACCTAA	1437				
DB	1381	ACCAACATGATCCAGCTGAGCAACCATTTGTCCACCTCTCTCCCACTCCACCTAA	1437				
		RESULT 2		US-09-835-147-25			
				Sequence 25, Application US/09835147			
				Patent No. US2002002277A1			
				GENERAL INFORMATION:			
				APPLICANT: Maliszewski, Charles R.			
				APPLICANT: Gayle III, Richard B.			
				APPLICANT: Price, Virginia L.			
				APPLICANT: Gimpel, Steven D.			
				TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment			
				FILE REFERENCE: 2879-US			
				CURRENT APPLICATION NUMBER: US/09/835,147			
				CURRENT FILING DATE: 2001-04-13			
				PRIOR APPLICATION NUMBER: US 60/104,585			
				PRIOR FILING DATE: 1998-10-16			
				PRIOR APPLICATION NUMBER: US 60/107,466			
				PRIOR FILING DATE: 1998-11-06			
				PRIOR APPLICATION NUMBER: US 60/149,010			
				PRIOR FILING DATE: 1999-08-13			
				PRIOR APPLICATION NUMBER: PCT/US99/22955			
				PRIOR FILING DATE: 1999-10-13			
				NUMBER OF SEQ ID NOS: 31			
				SOFTWARE: PatentIn Ver. 2.0			
				SEQ ID NO 25			
				LENGTH: 1464			
				TYPE: DNA			
				ORGANISM: Artificial Sequence			
				FEATURE:			
				NAME/KEY: CDS			
				LOCATION: (1)..(1461)			
				OTHER INFORMATION: Description of Artificial Sequence: Fusion			
				OTHER INFORMATION: construct of human CD39			
				US-09-835-147-25			
				Query Match		97.4%; Score 1400; DB 9; Length 1464;	
				Best Local Similarity		98.2%; Pred. No. 0;	
				Matches 1437; Conservative		0; Mismatches 0; Indels 27; Gaps 1;	
QY	1	ATGGCCCTGTGATCGACAGGATGCAACTCTCTGTGCAATGTCATTAAGTCTTGCACTT	60				
DB	1	ATGGCCCTGTGATCGACAGGATGCAACTCTCTGTGCAATGTCATTAAGTCTTGCACTT	60				

```
QY 61 GTCACAAACAGTGCACCTACTTCAAGTTCTCAAAAGAAAAACACAGCTAACTAGTTC---- 116
Db 61 GTCACAAACAGTGCACCTACTTCAAGTTCTCAAAAGAAAAACACAGCTAACTAGTTCAGGA 120
QY 117 -----NACCCAGAACNAAGCATTGCCAGNAACGTTAAAGTAT 153
Db 121 GACTCAAAAGATGACGATGACAAAACCCAGAACAAAGCAATGCCAGNAACGTTAAAGTAT 180
QY 154 GGGATTGTGCTGGATGCGGGTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCA 213
Db 181 GGGATTGTGCTGGATGCGGGTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCA 240
QY 214 GAAAGGAGAAATGACACAGCGGTGTGTCATCAAGTAGAAGAAATCAGGGTTAAAGTCT 273
Db 241 GAAAGGAGAAATGACACAGCGGTGTGTCATCAAGTAGAAGAAATCAGGGTTAAAGTCT 300
QY 274 GGAATCTCAAAATTTGTTTCAGAAAGTAAATGAATAGGCATTTACTGCTGATTTGCATG 333
Db 301 GGAATCTCAAAATTTGTTTCAGAAAGTAAATGAATAGGCATTTACTGCTGATTTGCATG 360
QY 334 GAAAGAGCTAGGGAAGTATCCAAAGTCCAGCACCAAGAGACACCCGGTTTACCTGGGA 393
Db 361 GAAAGAGCTAGGGAAGTATCCAAAGTCCAGCACCAAGAGACACCCGGTTTACCTGGGA 420
QY 394 GCCACGGCAGGCATGCGGTTGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTG 453
Db 421 GCCACGGCAGGCATGCGGTTGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTG 480
QY 454 GATGTTGGAGAGAGCTCAGCAACTACCCCTTTGACTTCCAGGGTGCAGGATCATTT 513
Db 481 GATGTTGGAGAGAGCTCAGCAACTACCCCTTTGACTTCCAGGGTGCAGGATCATTT 540
QY 514 ACTGCCCAAGAGAGGTCCTATCGCTGGATTACTATCACTATCTCTGCTGGCAAAATTC 573
Db 541 ACTGCCCAAGAGAGGTCCTATCGCTGGATTACTATCACTATCTCTGCTGGCAAAATTC 600
QY 574 AGTCAGAAAAAAGTGGTTTACGATAGTCCCATATGAACCAATTAATCAGSAAACCTTT 633
Db 601 AGTCAGAAAAAAGTGGTTTACGATAGTCCCATATGAACCAATTAATCAGSAAACCTTT 660
QY 634 GGAGCTTTGGACCTTGGGGAGCCCTACACAGTCACTTTTGTACCCCAAAACAGACT 693
Db 661 GGAGCTTTGGACCTTGGGGAGCCCTACACAGTCACTTTTGTACCCCAAAACAGACT 720
QY 694 ATCGAGTCCCCAGATAATGCTCTGCAATTTGSCCTCTATGSCAAGSACTACAACTGCTAC 753
Db 721 ATCGAGTCCCCAGATAATGCTCTGCAATTTGSCCTCTATGSCAAGSACTACAACTGCTAC 780
QY 754 ACACATAGCTTCTTGTGCTATGGGAAGGATCAGGCACCTTGGCAGAAAACCTGGCCAAAGAC 813
Db 781 ACACATAGCTTCTTGTGCTATGGGAAGGATCAGGCACCTTGGCAGAAAACCTGGCCAAAGAC 840
QY 814 ATTGAGTTGCAAGTAATGAATTTCTCAGGAGCCCATGCTTTTCATCTCGGATATAAGAG 873
Db 841 ATTGAGTTGCAAGTAATGAATTTCTCAGGAGCCCATGCTTTTCATCTCGGATATAAGAG 900
QY 874 GTAGTGAACGTAAGTGACCTTTACAAAGACCCCTGCACCAAGAGATTTGAGATGACTCTT 933
Db 901 GTAGTGAACGTAAGTGACCTTTACAAAGACCCCTGCACCAAGAGATTTGAGATGACTCTT 960
QY 934 CCATTTCCAGCAGTTTGAATCCAGGGTATTTGAAACTATCAACATGCCATCAAGCATC 993
Db 961 CCATTTCCAGCAGTTTGAATCCAGGGTATTTGAAACTATCAACATGCCATCAAGCATC 1020
QY 994 CTGAGCTCTTCAACACAGTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTTC 1053
Db 1021 CTGAGCTCTTCAACACAGTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTTC 1080
QY 1054 TTGCCACCACTCCAGGGGATTTTGGGCATTTTCAGCTTTTACTTTTGTGATGAGTTT 1113
Db 1081 TTGCCACCACTCCAGGGGATTTTGGGCATTTTTCAGCTTTTACTTTTGTGATGAGTTT 1140
```

```
QY 1114 TTAAACTTGCATCAGAGAAAAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTC 1173
Db 1141 TTAAACTTGCATCAGAGAAAAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTC 1200
QY 1174 TGTGCTCAGCCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAAAGTACCTG 1233
Db 1201 TGTGCTCAGCCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAAAGTACCTG 1260
QY 1234 AGTGAATACTGCTTTTCTGGTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTC 1293
Db 1261 AGTGAATACTGCTTTTCTGGTACCTACATTTCTCTCCCTCTTCTGCAAGGCTATCATTTTC 1320
QY 1294 ACAGCTGATTTCTGGAGACACATCCATTTTCATTTGSCAAGATCCAGGGCAGACGCCGCG 1353
Db 1321 ACAGCTGATTTCTGGAGACACATCCATTTTCATTTGGCAAGATCCAGGGCAGACGCCGCG 1380
QY 1354 TGGACTTTGGGCTACATGCTGAACCTGACCAACATGATCCCAAGCTGAGCAACCATTTGTC 1413
Db 1391 TGGACTTTGGGCTACATGCTGAACCTGACCAACATGATCCCAAGCTGAGCAACCATTTGTC 1440
QY 1414 ACACCTCTCTCCCACTCCACCTAA 1437
Db 1441 ACACCTCTCTCCCACTCCACCTAA 1464
```

RESULT 3

```
US-09-835-147-5
; Sequence 5, Application US/09835147
; Patent No. US2002002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; NAME/KEY: CDS
; LOCATION: (1)..(1362)
US-09-835-147-5
```

```
Query Match 95.0%; Score 1365; DB 9; Length 1365;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 73 GCACCTACTTCAAGTTCTACAAAGAAAAACACAGCTAACTAGTTCAACCCAGAACAAAGCA 132
Db 1 GCACCTACTTCAAGTTCTACAAAGAAAAACACAGCTAACTAGTTCAACCCAGAACAAAGCA 60
QY 133 TTGCAGAAAAACGTTAAGTATGGGATTTGTGCTGATGCGGTTCTTCTCACACAAGTTTA 192
Db 61 TTGCAGAAAAACGTTAAGTATGGGATTTGTGCTGATGCGGTTCTTCTCACACAAGTTTA 120
QY 193 TACATCTATAAGTGGCGCAGCAAGAAAGAGAAATCACACAGCGGTGCTCATCAAGTAGAA 252
```

121 TAACATCTATAAGTGGCCAGCAGAAAAAGGAGAAATGACACAGGCGTGGTGATCAAGTAGAA 180  
QY  
253 GAATGCAGGGTTAAAGTCTCGAATCTCAAAATTTGTTTCAGAAAAGTAATGAATAGGC 312  
Db  
181 GAATGCAGGGTTAAAGGCTCGGAATCTCAAAATTTGTTTCAGAAAAGTAATGAATAGGC 240  
QY  
313 ATTTCAGTCACTGATTCGATGGAAGAGCTPAGGGAAGTGAATCCAAAGGTCCCAAGCACCAG 372  
Db  
241 ATTTCAGTCACTGATTCGATGGAAGAGCTPAGGGAAGTGAATCCAAAGGTCCCAAGCACCAG 300  
QY  
373 GAGACACCCCTTTACCTGGGAGCCACGGCAGGATCGGTTGCTCAGGATGGAAAAGTGAA 432  
Db  
301 GAGACACCCCTTTACCTGGGAGCCACGGCAGGATCGGTTGCTCAGGATGGAAAAGTGAA 360  
QY  
433 GAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGGAGCCCTCAGCAACTACCCCTTTGAC 492  
Db  
361 GAGTTGGCAGACAGGGTTCTGGATGTGGTGAGAGGAGCCCTCAGCAACTACCCCTTTGAC 420  
QY  
493 TTCAGGGTGCCAGGATCATTTACTGSCCAAGAGAGAGGTCCTATGGCTGGATTACTATC 552  
Db  
421 TTCAGGGTGCCAGGATCATTTACTGSCCAAGAGAGAGGTCCTATGGCTGGATTACTATC 480  
QY  
553 AACTATCTGCTGGGCAAAATTCAGTCAGAAAAAAGGTGGTTTCAGCATAGTCCCATATGAA 612  
Db  
481 AACTATCTGCTGGGCAAAATTCAGTCAGAAAAAAGGTGGTTTCAGCATAGTCCCATATGAA 540  
QY  
613 ACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTCTACAAAGTCAC 672  
Db  
541 ACCAATAATCAGGAACCTTTGGAGCTTTGGACCTTTGGGGAGCCCTCTACAAAGTCAC 600  
QY  
673 TTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAAAGTCTGCAATTTGGCCCTAT 732  
Db  
601 TTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAAAGTCTGCAATTTGGCCCTAT 660  
QY  
733 GGCAAGGACTACAATGTCTACACATAGTCTTGTGCTATGGGAAGGATCAGGCAC 792  
Db  
661 GGCAAGGACTACAATGTCTACACATAGTCTTGTGCTATGGGAAGGATCAGGCAC 720  
QY  
793 TGGCAGAACTGGCAAGGACATTCAGGTTGGAAGTAATGAATTTCTCAGGAGCCCATGC 852  
Db  
721 TGGCAGAACTGGCAAGGACATTCAGGTTGGAAGTAATGAATTTCTCAGGAGCCCATGC 780  
QY  
853 TTTTCATCTCGATATAGAAGGTAGTGAAGTAAAGTACCTTTACAGACCCCTCGACC 912  
Db  
781 TTTTCATCTCGATATAGAAGGTAGTGAAGTAAAGTACCTTTACAGACCCCTCGACC 840  
QY  
913 AAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAATCCAGGGTATTTGAAACTAT 972  
Db  
841 AAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGAATCCAGGGTATTTGAAACTAT 900  
QY  
973 CAACAATGCCATCAAAAGCATCTGGAGCTCTTCAACACAGTTACTGCGCTTACTCCAG 1032  
Db  
901 CAACAATGCCATCAAAAGCATCTGGAGCTCTTCAACACAGTTACTGCGCTTACTCCAG 960  
QY  
1033 TGTGCTTCAATGGATTTTCTTGCCACCACTCAGGGGATTTTGGGGATTTTTCAGCT 1092  
Db  
961 TGTGCTTCAATGGATTTTCTTGCCACCACTCAGGGGATTTTGGGGATTTTTCAGCT 1020  
QY  
1093 TTTTACTTTTGTGATGAAGTTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAAAGGTG 1152  
Db  
1021 TTTTACTTTTGTGATGAAGTTTAAACTTGACATCAGAGAAAGTCTCTCAGGAAAAAGGTG 1080  
QY  
1153 ACTGAGATGATGAAAAAGTTCTGTGCTCAGCTTTGGAGGAGATATAAATCATCTTAGCT 1212  
Db  
1081 ACTGAGATGATGAAAAAGTTCTGTGCTCAGCTTTGGAGGAGATATAAATCATCTTAGCT 1140  
QY  
1213 GGAGTAAAGGAGAGTACCTGAGTGAATCTGCTTTTCTGGTACCTACATTTCTCCCTC 1272  
Db  
1141 GGAGTAAAGGAGAGTACCTGAGTGAATCTGCTTTTCTGGTACCTACATTTCTCCCTC 1200  
QY  
1273 CTTCTGCAAGGCTATCATTTTACAGCTGATTTCTCGGAGCAGCATCCATTTTCAATTTGCAAG 1332  
Db  
1201 CTTCTGCAAGGCTATCATTTTACAGCTGATTTCTCGGAGCAGCATCCATTTTCAATTTGCAAG 1260

QY 1333 ATCCAGGGCAGCGACGCGGCTGGACTTTTGGCTACTGCTGAACCTGACCAACATGATC 1392  
Db 1261 ATCCAGGGCAGCGACGCGGCTGGACTTTTGGCTACTGCTGAACCTGACCAACATGATC 1320  
QY 1393 CCAGCTGAGCAACCACTTTGTCCACACCTCTCTCCCACTCCACCTAA 1437  
Db 1321 CCAGCTGAGCAACCACTTTGTCCACACCTCTCTCCCACTCCACCTAA 1365

## RESULT 4

US-09-835-147-1  
; Sequence 1, Application US/09835147  
; Patent No. US2002002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Maliszewski, Charles R.  
; APPLICANT: Gayle III, Richard B.  
; APPLICANT: Price, Virginia L.  
; APPLICANT: Gimpel, Steven D.  
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment  
; FILE REFERENCE: 2879-US  
; CURRENT APPLICATION NUMBER: US/09/835,147  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/104,585  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 60/107,466  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: US 60/149,010  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/22955  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1599  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (67)..(1596)  
US-09-835-147-1

Query Match 91.8%; Score 1319.2; DB 9; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GTTCAACCCAGAACAAAGCATTTGCCAGAAAAAGTTGCGATTTGCTGGATGCGG 172  
Db 173 GGTTCACCCAGAACAAAGCATTTGCCAGAAAAAGTTGCGATTTGCTGGATGCGG 232  
QY 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAGGAGAGATGACACAG 232  
Db 233 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAGGAGAGATGACACAG 292  
QY 233 GCGTGGTGATCAAGTAGAAGAAATCAGGGTTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 292  
Db 293 GCGTGGTGATCAAGTAGAAGAAATCAGGGTTTAAAGGTCCTGGAATCTCAAAATTTGTTTC 352  
QY 293 AGAAAGTAAATGAATATAGGCATTTTACCTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGA 352  
Db 353 AGAAAGTAAATGAATATAGGCATTTTACCTGACTGATTTGCAATGGAAGAGCTAGGGAAGTGA 412  
QY 353 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACTGGGAGCCAGCGGATCGGCT 412  
Db 413 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACTGGAGGCCAGCGGATCGGCT 472  
QY 413 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGAGGTTTCTGGATGTGGTGGAGAGGCC 472  
Db 473 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGAGGTTTCTGGATGTGGTGGAGAGGCC 532  
QY 473 TCAGCAACTACCCCTTTGACTTTCCAGGGTGCCAGGATCATTTACTGGCCCAAGAGAGGTG 532  
Db 533 TCAGCAACTACCCCTTTGACTTTCCAGGGTGCCAGGATCATTTACTGGCCCAAGAGAGGTG 592

QY 533 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 592  
Db CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 652  
QY TCAGCATAGTCCCATATGAAACCAATATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 652  
Db TCAGCATAGTCCCATATGAAACCAATATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 712  
QY GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCCAGTCCCAAGATAATG 712  
Db GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCCAGTCCCAAGATAATG 772  
QY CTCTGCAATTTGCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 772  
Db CTCTGCAATTTGCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 832  
QY ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAAGGACATTCAGGTCGCAAGTAATG 832  
Db ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAAGGACATTCAGGTCGCAAGTAATG 892  
QY AAAATTTCTCAGGAGCCCATGCTTTCACTCTGGATATAAGAAAGTAGTGAACGTAAAGTGACC 892  
Db AAAATTTCTCAGGAGCCCATGCTTTCACTCTGGATATAAGAAAGTAGTGAACGTAAAGTGACC 952  
QY TTTTACAAGACCCCTGCAACCAAGAGATTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 952  
Db TTTTACAAGACCCCTGCAACCAAGAGATTGAGATGACTCTTCCATTTCCAGCAGTTTGAAA 1012  
QY TCCAGGATTTGGAAACTATCAACATGCCATCAAGCATCTCGAGCTTTCACACCA 1012  
Db TCCAGGATTTGGAAACTATCAACATGCCATCAAGCATCTCGAGCTTTCACACCA 1072  
QY GTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTCTTGCCACCACTCCAGGGGG 1072  
Db GTTACTGCGCTTACTCCAGTGTGCTTCAATGGGATTTCTTGCCACCACTCCAGGGGG 1132  
QY ATTTTGGGGCAATTTTCACTTTTACTTTTGTGATGAAGTTTAAACTTGACATCAGAGA 1132  
Db ATTTTGGGGCAATTTTCACTTTTACTTTTGTGATGAAGTTTAAACTTGACATCAGAGA 1192  
QY AAGTCTCTCAGGAAGGTGACTGAGATGATGAAGTTTCTGCTCAGGCTTGGGAGG 1192  
Db AAGTCTCTCAGGAAGGTGACTGAGATGATGAAGTTTCTGCTCAGGCTTGGGAGG 1252  
QY AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTCAGTGAATACTGCTTTTCTG 1252  
Db AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTCAGTGAATACTGCTTTTCTG 1312  
QY GTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCAATTTCAACAGCTGATTCCTGGGAGC 1312  
Db GTACCTACATTTCTCTCCCTCTCTGCAAGGCTATCAATTTCAACAGCTGATTCCTGGGAGC 1372  
QY ACATCCATTTTCAATTTGGCAAGATCCAGGCACGACGCGGCTGGACCTTGGGCTACATGC 1372  
Db ACATCCATTTTCAATTTGGCAAGATCCAGGCACGACGCGGCTGGACCTTGGGCTACATGC 1432  
QY TGAACCTTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA 1432  
Db TGAACCTTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA 1492  
QY 1433 CCTA 1436  
Db 1493 CCTA 1496

RESULT 5

US-10-646-308-29  
; Sequence 29, Application US/10646308  
; Publication No. US20040136992A1  
; GENERAL INFORMATION:  
; APPLICANT: BURTON, Paul B. J.  
; APPLICANT: DEISHER, Theresa A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE  
; FILE REFERENCE: 3432-B  
; CURRENT APPLICATION NUMBER: US/10/646.308  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: --to be assigned--  
; PRIOR FILING DATE: 2003-08-12  
; PRIOR APPLICATION NUMBER: 60/406,418  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 29  
; LENGTH: 1599  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (67)..(1596)  
US-10-646-308-29

Query Match 91.8%; Score 1319.2; DB 19; Length 1599;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GTTCAACCCAGAAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGGG 172  
Db 173 GGTTCAGCCAGAAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGGG 232  
QY 173 GTTCTTCTCACACAAGTTTATACATCTATAGTGGCCAGCAAAAGAGAGATGACACAG 232  
Db 233 GTTCTTCTCACACAAGTTTATACATCTATAGTGGCCAGCAAAAGAGAGATGACACAG 292  
QY 233 GCGTGGTGCACTCAAGTAGAAGAAATGCAAGGTTAAAGGTCCTGGAATCTCAAAAATTTGTTT 292  
Db 293 GCGTGGTGCACTCAAGTAGAAGAAATGCAAGGTTAAAGGTCCTGGAATCTCAAAAATTTGTTT 352  
QY 293 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTGCAATGGAAGAGCTAGGGAAGTGA 352  
Db 353 AGAAAGTAAATGAATAGGCAATTTACCTGACTGATTGCAATGGAAGAGCTAGGGAAGTGA 412  
QY 353 TTCCAAGGTCCTCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGCGCATGCGGT 412  
Db 413 TTCCNAGGTCCTCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGCGCATGCGGT 472  
QY 413 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGTTCTGGATGTGGTGAGAGAGGCC 472  
Db 473 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGTTCTGGATGTGGTGAGAGAGGCC 532  
QY 473 TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGGCCCAAGAGAGGTG 532  
Db 533 TCAGCAACTACCCCTTTGACTTCCAGGGTCCAGGATCATTTACTGGCCCAAGAGAGGTG 592  
QY 533 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 592  
Db 593 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAAACAAGTGGT 652  
QY 593 TCAGCATAGTCCCATATGAAACCAATATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 652  
Db 653 TCAGCATAGTCCCATATGAAACCAATATCAGGAACCTTTGGAGCTTTGGACCTTGGGG 712  
QY 653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 712  
Db 713 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATAATG 772  
QY 713 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 772  
Db 773 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 832  
QY 773 ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAAGGACATTCAGGTCGCAAGTAATG 832  
Db 833 ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAAGGACATTCAGGTCGCAAGTAATG 892  
QY 833 AAATTTCTCAGGAGCCCATGCTTTCACTCTGGATATAAGAAAGTAGTGAACGTAAAGTGACC 892

Db 893 AAATTCTCAGGACCACATGCTTTTCATCTCGGATATAAGAAAGGTAGTGAACGTAAAGTACC 952  
Qy 893 TTTCAGAGCCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCACAGCAGTTTGAA 952  
Db 953 TTTCAGAGCCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCACAGCAGTTTGAA 1012  
Qy 953 TCAGGGTATTGGAAACTATCAACAATGCATCAAGCATCTCGGAGCTCTTCAACACCA 1012  
Db 1013 TCAGGGTATTGGAAACTATCAACAATGCATCAAGCATCTCGGAGCTCTTCAACACCA 1072  
Qy 1013 GTTACTGCCCTTACTCCAGTGTGCCTTCAATGGGATTTTCTTGCACACACTCCAGGGG 1072  
Db 1073 GTTACTGCCCTTACTCCAGTGTGCCTTCAATGGGATTTTCTTGCACACACTCCAGGGG 1132  
Qy 1073 ATTTGGGGCATTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA 1132  
Db 1133 ATTTGGGGCATTTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTTGACATCAGAGA 1192  
Qy 1133 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAGAAAGTTCTGTCTCAGCGCTTGGGAGG 1192  
Db 1193 AAGTCTCTCAGGAAAGGTGACTGAGATGATGAAGAAAGTTCTGTCTCAGCGCTTGGGAGG 1252  
Qy 1193 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTCTG 1252  
Db 1253 AGATAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTCTG 1312  
Qy 1253 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGGAGC 1312  
Db 1313 GTACCTACATTTCTCCCTCTCTGCAAGGCTATCATTTTCACAGCTGATTTCTGGGAGC 1372  
Qy 1313 ACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGCGCTGGACTTTTGGGCTACATGC 1372  
Db 1373 ACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGCGCTGGACTTTTGGGCTACATGC 1432  
Qy 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCA 1432  
Db 1433 TGAACCTGACCAACATGATCCAGCTGAGCAACCAATTTGTCACACCTCTCTCCCACTCCA 1492  
Qy 1433 CCTA 1436  
Db 1493 CCTA 1496

RESULT 6

US-10-641-643-1475  
; Sequence 1475, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; Susan G. Stuart  
; Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/641,643  
; FILING DATE: 14-Aug-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1475:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1818 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g765255  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1475 :  
US-10-641-643-1475  
  
Query Match 91.8%; Score 1319.2; DB 18; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 113 GTTCAACCCAGAACAAAGCATTTGCCAGAAACGTTTAAAGTATGGGATTTGCTGGATGCGG 172  
Db 174 GGTTCACCCAGAACAAAGCATTTGCCAGAAACGTTTAAAGTATGGGATTTGCTGGATGCGG 233  
Qy 173 GTTCTTCTCACACAAGTTTATACATCTATAGTGGCCAGCAGAAAAGGAGNATGACACAG 232  
Db 234 GTTCTTCTCACACAAGTTTATACATCTATAGTGGCCAGCAGAAAAGGAGNATGACACAG 293  
Qy 233 GGTGCGTGCATCAAGTAGAAGTAAGTGCAGGTTTAAAGGTCTCTGAAATCTCAAAATTTGTTTC 292  
Db 234 GGTGCGTGCATCAAGTAGAAGTAAGTGCAGGTTTAAAGGTCTCTGAAATCTCAAAATTTGTTTC 353  
Qy 293 AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTGCAATGGAAGAGAGCTAGGGAAGTGA 352  
Db 354 AGAAAGTAAATGAATAGGCATTTTACCTGACTGATTGCAATGGAAGAGAGCTAGGGAAGTGA 413  
Qy 353 TTCCAAGGTCCAGCACCAGCAGACACCGGTTTACTCGGAGCCACGGCAGCATGCGGT 412  
Db 414 TTCCAAGGTCCAGCACCAGCAGACACCGGTTTACTCGGAGCCACGGCAGCATGCGGT 473  
Qy 413 TGCTCAGGATGAAAGTGAAGAGTTTGGCAGACAGCGGTTCTCGGATGTGTGGAGAGAGCC 472  
Db 474 TGCTCAGGATGAAAGTGAAGAGTTTGGCAGACAGCGGTTCTCGGATGTGTGGAGAGAGCC 533  
Qy 473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGGATCAATTAAGTCTGAGGAGGAGGTTG 532  
Db 534 TCAGCAACTACCCCTTTGACTTCCAGGGTGCAGGATCAATTAAGTCTGAGGAGGAGGTTG 593  
Qy 533 CCTATGGCTGGATTAATCAATCTATCTGCTGGGCAAAATTCAGTCAGAAAACAAGTGGT 592  
Db 594 CCTATGGCTGGATTAATCAATCTATCTGCTGGGCAAAATTCAGTCAGAAAACAAGTGGT 653  
Qy 593 TCAGCATAGTCCCATATGAACCAATAATCAAGAAAACCTTTGGAGCTTTGGACCTTGGGG 652  
Db 654 TCAGCATAGTCCCATATGAACCAATAATTCAGAAAACCTTTGGAGCTTTGGACCTTGGGG 713  
Qy 653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAAACAGACTATTCAGTCCCGAGATAATG 712  
Db 714 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAAACAGACTATTCAGTCCCGAGATAATG 773  
Qy 713 CTCTGCAATTTGCGCTCTATGCGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 772  
Db 774 CTCTGCAATTTGCGCTCTATGCGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 833  
Qy 773 ATGGGAAGGATCAGGCACCTCTGCGCAAAACTCGGCAAGGACATTCAGGTTTGAAGTAATG 832  
Db 834 ATGGGAAGGATCAGGCACCTCTGCGCAAAACTCGGCAAGGACATTCAGGTTTGAAGTAATG 893  
Qy 833 AAATTCTCAGGACCCCATGCTTTTCATCTCGGATATAAGAAAGGTAGTGAACGTAAAGTACC 892

Db 894 AAATTCTCAGGACCACCTGTTTCATCTCGGATATGAAGGTAGTGAACGTAAAGTGACC 953  
Qy 893 TTTTACAAGACCCCTGACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGA 952  
Db 954 TTTTACAAGACCCCTGACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGTTTGA 1013  
Qy 953 TCCAGGATATGGAACACTATCAACATGCGCATCAAGCATCCTGAGCTCTTCAACACCA 1012  
Db 1014 TCCAGGATATGGAACACTATCAACATGCGCATCAAGCATCCTGAGCTCTTCAACACCA 1073  
Qy 1013 GTTACTGCCCTTACTCCAGTGCTTCAATGGGATTTTCTGGCCACCCTCCAGGGGG 1072  
Db 1074 GTTACTGCCCTTACTCCAGTGCTTCAATGGGATTTTCTGGCCACCCTCCAGGGGG 1133  
Qy 1073 ATTTTGGGSCATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAACTTTGACATCAGAGA 1132  
Db 1134 ATTTTGGGSCATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAACTTTGACATCAGAGA 1193  
Qy 1133 AGTCTCTCAGGAAAAGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCCTGGGAGG 1192  
Db 1194 AGTCTCTCAGGAAAAGTGACTGAGATGATGAAAAGTTCTGTGCTCAGCCCTGGGAGG 1253  
Qy 1193 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1252  
Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTCTG 1313  
Qy 1253 GTACCTACATCTCTCCCTCTCTTCTGCAAGGCTATCATTTACAGCTGATTTCTCGGAGC 1312  
Db 1314 GTACCTACATCTCTCCCTCTCTTCTGCAAGGCTATCATTTACAGCTGATTTCTCGGAGC 1373  
Qy 1313 ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGACCGCGCTGGACTTTGGGCTACATGC 1372  
Db 1374 ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGACCGCGCTGGACTTTGGGCTACATGC 1433  
Qy 1373 TGAACCTGACCAACATGATCCAGCTGAGCAGCACTTCTCCACCTCTCTCCCACTCCA 1432  
Db 1434 TGAACCTGACCAACATGATCCAGCTGAGCAGCACTTCTCCACCTCTCTCCCACTCCA 1493  
Qy 1433 CCTA 1436  
Db 1494 CCTA 1497

RESULT 7

US-10-934-998-290  
; Sequence 290. Application US/10934998  
; Publication No. US20050153917A1  
; GENERAL INFORMATION:  
; APPLICANT: AL-MAHMOOD, SALMAN  
; APPLICANT: COLIN, SYLVIE  
; APPLICANT: SCHNEIDER, CHRISTOPHE  
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL  
; FILE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF  
; FILE REFERENCE: BMA-04-1206  
; CURRENT APPLICATION NUMBER: US/10/934,998  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR FILING DATE: 2003-03-04  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 290  
; LENGTH: 1818  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: Genbank/S73813  
; DATABASE ENTRY DATE: 1995-04-12  
US-10-934-998-290

Query Match 91.8%; Score 1319.2; DB 22; Length 1818;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 113 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTTAAGTATGGGATTTGCTGGATGGG 172  
Db 174 GTTCAACCCAGAACAAAGCATTTGCCAGAAAACGTTTAAGTATGGGATTTGCTGGATGGG 233  
Qy 173 GTTCTCTTCACACAAGTTTATACATCTATATAGTGGCCAGCAAAAAGAGAAATGACACAG 232  
Db 234 GTTCTCTTCACACAAGTTTATACATCTATATAGTGGCCAGCAAAAAGAGAAATGACACAG 293  
Qy 233 GCGTGGTGCATCAAGTAGAAGATGACGGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTC 292  
Db 294 GCGTGGTGCATCAAGTAGAAGATGACGGGTTAAAGTCTCTGGAATCTCAAAATTTGTTTC 353  
Qy 293 AGAAGTAAATGAATAGGCATTTACCTGACTGATTTGCATGGAAGAGCTAGGGAAGTGA 352  
Db 354 AGAAGTAAATGAATAGGCATTTACCTGACTGATTTGCATGGAAGAGCTAGGGAAGTGA 413  
Qy 353 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGT 412  
Db 414 TTCCAAGGTCCAGCACCAAGAGACACCCGTTTACCTGGGAGCCACGGCAGGCATGCGGT 473  
Qy 413 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGATGTGTGGAGAGAGCC 472  
Db 474 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGATGTGTGGAGAGAGCC 533  
Qy 473 TCAGCAACTACCCCTTTGACTTCCAGGTCGCCAGGATCATTTACTGGCCAAAGGAAAGTG 532  
Db 534 TCAGCAACTACCCCTTTGACTTCCAGGTCGCCAGGATCATTTACTGGCCAAAGGAAAGTG 593  
Qy 533 CCTATGGCTGATTTACTATCAACTATCTGTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 592  
Db 594 CCTATGGCTGATTTACTATCAACTATCTGTGGGCAAAATTCAGTCAGAAAAACAAGGTGT 653  
Qy 593 TCAGCATAGTCCCATATGAAAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGG 652  
Db 654 TCAGCATAGTCCCATATGAAAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGG 713  
Qy 653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCAAGTAATG 712  
Db 714 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCAAGTAATG 773  
Qy 713 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGCT 772  
Db 774 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGCT 833  
Qy 773 ATGGAAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 832  
Db 834 ATGGAAAGGATCAGGCACTCTGGCAGAAACTGGCCAAAGGACATTCAGGTTGCAAGTAATG 893  
Qy 833 AAATTTCTCAGGACCCCATGCTTTCATCTGTGATATAGAAGGTAGTGAACGTAAAGTACC 892  
Db 894 AAATTTCTCAGGACCCCATGCTTTCATCTGTGATATAGAAGGTAGTGAACGTAAAGTACC 953  
Qy 893 TTTTACAAGACCCCTGCAACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGATTTGAAA 952  
Db 954 TTTTACAAGACCCCTGCAACCAAGAGATTTGAGATGACTCTTCCATTTCCAGCAGATTTGAAA 1013  
Qy 953 TCCAGGGTATTTGAAAACCTATCAACAAATGCCATCAAGCATCCTGGAGCTCTTCAACACCA 1012  
Db 1014 TCCAGGGTATTTGAAAACCTATCAACAAATGCCATCAAGCATCCTGGAGCTCTTCAACACCA 1073  
Qy 1013 GTTACTGCCCTTACTCCAGTGCTTCAATGGGATTTTCTTGGCCACCCTCCAGGGGG 1072  
Db 1074 GTTACTGCCCTTACTCCAGTGCTTCAATGGGATTTTCTTGGCCACCCTCCAGGGGG 1133  
Qy 1073 ATTTTGGGSCATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAACTTTGACATCAGAGA 1132  
Db 1134 ATTTTGGGSCATTTTTCAGCTTTTACTTTTGTGATGAAGTTTTTAACTTTGACATCAGAGA 1193  
Qy 1133 AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTTGGGAGG 1192



Db 1194 AGTCTCTCAGGAAAGGTGACTGAGATGATGAAAAGTTCTGTCTCAGCCCTGGGAGG 1253  
QY 1193 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTAACTGAGTGAATCTGCTTTCTG 1252  
Db 1254 AGATAAAACATCTTACGCTGGAGTAAAGGAGAGTAACTGAGTGAATCTGCTTTCTG 1313  
QY 1253 GTACCTACATCTCTCCCTCTCTCTGCAAGGCTATCATTTCCACGCTGATTCCTGGAGC 1312  
Db 1314 GTACCTACATCTCTCCCTCTCTCTGCAAGGCTATCATTTCCACGCTGATTCCTGGAGC 1373  
QY 1313 ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGACCGCGCTGGACTTTGGGCTACATGC 1372  
Db 1374 ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGACCGCGCTGGACTTTGGGCTACATGC 1433  
QY 1373 TGAACCTGACCAACATGATCCCAAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1432  
Db 1434 TGAACCTGACCAACATGATCCCAAGCTGAGCAACCATTTGTCACACCTCTCTCCCACTCCA 1493  
QY 1433 CCTA 1436  
Db 1494 CCTA 1497

RESULT 8

US-10-934-998-46  
; Sequence 46, Application US/10934998  
; Publication No. US20050153917A1  
; GENERAL INFORMATION:  
; APPLICANT: AL-MAHMOOD, SALMAN  
; APPLICANT: COLIN, SYLVIE  
; APPLICANT: SCHNEIDER, CHRISTOPHE  
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL  
; TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF  
; FILE REFERENCE: BMA-04-1206  
; CURRENT APPLICATION NUMBER: US/10/934,998  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: PCT/FR03/00695  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: FR02/02717  
; PRIOR FILING DATE: 2002-03-04  
; PRIOR APPLICATION NUMBER: FR02/04546  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 46  
; LENGTH: 2081  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: GS-N45  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GENBANK/AJ131313  
; DATABASE ENTRY DATE: 2000-01-19  
; RELEVANT RESIDUES: (1)..(2081)  
US-10-934-998-46

Query Match 91.8%; Score 1319.2; DB 22; Length 2081;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 113 GTTCAACCCAGACAAGCATTCCAGAAACGTTAAGTATGGATTGCTGGATGCGG 172  
Db 311 GGTGACCCAGACAAGCATTCCAGAAACGTTAAGTATGGATTGCTGGATGCGG 370  
QY 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAAGGAGAATGACACAG 232  
Db 371 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGACAGAAAAAGGAGAATGACACAG 430  
QY 233 GCGTGTGTCATCAAGTAGAAGAAATGAGGGTTAAAGCTTGAATCTCAAAATTTGTTTC 292  
Db 431 GCGTGTGTCATCAAGTAGAAGAAATGAGGGTTAAAGCTTGAATCTCAAAATTTGTTTC 490

QY 293 AGAAAGTAAATAGGCATTTACCTGACTGATTGTCATGGAAGAGAGCTAGGGAAGTGA 352  
Db 491 AGAAAGTAAATAGGCATTTACCTGACTGATTGTCATGGAAGAGAGCTAGGGAAGTGA 550  
QY 353 TTCCAAGGTCCAGCAACAAAGAGACACCCGTTTAACTCTGGAGGCCACGGCAGGCATGCGGT 412  
Db 551 TTCCAAGGTCCAGCAACAAAGAGACACCCGTTTAACTCTGGAGGCCACGGCAGGCATGCGGT 610  
QY 413 TGCTCAGCATGGAAGTGAAGTGGGAGACAGAGGTTCTGGATGTTGGTGGAGAGAGGCC 472  
Db 611 TGCTCAGCATGGAAGTGAAGTGGGAGACAGAGGTTCTGGATGTTGGTGGAGAGAGGCC 670  
QY 473 TCAGCAACTACCCCTTTTACCTTCCAGGGTGCAGAGTCAATTTACTGCGCCCAAGAGGAGGTG 532  
Db 671 TCAGCAACTACCCCTTTTACCTTCCAGGGTGCAGAGTCAATTTACTGCGCCCAAGAGGAGGTG 730  
QY 533 CCTATGGCTGGATTAATCAATCTCTGCTGGGCAAAATTCAGTGCAGAAAAACAAGTGTGT 592  
Db 731 CCTATGGCTGGATTAATCAATCTCTGCTGGGCAAAATTCAGTGCAGAAAAACAAGTGTGT 790  
QY 593 TCAGCATAGTCCCATATGAAACCAATATCAAGAAACCTTTTGGAGCTTTGGACCTTTGGGG 652  
Db 791 TCAGCATAGTCCCATATGAAACCAATATCAAGAAACCTTTTGGAGCTTTGGACCTTTGGGG 850  
QY 653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATG 712  
Db 851 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCCAGATAATG 910  
QY 713 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 772  
Db 911 CTCTGCAATTTGCGCTCTATGGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCT 970  
QY 773 ATGGCAAGGATCAGCACTCTGCGAGAACTCGCCAAAGGACATTCAGGTTGCAAGTAATG 832  
Db 971 ATGGCAAGGATCAGCACTCTGCGAGAACTCGCCAAAGGACATTCAGGTTGCAAGTAATG 1030  
QY 833 AAATTTCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAGTACC 892  
Db 1031 AAATTTCTCAGGACCCATGCTTTTCATCTCTGGATATAAGAAAGGTAGTGAACGTAAGTACC 1090  
QY 893 TTTCACAAACCCCTTGCCACAAAGATTTGAGATGACTCTTCCATTCACAGCAGTTTGAAA 952  
Db 1091 TTTCACAAACCCCTTGCCACAAAGATTTGAGATGACTCTTCCATTCACAGCAGTTTGAAA 1150  
QY 953 TCCAGGTTATTCGAAACTATCAACATGCTCAAGAGTCTCTGAGCTCTTCAACACCA 1012  
Db 1151 TCCAGGTTATTCGAAACTATCAACATGCTCAAGAGTCTCTGAGCTCTTCAACACCA 1210  
QY 1013 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGGCCACACTCCAGGGG 1072  
Db 1211 GTTACTGCCCTTACTCCCAAGTGTGCTTCAATGGGATTTTCTTGGCCACACTCCAGGGG 1270  
QY 1073 ATTTTGGGCAATTTTCAAGTGTGATGAAAGTTTAACTTTGACATCAGAGA 1132  
Db 1271 ATTTTGGGCAATTTTCAAGTGTGATGAAAGTTTAACTTTGACATCAGAGA 1330  
QY 1133 AGTCTCTCAGAAAGGTGACTGAGATGATCAAAAGTTCTGTGCTCAGCCTTTGGAGG 1192  
Db 1331 AGTCTCTCAGAAAGGTGACTGAGATGATCAAAAGTTCTGTGCTCAGCCTTTGGAGG 1390  
QY 1193 AGATAAAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTCTG 1252  
Db 1391 AGATAAAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTGAGTGAATACTGCTTTCTG 1450  
QY 1253 GTACCTACATCTCTCCCTCTCTGCAAGGCTATCATTTTCACAGCTGATTCCTGGAGC 1312  
Db 1451 GTACCTACATCTCTCCCTCTCTGCAAGGCTATCATTTTCACAGCTGATTCCTGGAGC 1510  
QY 1313 ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGACCGCGCTGGACTTTGGGCTACATGC 1372  
Db 1511 ACATCCATTTTCAATGGCAAGATCCAGGCGAGCGACCGCGCTGGACTTTGGGCTACATGC 1570  
QY 1373 TGAACCTGACCAACATGATCCCAAGCTGAGCAACCATTTGTCCACACTCTCTCTCCCACTCCA 1432



Db 1571 TGAACCTGACCAACATGATCCAGCTGAGCAACCATGTCACACACTCTCTCCCACTCCA 1630  
Qy 1433 CCTA 1436  
Db 1631 CCTA 1634

RESULT 9

US-10-240-965-242  
; Sequence 242, Application US/10240965  
; Publication No. US20030165924A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: SHIFFMAN, Dov  
; APPLICANT: SOMOGYI, Roland  
; APPLICANT: LAWN, Richard M.  
; APPLICANT: SEILHAMER, Jeffrey J.  
; APPLICANT: PORTER, Gordon J.  
; APPLICANT: MIKITA, Thomas  
; APPLICANT: TAI, Julie  
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION  
; FILE REFERENCE: PA-0025 PCT  
; CURRENT APPLICATION NUMBER: US/10/240,965  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 60/195,106  
; PRIOR FILING DATE: 2000-04-05  
; NUMBER OF SEQ ID NOS: 276  
; SOFTWARE: PERL Program  
; SEQ ID NO 242  
; LENGTH: 4411  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030165924A1 347965.2  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 3369  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-240-965-242

Query Match 91.8%; Score 1319.2; DB 16; Length 4411;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 113 GTTCAACCCAGAACAGCATGCCAGAAAACGTTAAGTATGGGATTTGCTGGATGCGG 172  
Db 184 GGTGACCCAGAACAAAGCATTTGCCAGAAAACGTTAAGTATGGGATTTGCTGGATGCGG 243  
Qy 173 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGAGAAATGACACAG 232  
Db 244 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGAGAAATGACACAG 303  
Qy 233 GCGTGGTGATCAAGTAGAAGATCGAGGTTAAAGGTCCTGGAAATCTCAAAAATTTGTTTC 292  
Db 304 GCGTGGTGATCAAGTAGAAGATCGAGGTTAAAGGTCCTGGAAATCTCAAAAATTTGTTTC 363  
Qy 293 AGAAGTAAATGAATAGCATTTTACCTGATGATGATGATGATGATGATGATGATGATGATGAT 352  
Db 364 AGAAGTAAATGAATAGCATTTTACCTGATGATGATGATGATGATGATGATGATGATGATGAT 423  
Qy 353 TTCCAAAGTCCCAGCAGCAAGAGACACCGCTTTTACCTGGAGCCACGCGCATGCGGT 412  
Db 424 TTCCAAAGTCCCAGCAGCAAGAGACACCGCTTTTACCTGGAGCCACGCGCATGCGGT 483  
Qy 413 TGCTCAGGATGGAAGTAGAAGTTGGCAGACAGGTTCTGGATGTGGTGGAGAGAGGCC 472  
Db 484 TGCTCAGGATGGAAGTAGAAGTTGGCAGACAGGTTCTGGATGTGGTGGAGAGAGGCC 543  
Qy 473 TCAGCAACTACCCCTTTGACTTCCAGGTCGCCAGGATCATTAAGTGGCCAAAGGAAGGTG 532  
Db 544 TCAGCAACTACCCCTTTGACTTCCAGGTCGCCAGGATCATTAAGTGGCCAAAGGAAGGTG 603

RESULT 10  
US-10-934-998-147/c  
; Sequence 147, Application US/10934998  
; Publication No. US20050153917A1  
; GENERAL INFORMATION:  
; APPLICANT: AL-MAHMOOD, SALMAN  
; APPLICANT: COLIN, SYLVIE

Qy 533 CCTATGGCTGGATTACTCAACTATCTGCTGGGCAAAATTCAGTCCAGAAAAACAAGGTGCT 592  
Db 604 CCTATGGCTGGATTACTCAACTATCTGCTGGGCAAAATTCAGTCCAGAAAAACAAGGTGCT 663  
Qy 593 TCAGCATAGTCCCATATGAAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 652  
Db 664 TCAGCATAGTCCCATATGAAACCAATATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG 723  
Qy 653 GAGCCTCTACACAAGCTCACTTTTGTACCCCAAAACAGACTATCAGTCCCGCAGATAATG 712  
Db 724 GAGCCTCTACACAAGCTCACTTTTGTACCCCAAAACAGACTATCAGTCCCGCAGATAATG 783  
Qy 713 CTCTGCAATTTTGCCTCTATGSCAAGGACTACAATGTCTACACATAGCTTCTTTGTGCT 772  
Db 784 CTCTGCAATTTTGCCTCTATGSCAAGGACTACAATGTCTACACATAGCTTCTTTGTGCT 843  
Qy 773 ATGSGAAGGATCAGGCACCTCTGGCAGAAAATGCGCCAAAGACATTTCAGGTTGCAAGTAATG 832  
Db 844 ATGSGAAGGATCAGGCACCTCTGGCAGAAAATGCGCCAAAGACATTTCAGGTTGCAAGTAATG 903  
Qy 833 AAATTTCTCAGGACCCATGCTTTTCACTCTGGATATAAGAAAGTGTGAACGTAAGTGACC 892  
Db 904 AAATTTCTCAGGACCCATGCTTTTCACTCTGGATATAAGAAAGTGTGAACGTAAGTGACC 963  
Qy 893 TTTACAAGACCCCTTGCCACCAAGGATTTGAGATGACTCTTCCATTCCAGCAGATTTTGAAA 952  
Db 964 TTTACAAGACCCCTTGCCACCAAGGATTTGAGATGACTCTTCCATTCCAGCAGATTTTGAAA 1023  
Qy 953 TCCAGGGTATTTGGAAAACCTATCAACAATGCCATCAAAGCATCTCTGAGCTCTTCAACACCA 1012  
Db 1024 TCCAGGGTATTTGGAAAACCTATCAACAATGCCATCAAAGCATCTCTGAGCTCTTCAACACCA 1083  
Qy 1013 GTTACTGCCCTTACTCCCAGTGTGCTTCAATGGGATTTTCTGCGCCACACTCCAGGGGG 1072  
Db 1084 GTTACTGCCCTTACTCCCAGTGTGCTTCAATGGGATTTTCTGCGCCACACTCCAGGGGG 1143  
Qy 1073 ATTTTGGGGCATTTTTCAGCTTTTGTGATGAAGTAACTTTTAACTTGACATCAGAGA 1132  
Db 1144 ATTTTGGGGCATTTTTCAGCTTTTGTGATGAAGTAACTTTTAACTTGACATCAGAGA 1203  
Qy 1133 AAGTCTCTCAGAAAAGGTGACTGAGATGATGATAAGTCTCTGCTCAGCCTTGGAGG 1192  
Db 1204 AAGTCTCTCAGAAAAGGTGACTGAGATGATGATAAGTCTCTGCTCAGCCTTGGAGG 1263  
Qy 1193 AGATAAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1252  
Db 1264 AGATAAAAACATCTTACGCTGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTG 1323  
Qy 1253 GTACTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTCAAGCTGATTTCTCTGGAGC 1312  
Db 1324 GTACTACATTTCTCTCCCTCTCTGCAAGGCTATCATTTCAAGCTGATTTCTCTGGAGC 1383  
Qy 1313 ACATCCATTTTCAATTTGGCAAGATCCAGGCGACGCGGCTGGACTTTGGGCTACATGC 1372  
Db 1384 ACATCCATTTTCAATTTGGCAAGATCCAGGCGACGCGGCTGGACTTTGGGCTACATGC 1443  
Qy 1373 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA 1432  
Db 1444 TGAACCTGACCAACATGATCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCA 1503  
Qy 1433 CCTA 1436  
Db 1504 CCTA 1507

; APPLICANT: SCHNEIDER, CHRISTOPHE  
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL  
; FILE REFERENCE: BMA-04-1206  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: PCT/FR03/00695  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: FR02/02717  
; PRIOR FILING DATE: 2002-03-04  
; PRIOR APPLICATION NUMBER: FR02/04546  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 147  
; LENGTH: 704  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-934-998-147

Query Match 44.6%; Score 640.2; DB 22; Length 704;  
Best Local Similarity 99.5%; Pred. No. 1.6e-192;  
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 792 CTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGGACCCCATG 851  
Db |||||||  
QY 704 CTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGGACCCCATG 645  
Db |||||||  
QY 852 CTTTTCATCTGGATATAAGAAGGTAGTGAACGTAAGTGACCTTTTACAAGACCCCTTGAC 911  
Db |||||||  
QY 644 CTTTTCATCTGGATATAAGAAGGTAGTGAACGTAAGTGACCTTTTACAAGACCCCTTGAC 585  
Db |||||||  
QY 912 CAAGAGATTGAGATGACTCTCCATTCAGGAGTTTGAATCCAGGGTATTGGAAACTA 971  
Db |||||||  
QY 584 CAAGAGATTGAGATGACTCTCCATTCAGGAGTTTGAATCCAGGGTATTGGAAACTA 525  
Db |||||||  
QY 972 TCAACAATGCGCATCAAGGACATCTGGAGCTCTTCAACACAGTTACTGCCCTTACTCCCA 1031  
Db |||||||  
QY 524 TCAACAATGCGCATCAAGGACATCTGGAGCTCTTCAACACAGTTACTGCCCTTACTCCCA 465  
Db |||||||  
QY 1032 GTGTGCTTCAATGGGATTTTCTTGCCACCACCTCCAGGGGGATTTTGGGGCATTTTTCAGC 1091  
Db |||||||  
QY 464 GTGTGCTTCAATGGGATTTTCTTGCCACCACCTCCAGGGGGATTTTGGGGCATTTTTCAGC 405  
Db |||||||  
QY 1092 TTTTACTTTGATGAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGT 1151  
Db |||||||  
QY 404 TTTTACTTTGATGAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGT 345  
Db |||||||  
QY 1152 GACTGAGATGATGAAAAGTTCTGTCTCAGCCTTGGGAGGAGATAAAAACATCTTACGC 1211  
Db |||||||  
QY 344 GACTGAGATGATGAAAAGTTCTGTCTCAGCCTTGGGAGGAGATAAAAACATCTTACGC 285  
Db |||||||  
QY 1212 TGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTGTGTACCTACATTTCTCTCCCT 1271  
Db |||||||  
QY 284 TGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTGTGTACCTACATTTCTCTCCCT 225  
Db |||||||  
QY 1272 CTTTCTGCAAGGTATCATTTTCAAGTGTCTGAGGAGCATCATTTTCAATGGCAA 1331  
Db |||||||  
QY 224 CTTTCTGCAAGGTATCATTTTCAAGTGTCTGAGGAGCATCATTTTCAATGGCAA 165  
Db |||||||  
QY 1332 GATCCAGGGCAGCGCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGAT 1391  
Db |||||||  
QY 164 GATCCAGGGCAGCGCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGAT 105  
Db |||||||  
QY 1392 CCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCACCTA 1436  
Db |||||||  
QY 104 CCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCACCTA 60  
Db |||||||

RESULT 11  
US-10-934-998-193/c  
; Sequence 193, Application US/10934998  
; Publication No. US20050153917A1

; GENERAL INFORMATION:  
; APPLICANT: AL-MAHMOOD, SALMAN  
; APPLICANT: COLIN, SYLVIE  
; APPLICANT: SCHNEIDER, CHRISTOPHE  
; TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL  
; FILE REFERENCE: BMA-04-1206  
; CURRENT APPLICATION NUMBER: US/10/934,998  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: PCT/FR03/00695  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: FR02/02717  
; PRIOR FILING DATE: 2002-03-04  
; PRIOR APPLICATION NUMBER: FR02/04546  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 193  
; LENGTH: 6164  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-934-998-193

Query Match 44.6%; Score 640.2; DB 22; Length 6164;  
Best Local Similarity 99.5%; Pred. No. 6e-192;  
Matches 642; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 792 CTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGGACCCCATG 851  
Db |||||||  
QY 1811 CTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATGAATTTCTCAGGGACCCCATG 1752  
Db |||||||  
QY 852 CTTTTCATCTGGATATAAGAAGGTAGTGAACGTAAGTGACCTTTTACAAGACCCCTTGAC 911  
Db |||||||  
QY 1751 CTTTTCATCTGGATATAAGAAGGTAGTGAACGTAAGTGACCTTTTACAAGACCCCTTGAC 1692  
Db |||||||  
QY 912 CAAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAATCCAGGGTATTGGAAACTA 971  
Db |||||||  
QY 1691 CAAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAATCCAGGGTATTGGAAACTA 1632  
Db |||||||  
QY 972 TCAACAATGCGCATCAAGGACATCTGGAGCTCTTCAACACAGTTACTGCCCTTACTCCCA 1031  
Db |||||||  
QY 1631 TCAACAATGCGCATCAAGGACATCTGGAGCTCTTCAACACAGTTACTGCCCTTACTCCCA 1572  
Db |||||||  
QY 1032 GTGTGCTTCAATGGGATTTTCTTGCCACCACCTCCAGGGGGATTTTGGGGCATTTTTCAGC 1091  
Db |||||||  
QY 1571 GTGTGCTTCAATGGGATTTTCTTGCCACCACCTCCAGGGGGATTTTGGGGCATTTTTCAGC 1512  
Db |||||||  
QY 1092 TTTTACTTTGATGAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGT 1151  
Db |||||||  
QY 1511 TTTTACTTTGATGAAGTTTAACTTGACATCAGAGAAAGTCTCTCAGGAAAGGT 1452  
Db |||||||  
QY 1152 GACTGAGATGATGAAAAGTTCTGTCTCAGCCTTGGGAGGAGATAAAAACATCTTACGC 1211  
Db |||||||  
QY 1451 GACTGAGATGATGAAAAGTTCTGTCTCAGCCTTGGGAGGAGATAAAAACATCTTACGC 1392  
Db |||||||  
QY 1212 TGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTGTGTACCTACATTTCTCTCCCT 1271  
Db |||||||  
QY 1391 TGGAGTAAAGGAGAGTACCTGAGTGAATACTGCTTTTCTGTGTACCTACATTTCTCTCCCT 1332  
Db |||||||  
QY 1272 CTTTCTGCAAGGTATCATTTTCAAGTGTCTGAGGAGCATCATTTTCAATGGCAA 1331  
Db |||||||  
QY 1331 CTTTCTGCAAGGTATCATTTTCAAGTGTCTGAGGAGCATCATTTTCAATGGCAA 1272  
Db |||||||  
QY 1332 GATCCAGGGCAGCGCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGAT 1391  
Db |||||||  
QY 1271 GATCCAGGGCAGCGCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGAT 1212  
Db |||||||  
QY 1392 CCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCACCTA 1436  
Db |||||||  
QY 1211 CCCAGCTGAGCAACCATTTGTCCACACCTCTCTCCCACTCCACCTA 1167  
Db |||||||

RESULT 12

```
US-09-918-995-24656
; Sequence 24656, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24656
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-24656

Query Match      28.8%; Score 414; DB 10; Length 475;
Best Local Similarity 96.6%; Pred. No. 1.5e-120;
Matches 423; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 665 AAGTCACTTTTGTACCCCAAAACAGACTATCGAGTCCCAAGATATGCTCTGCAATTC 724
DB 38 AGGGCACTTTATGTACCCCTAAACAGACTATCGAGTCCCAAGATATGCTCTGCAATTC 97
QY 725 GCCTCTATGGCAAGGACTACAATGTCTACACATAGTCTTGTGCTATGGGAGGATC 784
DB 98 ACTCTATGGCAGGACTACAATGTCTACACATAGTCTTGTGCTATGGGAGGATC 157
QY 785 AGGCACTCTGGCAGAACTGGCCAAAGGACATTCAGGTTGCAAGTAATGAAATTTTCAGGG 844
DB 158 ATGCACTCTGGCATAAATCGGCAAGGACATTCAGGTTGCAAGTAATGAAATTCACAGG 217
QY 845 ACCCATGCTTTCATCTCGATATAGAAGGTAGTGAACGTAAAGTGAACCTTTACAGACCC 904
DB 218 ACCCATGCTTTCATCTCGATATAGAAGGTAGGAACTGAAGAGACCTTTTACAGACCC 277
QY 905 CTGGCACCAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAATCCAGGGTATTG 964
DB 278 CTGGCACCAGAGATTGAGATGACTCTTCCATTCAGCAGTTTGAATCCAGGGTATTG 337
QY 965 GAACTATCAACAATGCCATCAAGCATCTCGAGCTTTCAACACCAGTTACTGCCCTT 1024
DB 338 GAACTATCATCAATGCCATCAAGCATCTCGAGCTTTCAACACCAGTTACTGCCCTT 397
QY 1025 ACTCCAGTGTGCTTCAATGGATTCTTCCACCACTCCAGGGGATTTTGGGGCAT 1084
DB 398 ACTCCAGTGTGCTTCAATGGATTCTTCCACCACTCCAGGGGATTTTGGGGCAT 457
QY 1085 TTTTCAGCTTTTACTTTG 1102
DB 458 TTTTCAGCTTTTACTTTG 475

RESULT 13
US-09-918-995-23052
; Sequence 23052, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23052

US-09-918-995-23052
; Length: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)....(484)
; OTHER INFORMATION: n = A, T, C or G
US-09-918-995-23052

Query Match      26.4%; Score 379; DB 10; Length 484;
Best Local Similarity 100.0%; Pred. No. 2.1e-109;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1058 CACCACCTCCAGGGGATTTTGGGCAATTTTCAGCTTTTCTTTGTGATGAAGTTTTTAA 1117
DB 50 CACCACCTCCAGGGGATTTTGGGCAATTTTCAGCTTTTCTTTGTGATGAAGTTTTTAA 109
QY 1118 ACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAGAAAGTTCTGTG 1177
DB 110 ACTTGACATCAGAGAAAGTCTCTCAGGAAAGGTGACTGAGATGATGAAGAAAGTTCTGTG 169
QY 1178 CTCAGCCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTCAGTG 1237
DB 170 CTCAGCCTTGGGAGGAGATAAAACATCTTACGCTGGAGTAAAGGAGAAAGTACCTCAGTG 229
QY 1238 AATACCTGCTTTTCTGGTACCTACATTTCTCTCCCTCTCTCTCAAGGCTATCATTTCCACAG 1297
DB 230 AATACCTGCTTTTCTGGTACCTACATTTCTCTCCCTCTCTCTCAAGGCTATCATTTCCACAG 289
QY 1298 CTGATTCCTGGGAGGACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGCGGTGGA 1357
DB 290 CTGATTCCTGGGAGGACATCCATTTTCATTTGGCAAGATCCAGGCGAGCGCGGTGGA 349
QY 1358 CTTTGGGCTACATGCTGAACCTGACCAACATGATCCAGCTCAGCAACCATTTGTCCACAC 1417
DB 350 CTTTGGGCTACATGCTGAACCTGACCAACATGATCCAGCTCAGCAACCATTTGTCCACAC 409
QY 1418 CTCTCTCCCACTCCACCTA 1436
DB 410 CTCTCTCCCACTCCACCTA 428

RESULT 14
US-10-002-631C-275/c
; Sequence 275, Application US/10002631C
; Publication No. US20030157486A1
; GENERAL INFORMATION:
; APPLICANT: Graff, Jonathan M.
; TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
; FILE REFERENCE: A34943 090495.0243
; CURRENT APPLICATION NUMBER: US/10/002,631C
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/300,309
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 275
; LENGTH: 703
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (656)....(698)
; OTHER INFORMATION: n = A, C, G, or T
US-10-002-631C-275

Query Match      23.4%; Score 335.8; DB 16; Length 703;
Best Local Similarity 80.2%; Pred. No. 1.6e-95;
Matches 394; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 118 ACCCAGAACAAAGCATTTGCCAGAAACCGTTAAGTATGGGATTTGCTCGATCGGGTCT 177
```

Db 547 ACCGAGAACAACTTTGTCAGAAAATGTTAAGTATGGGATTGTGTTGATGCGGGTCA 488  
Qy 178 TCTCACAAAGTTTATACATCTATAGTGGCCAGCAGAAAAGAGAAATGACACAGCGGTG 237  
Db 487 TCTCACAAACCTGTACATCTACAAGTGGCCGCGGAGAGAGAAATGACACAGGGGTG 428  
Qy 238 GTGCATCAAGTAGAAGATGSCGGGTTAAAGTTCCTGGAAATCTCAAAAATTTGTTACAGAA 297  
Db 427 GTGCAGAGTTAGAGGAATGCCAAGTGAAGGTCCTGGAAATCTCAAAAATATGCTCAGAAA 368  
Qy 298 GTAATGAATAGGCAATTTACCTGACTGATTTGATGCAAGAAAGCTTAGGGAAGTATCCA 357  
Db 367 ACAGATGAATCGGTGCGTACCTGGCCGAATGCAATGGAATCTCCACCGAACTGATACCA 308  
Qy 358 AGTCCGAGCACCAAGAGACACCCGTTTACCTGGAGCCACGCCAGGCATGCGGTTGCTC 417  
Db 307 ACATCCAAGCATCACCAGATCTCTGTACTCTGGAGCCACAGCAGGCATGCGCTTGCTT 248  
Qy 418 AGGATGGAAGTGAAGATTTGGCAGACAGGGTTCTGATGTGTTGGAGAGGAGCCTCAGC 477  
Db 247 AGAATGGAAGCGAACAATCGGCAGACGAGTCTGCTGCAATGTCACCAAGCCTTAAG 188  
Qy 478 AACTACCCCTTTGACTTCCAGGCTGCCAGGATCAATTAAGTGGCAAGAGGAGTGCCTAT 537  
Db 187 AGCTACCCCTTTGACTTCCAGGCTGCCAAGATCATCACTGGAACAAGGAGGTCCTAT 128  
Qy 538 GGCTGGAATTAATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAACAAGGTTGCTCAGC 597  
Db 127 GGCTGGAATTAATCAACTATCTGCTGGGCAAAATTCAGTCAGAAAACAAGGTTGCTCAGC 68  
Qy 598 ATAGTCCCATTA 608  
Db 67 CTCACTTCAGA 57

## RESULT 15

US-09-923-304-3  
; Sequence 3, Application US/09923304  
; Patent No. US20020081612A1  
; GENERAL INFORMATION:  
; APPLICANT: KATZ, RUTH  
; APPLICANT: JIANG, FENG  
; TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS  
; FILE REFERENCE: UTSC:658US  
; CURRENT APPLICATION NUMBER: US/09/923, 304  
; CURRENT FILING DATE: 2001-08-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2797  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(1672)  
US-09-923-304-3

Query Match 20.3%; Score 291; DB 9; Length 2797;  
Best Local Similarity 54.3%; Pred. No. 7e-81;  
Matches 707; Conservative 0; Mismatches 575; Indels 21; Gaps 5;

Qy 120 CAGAACAAAGCATTCGCCAGAAACGTTAAGTATGGATGTGCTCGATGCGGGTCTTTC 179  
Db 220 CAAGCAAGAGGTCTCCCTCCAGGACTGAAGTATGTGTTGCTGGATGCGGGTCTTTC 279  
Qy 180 TCACAAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAAATGACACAGCGGTGTT 239  
Db 280 AAGAACACAGTCTACGTGTATCAATGGCCAGCAGAAAAGAGAAATATACCGAGTGGT 339  
Qy 240 GCATCAAGTAAAGAAATGCAAGGTTTAAAGTCTCGAATCTCAAAATTTGTTCAAGAAAT 299  
Db 340 CAGTCAAACTTCAAAATGTAGTGTGAAGGCTCTGGAATCTCCAGCTATGGAATTAACCC 399

Qy 300 AAATGAATAGGCAATTTACCTGACTGATTTGCATGGAAAGAGCTAGGGAAGTGAATTCACAG 359  
Db 400 CCAAGATGTCCCAAGAGCCTTTGAGAGATGTATGCAAAAGTCAAGGGGCGAGTTCCATC 459  
Qy 360 GTCCAGACCAAGAGACACCCGTTTACCTGGAGCCACGGCAGGCATGCGGTGTGCTAG 419  
Db 460 CCACCTCCAGGATCCACCCCATTTACCTGGAGCCACGGCTGGGATGCGCTTGCTGAG 519  
Qy 420 GATGAAAGTGAAGATTTGGCAGACAGGGTTCTGATGTGGTGGAGAGGAGCCTCAGCAA 479  
Db 520 GTTGCAAAATGAAACAGCAGCTAAATGAAATCTTGAAGCATCCAAAGCTACTTCAAGTC 579  
Qy 480 CTACCCCTTTGACTTCCAGGCTGCCAGGATCAATTAAGTGGCCCAAGAGGAGTGCCTATGG 539  
Db 580 CCAGCCCTTTGACTTTAGGGGTGCTCAAAATCATTTCTGGCAGAAAGAGGGGTATATGG 639  
Qy 540 CTGGATTAATCAATCACTATCTGCTGGGCAAAATTCAGTTCAGAAAACAAGGTGTTCAAGAT 599  
Db 640 ATGGATTAAGCACTATTTAATGGAAATTTCTGGAGAAAGAACTCTGGCAGCATGTG 699  
Qy 600 AGTCCCATATGAACCAATTAATCAGGAACCTTTGGAGCTTTGGAGCTTTGGGGGAGCCCTC 659  
Db 700 GGTGC-----ACCCGCAATGGAGTGGAAACACGGGTGCCCTTGAAGTGGTGGCTTC 753  
Qy 660 TACACAAGTCACTTTGTACCCCAAAACCCAGACTATCGAGTCCCCAGATAATGCTCTGCA 719  
Db 754 CACCCAAATATCTTCGTGGCAGGAGAGAGATGGATCTGAACACACAGGCATCATGCA 813  
Qy 720 APTTCGCTCTATGCAAGGACTACAATGTCTACACATAGCTTCTTGTGCTATGGGAA 779  
Db 814 GGTGTCCTGTATGCTACGTATACCGCTCTACACACACAGCTTCCAGTGTCTATGGCG 873  
Qy 780 GGATCAGGCACCTCTGGCAGAAACTGGCCNAGACATTCAGGTTGCAAGTGAATGAAT---T 836  
Db 874 GAATGAGGCTGAGAAGAGTTTCTGGCAATGCTCTCGCAATTCCTCTACCAAAACCA 933  
Qy 837 TCTCAGGGACCCATGCTTTTCATCTCTGGATATAAGAAAGTAGTGAACGTAAGTGACCTTTA 896  
Db 934 TCTCAACATCTCTGTACCTCTGGGATTTAGCATCAGCTTCACCATGGGCCATGTATT 993  
Qy 897 CAAGACCCCTTCAC-----CAAGAGATTTGAGATGACTTTTCCATTTCCAGCAGTTTGA 950  
Db 994 TGATAGCTGTGCACTGTGGACAGAGGCCAGAAAGTTATAACCCCAATGATGTATCATC 1053  
Qy 951 AATCCAGGATTTGAAACTATCAACATGCCATCAAGCATCCTGGAGCTCTTCAACAC 1010  
Db 1054 TTTTGAAGGAAGTGGGACCCCATCTCTGTGTGAAGAGAGGTTCCCATATTTGACTTT 1113  
Qy 1011 CAGTTACTGSCCTTACTCCAG---TGTCCTTCAATGGGATTTTCTGCCACCACTCCA 1067  
Db 1114 CAAGCTTGCCATGATCAAGAAACCTGTCTTTTGTATGGGGTTATCAGCCAAAGATTAA 1173  
Qy 1068 GGGGATTTTGGGCATTTTTCAGCTTTTTCATTTTGTGATGAAGTTTAACTTGACATC 1127  
Db 1174 AGGGCATTTTGTGGCTTTTGCAGGATTTCTACTACACAGCCAGTGTCTTTAAATCT---TTC 1230  
Qy 1128 AGAGAAAGTCTCTCAGAAAAGGTGACTGAGATGATGAAAAGTTTGTGCTCAGCCTTG 1187  
Db 1231 AGGTAGCTTTTCCCTGGACACCTTCAACTCCAGCACCTGGAAATTTTGTCTCAGAAATTTG 1290  
Qy 1188 GGAGAGATATAAACAATCTTACGCTGGAGTAAGGAGAGTACCTGAGTGAATACTGCTT 1247  
Db 1291 GAGTCAGCTCCCATGCTGCTCTCCCAATTTGATGAGGTATATGCCGCTCTTACTGCTT 1350  
Qy 1248 TTCTGGTACCTACATTTCTCTCCCTCTCTCTCAAGGCTATCATTTTCAAGCTGATTCCTG 1307  
Db 1351 CTCAGCCAACTACATCTACCACTTGTGTGAACGGTTACAAATTCACAAATTCACAGAGAGACTTG 1410  
Qy 1308 GGAGCACATCCATTTCAATGGCAAGATCCAGGGCAGCGCGGTGAGCTTTGGGCTA 1367  
Db 1411 GCCCCAAATACACTTTGAAAAAAGAGTGGGGAATAGCAGCATAGCCTGTGCTCTTGGCTA 1470  
Qy 1368 CATGCTGAACCTGACCAACATGATCCAGCTCAGCAACCATTTG 1410

Db 1471 CATGCTCAGCCTGACCAACCAAGATCCAGCTGAAAGCCCTCTG 1513

Search completed: September 22, 2005, 04:37:25  
Job time : 1045.08 secs

**THIS PAGE BLANK (USPTO)**

**THIS PAGE BLANK (USPTO)**